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Copyright (c) 1993 - 2004 Compugen Ltd.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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ABB80521

ID ABB80521

NO B-09

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                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
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                           ABB80566 standard; peptide; 11 AA.
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                                                                                                                             'note= "Valy1 carbony1 forming keto-amide linkage with
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                                                              'note= "N-terminal acetyl"
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Location/Qualifiers
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80559 standard; peptide; 11 AA.
                                             Brunck TK;
                                                                                                                                                                        English.
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                                                                                                                                                                        Claim 17; Page 65; 69pp;
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                               Lim-Wilby M, Levy OE,
               (CORV-) CORVAS INT INC
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Local Sim.
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ABB80559
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                                                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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100.0%; Pred. No. 0.002;
iive 0; Mismatches 0; Indels
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/note= "C-terminal amide"
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nes 11; Conservative
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Best Local Si
Matches 11;
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ABB80567 RESULT

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Gaps

ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
                                                                                                                                                                                                                                                                                                                                           ABB80526 standard; peptide; 11 AA.
                                                         Claim 17; Page 65; 69pp; English
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(first entry

'note= "Norvaly1 carbony1 forming keto-amide linkage with

residue 7"

/note= "C-terminal amide" note= "D-form residue" note= "D-form residue"

Brunck TK;

Claim 17; Page 64; 69pp; English.

note= "N-terminal acetyl'

Location/Qualifiers

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        The sequence represents a peptide compound of the invention having the peptides of the invention are alpha *ketoamide peptide analogues. The peptides have invention are alpha *ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with RICV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44
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                                                                                                                                                               Score 50; DB 5; Length 11;
Pred. No. 0.002;
0; Mismatches 0; Indels
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100.0%;
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                                                                                                                                                                                 Similarity
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Best Local S:
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96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels

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EEVVPXGMSYS

Sequence 11 AA;

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virudide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                  'note= "Norvaly1 carbony1 forming keto-amide linkage with
                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
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                                                                                                                                                                                                                                                                    'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                   'note= "D-form residue"
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                 ABB80561 standard; peptide; 11 AA.
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Best Local Similarity
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                                   Gaps
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virucide.
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DB 5; Length 11;
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thes 0; Indels
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0; Mismatches
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                 l Similarity 100.0%; Pi
11; Conservative 0;
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                                                                                                                                                                                                                                     /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4
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Pred. No. 0.013;
0; Mismatches 1; Indels
                                                                                                                                                                                                                 'note= "N-terminal acetyl"
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90.9%;
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                                                      "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
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                                  note= "N-terminal acetyl"
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Matches 10, Conservative
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                                                                                     Misc-difference
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                          ___/note= "C-terminal amide"
                              /note= "D-form residue"
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residue 7"
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                 Misc-difference 8
                                                                                          WO200208251-A2
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Search completed: June 3, 2004, 11:48:22 Job time: 45.9333 secs 1 EEVVPXGMDYS 11 셤

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Score 46; DB 5; Length 11; Pred. No. 0.013; 0; Mismatches 1; Indels

Query Match
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Sequence 3738, Application US/09134000C

Sequence 3738, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:
APPLICANT: LYND DOUGETEE-Stamm et al
APPLICANT: LYND DOUGETEE-Stamm et al
APPLICANT: LYND NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERACCCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DATE: 1998-03-13
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

SPRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NO 3738

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US-09-408-020-4
i Sequence 4, Application US/09408020
i Sequence 4 Application US/09408020
i Patent No. 6632937
i GENERAL INFORMATION:
i APPLICANT: Swanson, Ronald V.
i APPLICANT: Schleper, Christa
i TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
i TITLE OF INVENTION: NUMBER: US/09/408,020
i CURRENT RILING DATE: 1999-09-29
i PRIOR APPLICATION NUMBER: 60/102,294
i RIOR FILING DATE: 1998-09-29
i NUMBER OF SEQ ID NOS: 123
i SOPTWARE: FastSEQ for Windows Version 3.0
i LENGTH: 3472
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4; Mismatches 1; Indels
                                      US-08-464-517-6
US-08-264-377-6
US-08-264-377-6
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US-08-246-361A-6
US-08-246-361A-23
US-08-246-361A-23
US-08-465-371A-23
US-08-46-361A-23
US-08-46-361A-23
US-08-46-361A-120-8
US-08-46-517-120-8
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CRGANISM: Cenarchaeum symbiosum
US-09-408-020-4
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ORGANISM: Enterococcus faecalis
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54.5%;
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Sequence 73, Appl
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Sequence 2902, Ap
Sequence 7885, Appl
Sequence 3, Appli
Sequence 236, Appl
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-540-236-2902
US-09-740-352-7885
US-09-760-946-3
US-08-637-759B-236
US-08-637-759B-236
US-08-637-355A-236
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US-08-464-517-22
US-08-246-361A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                     otal number of hits satisfying chosen parameters:
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US-07-667-711B-4
US-08-193-977-7
                                                                                                                                                                                                                                                                                                                                                                                                          389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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1394
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382
947
1191
1407
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102
1102
1152
1732
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Perfect score:
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Gaps

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Patent No. 6562958
GENERAL INFORMATION
APPLICANT: GAYY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BADVANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GGT09-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7885
LENGTH: 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cameron, Dale R.
APPLICANT: Cameron, Dale R.
APPLICANT: Gancon, Dale R.
APPLICANT: Ghicher, Anne-Marie
APPLICANT: Ghicher, Mathalie
APPLICANT: Ghicher, Nathalie
APPLICANT: Ghicher, Nathalie
APPLICANT: Halmos, Teddy
APPLICANT: Lilias-Brunds Perceyclic Peptides Active Against the Hepatitis C Virus
FILE REFERENCE: 13/076-1-C1
CURRENT PAPLICANTON NUMBER: US 09/760,946
CURRENT FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 12
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Pred. No. 2.5e+02;
2; Mismatches 1; Indels
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Pred. No. 1.7;
4; Mismatches 2; Indels
Sequence 7885, Application US/09328352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09760946
Patent No. 6608027
GENERAL INPORMATION:
APPLICANT: Teantrizos, Youla S.
APPLICANT: Cameron, Dale R.
APPLICANT: Faucher, Anne-Marie
APPLICANT: Ghiro, Elise
                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09760946 Patent No. 6608027 GENERAL INFORMATION: APPLICANT: Fsantrizes, Youla S.
                                                                                                                                                                                                                                                                                                                                                           65.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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US-09-760-946-2
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US-09-760-946-3
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Patent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2902
LENGTH: 1191
                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-228-986-73
US-09-228-986-73
US-09-228-986-73
Sequence 73, Application US/09228986
Parent No. 6359198
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
CURRENT APPLICANTON NUMBER: US/09/228,986
CURRENT APPLICATION NUMBER: US/09/228,986
NUMBER OF SEQ ID NOS: 130
SEQ ID NOS: 130
SEQ ID NO 73
LENGTH: 947
                   NAME/KEY: MISC FEATURE

LOCATION: (328)

LOCATION: (328)

CHER INFORMATION: Amino acids 327 & 328 are Xaa wherein Xaa = any amino acid. US-09-134-000C-3738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%; Score 34; DB 4; Length 947; 66.7%; Pred. No. 1.6e+02; ive 2; Mismatches 1; Indels
                                                                                                                                Query Match 69.2%; Score 36; DB 4; Length 382; Best Local Similarity 66.7%; Pred. No. 22; Marches 1; Indels Matches 1; Indels
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                     332 LIPEGMSYS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: M.catarrhalis
US-09-540-236-2902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        686 VMPSGISYS 694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EVVPXGMSY 10
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US-09-540-236-2902
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US-09-328-352-7885
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LENGTH: 45 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: process
TRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-637-759B-236
      SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acide
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APPLICANT: Goudreau, Nathalie
APPLICANT: Halmos, Tredy
APPLICANT: Llanes, Tredy
APPLICANT: Llinas-Brunet, Montse
TITLE OF INVENTION: Macrocyclic Peptides Active Against the Hepatitis C Virus
FILE REFERENCE: 13/0761-C1
CURRENT APPLICATION NUMBER: US/09/760,946
CURRENT FILING DATE: 2001-08-23
PRIOR PAPLICATION NUMBER: US 69/542,675
PRIOR APPLICATION NUMBER: US 60/128,011
PRIOR APPLICATION NUMBER: US 60/128,011
PRIOR APPLICATION NUMBER: US 60/128,011
NUMBER OF SEQ ID MOS: 5
SOFTWARE: Patentin version 3.1
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63.5%; Score 33; DB 4; Length 12;
Best Local Similarity 45.5%; Pred. No. 1.7;
Matches 5; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1) OTHER INPORMATION: Asp at position 1 is biotinylated NAME/KEY: MOLRES
                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: Tracer for NS3 protease assay NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DDIVPCSMSYT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMSYS 11
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                                                                                                                                                                                            SEQ ID NO 3
LENGTH: 12
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Gabs
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Score 33; DB 2; Length 45;
Pred. No. 7.8;
1; Mismatches 3; Indels
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Pred. No. 7.8;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IMP PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/871,355A

FILING DATE: 09-JUN-1997

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: PCT/GB95/02875

FLING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Pabet, Patea 1.

REGISTRACE/DOCKET NUMBER: RPMS 101 CON

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPRAK: (404) 873-8794

INFORMATION FOR SEQ ID NO: 236:

SEQUENCE CHRARACTERISTICS:

LEASTH: 45 anino acids

LEATH: 45 anino acids
                                                                                                                                                                                                                                Patent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TILE OF INVENTION:
INTERE OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabet
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
                                                                                                                                                                                          63.5%;
Similarity 60.0%; 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.5
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                       ||: | | ||
EEISPLGWSY 10
                                                                                1 EEVVPXGMSY 10
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  Query Match
Best Local Similarity
Matches 6; Conserva
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Sequence 66, Application US/09357952

Retent No. 6248904

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Yang, Wu
ITTLE OF INVENTION: Pluorescence Screening Assays for Caspases, Peptidases, Proteases
ITTLE OF INVENTION: Pluorescence Screening Assays for Caspases, Peptidases, Proteases
ITTLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735.003001
CURRENT APPLICATION NUMBER: US/09/357,952
CURRENT PAPLICATION NUMBER: US 60/093,642
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                                                                                                                                                                                                                      RESULT 12
5177197
Patent No. 5177197
MENGINEL SANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
MENSTEDT, CHRISTER; HELLMAN, ULF; MIXAZONO, KOHEI; CLAESSON-WELSH,
LENA, HELDIN, CARL-HENRIN
TITLE OF INVERTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%; Score 33; DB 6; Length 1394; 45.5%; Pred. No. 3.9e+02; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 6; Length 410;
Pred. No. 97;
3; Mismatches 3; Indels
   3; Indels
   3; Mismatches
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Best Local Similarity 45.5
Matches 5; Conservative
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Best Local Similarity 45.5
Matches 5; Conservative
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399 KEICPGGMGYT 409
   5; Conservative
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52 KEICPGGMGYT 62
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LENGTH: 1394
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;Patent No. 5177197
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      Matches
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517197-51
FALENT NO. 5177197
FARMARY, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
FARMSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
LENA, HELDIN, CARL-HENRIK
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING;
HUMAN TRANSFORMING GROWTH FACTOR-BETAI-BINDING PROTEIN
CURRENT APPLICATION DATA;
CURRENT APPLICATION DATA;
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%; Score 33; DB 4; Length 45; 60.0%; Pred. No. 7.8; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 65;
US-09-201-945-236
Sequence 236, Application US/09201945
Patent No. 6342215
GENERAL INFORMATION:
APPLICANT:
David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabet
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STARET: USA
COUNTRY: Georgia
COUNTRY: Georgia
CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSIFICATION NUMBER: US/09/201,945
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/637,759
FILING DATE:
CALLOR 
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Pred. No. 12;
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 101
TELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8794
TELEPKY: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236: SEQUENCE CHARACTER (2010)
SEQUENCE CHARACTER (2010)
SEQUENCE CHARACTER (2010)
SEQUENCE TARACTER (2010)
SEQUENCE TARACTER (2010)
STRANDENES: SINGLE
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Best Local Similarity
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Matches 6; Conserv
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; LENGTH: 65
5177197-51
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Sequence 66, Application US/09521650
Sequence 66, Application US/09521650
Patent No. 6335429
GENERAL INFORMATION:
APPLICANT: Well, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drew, John F.W.
APPLICANT: Dremening Assays for Whole-Cell Fluorescence
TITLE OF INVENTION: USE Thereof
TITLE OF INVENTION WIMBER: US/09/521,650
CURRENT FILING DATE: 1998-10-09
EARLIER PILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 09/061,582
EARLIER APPLICATION NUMBER: US 09/061,582
EARLIER PILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 10
THENGTH: 10
THENGTH: 10
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                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
'S-09-357-952-66
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
IS-09-521-650-66
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61.5%; Score 32; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.3;
Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                       Query Match 61.5%; Score 32; DB 3; Length 10; Best Local Similarity 50.0%; Pred. No. 2.3; Matches 5; Conservative 3; Mismatches 2; Indels
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 10
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(without alignments)
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/ cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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/ cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1155919 seqs, 281338677 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 EEVVPXGMSYS 11
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %

No. Score Match Length DB ID

Sequence 5, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 7, Appliance 7, Appliance 7, Appliance 8, Appliance 9, Appliance 8, Appliance 9, Appliance 8, Appliance 9, Appliance 9, Appliance 9, Appliance 8, Appliance 9, Appli

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12 US-09-909-164-2 12 US-09-909-164-2 12 US-09-909-164-2	12 US-09- 12 US-09- 12 US-09- 12 US-09-	12 US-09-909-164- 12 US-09-909-164- 12 US-09-909-164- 12 US-09-909-164-	12 US-09-909-164- 12 US-09-909-164- 12 US-09-909-164- 12 US-09-909-164- 12 US-09-909-164-	12 US-09-909-164 12 US-09-909-164 12 US-09-909-164 12 US-09-909-164 12 US-09-909-164	11 12 US-09-909-164-41 11 12 US-09-909-164-45 11 12 US-09-909-164-46 11 12 US-09-909-164-36 11 12 US-09-909-164-34 11 12 US-09-909-164-38 11 12 US-09-909-164-38
24.44.5	9 45 86. 0 44 84. 1 44 84. 2 44 84.	8 8 8 8 1 4 4 4 0 0	41 78. 9 41 78. 1 41 78.	76. 76. 76.	38 40 40 41 41 42 43 43 43 43 44 45 45 45 45 45 45 45 45 45

ALIGNMENTS

00-90-164-5 00-90-164-5 00-90-164-5 EXERAL INFORMATION: EXERTINES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS CHILL REFERENCE: EXERTION: EXERTINES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS CHILL EXERENCE: EXERTINES:	
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тедк	Length 11;
P P P P P P P P P P P P P P P P P P P	Len
EUI EUI	12;
- SEI	DB 12;
UET 1 9-909-164-5 9-909-164-5 9-909-164-5 9-909-164-5 PULCATION NO. UG20020069702A1 NERAL INFORMATION: UG20020069702A1 NERAL INFORMATION: UG20020069702A1 NERAL INFORMATION: UG20020069702A1 DEPLICANT: UG2V, Odile E PPLICANT: UG2V, Odile E PPLICANT: UG2V, Odile E PPLICANT: UG3V, Odile E PPLICANT: UG3VENT: UG3	
nc. A.S. 1zed	Score 50;
SULT 109-909-164-5 Sequence 5. Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION: APPLICANT: Corvas International, Inc. APPLICANT: Lim-Wilby, Marguerita APPLICANT: Brunck, Terence K TITLE OF INVENTION: UNOVEL FFFTIDES AS NS- FILE REFERENCE: IN01192-US FUCRENT FILING DATE: 2003-03-25 RIOR APPLICATION NUMBER: 60/220,101 NUMBER: OF SEQ ID NOS: 62 SOFTWARE: PATOR OF SEG ID NOS: 62 SOFTWARE: PAT TYPE: NOD RES LOCATION: (1)(1) OTHER INFORMATION: ALINE-(CO) FEATURE: NAME/KEY: MISC_FEATURE NAME/KEY: MISC_FEATURE NAME/KEY: MISC_FEATURE NAME/KEY: MOD RES LOCATION: (1)(1) OTHER INFORMATION: AMIDATION OTHER INFORMATION: AMIDATION OTHER REFORMATION: AMIDATION	SGO
UT 1 9-909-164-5 9-909-164-5 9-909-164-5 Juptence 5. Application US/09909164 NERAL INFORMATION: NERAL INFORMATION: NERAL INFORMATION: DEPLICANT: Lim-Wilby, Marguerita PPLICANT: Bruck, Terence K ITLE OF INVENTION: 10072-05 UNRENT PELLICATION NUMBER: 06/220, 1000-07-21 UNBER OF SEQ ID NOS: 62 OFTWARE: PATON SEG ID NOS: 62 OFTWARE: PATON SEG ID NOS: 62 OFTHER INFORMATION: 11-mer synthee PRAYURE: OTHER INFORMATION: 11-mer synthee PRAYURE: OTHER INFORMATION: 0.1-mer synthee PRAYURE: OTHER INFORMATION: 0.1-mer synthee PRAYURE: COCATION: (1)(1) OTHER INFORMATION: 0.1-mer synthee PRAYURE: COCATION: (1)(1) OTHER INFORMATION: 0.1-welline-(CO) PRAYURE: NAME/KEY: MOD RES LOCATION: (1)7(11) OTHER INFORMATION: AMIDATION 9-909-164-5	 æ
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pplication US/099 0. US20020068702A MATION: Corvas Internation Lim wilby, Margue Levy, Odile E BENINGY, Terence K ENTION: NOVEL PF CE: IN01192-US TCATION: NUMBER: 60/ CE: IN01192-US ATION NUMBER: 60/ ID AND: 62 Centin version 3. Inficial sequenc MATION: 11-mer sy CD RES 1)(1) MATION: 11-mer sy CD RES 1)(1) MATION: 10-valine MATION: norvaline COD RES 6)(6) MATION: norvaline COD RES 10(1) MATION: AUDATION MATION: NOVALINE COD RES 10(1) MATION: AUDATION MATION: NOVALINE COD RES 1(1)	
RESULT 1 18-09-909-164-5 Sequence 5, Application US/0990 Publication No. US20020068702A1 GENERAL INFORMATION: APPLICANT: Corvas Internationa APPLICANT: Lim wilby, Marguer: APPLICANT: Lim wilby, Marguer: APPLICANT: Levy, Odile E APPLICANT: Lim of INVERIENCE: 1001192-US CURRENT APPLICATION NUMBER: 60/2 PRIOR PLING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 62/2 NUMBER OF SEQ ID NOS: 62/2 NUMBER OF SEQ ID NOS: 61/2 NUMBER OF SEG ID NOS: 61/2 NUMBER OF SEG ID NOS: 61/2 NUMBER NUMBER: NUMBER: NOD RES NUMBER NUMBER: NUMBER: NOD RES NUMBER NUMBER: NUMBER	ch
SULT 1 -09-909-164- Sequence 5, Publication APPLICANT:	Query Match
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RESULT 1 US-09-909-164-5 Sequence 5, A Publication N GENERAL INFOR APPLICANT:	8

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MSPG19-164-10
Sequence 10, Application US/09909164
Fublication No. US20020068702A1
Sequence 10, Application US/09909164
Fublication No. US20020068702A1
GENERAL INFORMATION
SEPTICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: NOVIDER: 2003-03-25
FILE REFERENCE: 2003-03-25
FRICK APPLICATION NUMBER: 60/220,101
PRICK FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NOS: 62
SEQ ID NO 10
SEQ ID NO 10
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0.0014;
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96.2%; Score 50; DB
Best Local Similarity 100.0%; Pred. No. 0.(
Matches 11; Conservative 0; Mismatches
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THER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                         LOCATION: (6). (6) OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (8). (8)
COTHER INFORMATION: D-amino acid
US-09-909-164-9
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NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                            FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
PEATURE:
NUMBER OF SEQ ID NOS: 62
SOFWHARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 11
                                                                              TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: artificial sequence
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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                                                                                                                                           Sequence 9, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim.Walby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
ILLE ON INVENTION: NOVE PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
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VTHER INFORMATION: 11-mer synthesized according to example 1
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    100.0%; Pred. No. 0.0014; ive 0, Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD_RES
LOCATION: (1) 7.(1)
OTHER INFORMATION: ACETYLATION
FEATURE: NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE: NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
FEATURE:
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ORGANISM: artificial sequence
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LOCATION: (11)...(11)
OTHER INPERMATION: AMIDATION
US-09-909-164-6
                           11; Conservative
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                                                                 1 EEVVPXGMSYS 11
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  Best Local Similarity
Matches 11; Conserv
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96.2%; Score 50; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                         PEATURE:
OTHER INFORMATION: 11-mer synthesized according to example PEATURE:
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100.0%; Pred. No. 0.0014;
tive 0; Mismatches 0;
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NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
COTHER INFORMATION: norleucine-(CO)
US-09-909-164-49
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NAME/KEY: MOD RES

LOCATION: (11)...(11)

OTHER INFORMATION: AMIDATION

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (6)...(6)

US-09-909-164-48
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OTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                     NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
                                                                                  TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 11; Conservative
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NAME/KEY: MOD_RES
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                                                                                                                                                                                                                                                                            Sequence 47. Application US/09909164
Sequence 47. Application US/09909164
Sequence 47. Application No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby
APPLICANT: Lim-Wilby
APPLICANT: Lim-Wilby
APPLICANT: NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 47
LENGTH: 11
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Sequence 48, Application US/09909164
Sequence 48, Application US/09909164
Sequence 48, Application US/09008702A1
GENERAL INFORMATION:
APPLICAMT: Corvas International, Inc.
APPLICAMT: Lim.Wilby, Marguerita
APPLICAMT: Lim.Vilby, Marguerita
APPLICAMT: Lim.Vilby, Marguerita
APPLICAMT: Lim.Vilby, Marguerita
APPLICAMT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPAITILS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
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                                                            Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
  OTHER INFORMATION: D-amino acids JS-09-909-164-10
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OTHER INFORMATION: ACETYLATION
FEATURE:
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CTHER INFORMATION: valine-(CO)
JS-09-909-164-47
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                   1 EEVVPXGMSYS 11
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NAME/KEY: MISC_FEATURE
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NAME/KEY: MOD_RES
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Sequence 52, Application US/09909164

| Sequence 52, Application No. US20020068702A1
| Publication No. US20020068702A1
| GENERAL INPORMATION:
| APPLICANT: Lim-Wilby, Marguerita
| TITLE OF INTENTION: NOWBER: US/09/909,164
| CURRENT FILING DATE: 2000-07-21
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SEQ ID NO 52
| LENGTHALE: Patentin version 3.1
| LENGTH: 11
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96.2%; Score 50; DB 12; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0014;

Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/CHATTON: (6)...(6); COTHER INFORMATION: (8,8)-allothreonine-(CO)US-09-909-164-51
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; OTHER INFORMATION: propynyl glycine-(CO)
US-09-909-164-52
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                                                            OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
NAME: 
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FRATURE: NAME/KEY: MOD_RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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US-09-909-164-8
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                                                                                                                                          US-09-909-164-50

Sequence 50, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Curves International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
FILE REPERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
PRIOR PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 50
LENGTH: 11
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Sequence 5.1, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS 'NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: INO1192-US

CURRENT PRILING DATE: 2000-07-25

FRICK APPLICATION NUMBER: 60/220,101

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PALENTH VERSION 3.1

SEQ ID NO 51

LENGTH: 11

LENGTH: 11

LENGTH: 11
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ORGANISM: artificial sequence
FEATURE:
FEATURE:
FEATURE:
FEATURE:
FOCATION: 11.-mer synthesized according to example 1
FEATURE:

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; OTHER INFORMATION: 2-amino-butyric acid-(CO)
US-09-909-164-50
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ORGANISM: artificial sequence
FEATURE:
EEVVPXGMSYS 11
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INO1192-US
CURRENT APPLICATION NUMBER: US/09/909,164
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTION OF 52
SOFTWARE: PATENTION OF 52
SOFTWARE: PATENTION OF 52
SOFTWARE: ATCHING PATENTION OF 53
LENGTH: 11
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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88.5%; Score 46; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                      FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (6)...(6)

OTHER INFORMATION: norvaline-(CO)

FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (8)...(8)

OTHER INFORMATION: D-amino acid
US-09-909-164-12
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NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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// LOCATION: (8)..(9)

// OTHER INFORMATION: D-amino acids
US-09-909-164-13
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                  NAME/KEY: MOD RES LOCATION: (11\overline{1})...(11) OTHER INFORMATION: AMIDATION
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Matches 10; Conservative
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1S-09-909-164-12

Sequence 12, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

LENGTH 111

LENGTH 111
                  APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Law, Mibby, Marguerita
APPLICANT: Law, Odile B
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES. AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 8
LENGTH: 11
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Pred. No. 0.0091;
0; Mismatches 1; Indels
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OTHER INFORMATION: ACETYLATION
FRATURE:
FRATURE:
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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Length 11;
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0; Mismatches 1.
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OTHER INFORMATION: norvaline-(CO)
FEATURE:
                                  LOCATION: (1) ... (1)
POTHER INFORMATION: ACETYLATION
PEATURE:
NAME/KEY: MOD RES
LOCATION: (11) ... (11)
PEATURE:
NAME/KEY: MISC_FEATURE
NAME/KEY: MISC_FEATURE
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| LOCATION: (8) ...(8)
| CTHER INFORMATION: D-amino acid
US-09-909-164-11
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Best Local Similarity 90.9%;
Matches 10; Conservative (
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| Sequence 11. Application US/09909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc. APPLICANT: Lawy, Odile E
| APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TILLE REPRESENCE: 100192-05
| TILLE REPRESENCE: 100192-05
| TILLE APPLICATION NUMBER: US/09/909,164
| CURRENT FILING DATE: 2003-03-25
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| LENGTH: 11
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PERATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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ORGANISM: artificial sequence
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                                  Sequence 7, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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NAME/KEY: MISC FEATURE
LOCATION: (9) ... (9)
OTHER INFORMATION: D-amino acid
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.9%;
Matches 10; Conservative (
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COTHER INFORMATION: AMIDATION
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GenCore version 5.1.6
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31	33	63.5	1712	7	A38261	masking protein pr
32	32	61.5	84	Ŋ	E97333	hypothetical prote
33	32	61.5	175	N	PQ0616	transport protein
34	32	61.5	223	N	T01457	rho protein GDP-di
35	32	61.5	279	N	B72481	hypothetical prote
36	32	61.5	288	N	JC4011	cyclin D2 - rat
37	32	61.5	288	N	I58372	cyclin D2 - rat
38	32	61.5	289	N	A41984	cyclin D2 - mouse
39	32	61.5	289	~	A42822	cyclin D2 - human
40	32	61.5	291	N	S57922	cyclin D1 - Africa
41	32	61.5	291	N	S57925	cyclin D2 - Africa
42	32	61.5	291	~	JC4579	cyclin D2 - chicke
43	32	61.5	291	N	\$62730	cyclin D1 - zebra
44	32	61.5	292	N	B42822	cyclin D3 - human
45	32	61.5	295	~	A38977	cyclin D1 - human
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hypothetical protein present asking protein protein transport protein rho protein GDP-di hypothetical protein the protein GDP-di hypothetical protein GYClin D2 - rat cyclin D2 - human cyclin D2 - human cyclin D2 - Africa cyclin D2 - Africa cyclin D2 - Chicke cyclin D3 - Africa cyclin D3 - Africa cyclin D3 - human cyclin D1 - thuman cyclin D1 - thuman	ENTS	chaeum symbiosum ision 11-Jan-2000 #text_change 18-Feb-2000 ston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V. chromosomal variation in natural populations of the 98422450; PMID:9748430 [from GB/EMBL/DDBJ] ; NID:g3599393; PID:g3599394; PIDN:AAC62699.1	73		ist (Schizosaccharomyces pombe) 03-Dec-1999 #text_change 03-Dec-1999 Rajandream, M.A.; Barrell, B.G. ember 1999 GB/EWBL/DDBJ	ъвбоол5.1; GSPDB:GN00066; SPDB:SPAC869.05с .d с869	7; DB 2; Length 840; 5, 21; atches 1; Indels 0; Gaps 0;	
1704456 B348261 B348261 F00616	ALIGNMENT	Cenarchaeum symbiosum e_revision 11-Jan e_revision 11-Jan f. 1998 veals chromosomal MUID:98422450; PM lated from GB/EMB	Score 38; DB Pred. No. 60; 4; Mismatches		n cea	9; PIDN:CAB6 2h-; cosmid	Score 37; Pred. No. 1; Mismate	
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U U U U U U U U U U U U U U U U U U U		RESULT 1 Tal308 hypothetical 367K protein - Cenarchaeum (f. Specielse: Cenarchaeum symbiosum C; Specielse: Cenarchaeum symbiosum C; Date: 11-Jan-2000 #sequence_revision 1: C; Accession: T31308 R; Schleper, C; DeLong, E.F.; Preston, C. J. Bacteriol. 180, 5003-5009, 1998 A; Title: Gencmic analysis reveals chromon, A; Reference number: 220994; MUID: 9842245; A; Accession: T31308 A; Status: preliminary; translated from Gi A; Molecule type: DNA A; Residues: 1-3472 < SCH> A; Accession: Cenarchaes: RBEL: AP083072; NID: G; C; C; Conarchaeum symbiosum hypocapamily: Cenarchaeum symbiosum hypocapamily: Cena	Query Best 1 Matche	o d	RESULT 2 T19116 probable sulfate permease - fission 1 C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revisit C;Accession: T39116 R;Hunt, C.; Aves, S.; McDougall, R.C submitted to the EMBL Data Library, A;Reference number: Z21829 A;Reference number: Z21829 A;Reteurs: prediminary; translated fro	A,Resid A,Resid A,Exper C,Genet A,Genet A,Map p	Query N Best Lo Matches	\$ £

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A;Gross-references: EMBL:Z81109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10 A;Experimental source: clone R10D12
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C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Accession: S57808
A;Niligan, S.B.; Gasser, C.S.
A;Niligan, S.B.; Gasser, C.S.
A;Nilie: Nature and regulation of pistil-expressed genes in tomato.
A;Reference number: S57808; MUID:95375233; PMID:7647301
A;Accession: S57810
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C;Species: Rattus norvegicus (Norway rat)
C;Species: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: $22-93; I786 56
R;Mitchelmore, C:; Traboni, C: Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein R10D12.10 - Caenorhabditis elegans
Cyspecies: Gaenorhabditis elegans
Cybate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
CyAccession: T24111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary, nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-25 AML>
A;Cross-references: EMBL:U20592; NID:g924625; FIDN:AAA80497.1; PID:g924626
C;Superfamily: plant Kunitz-type proteinase inhibitor
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                                                                             Gaps
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                                                                             ;
2; Length 1498;
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Pred. No. 13;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.3%; Score 35; DB 2; Length 425; 50.0%; Pred. No. 26; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                aypothetical protein precursor (clone TPP11) - tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary, translated from GB/EMBL/DDBJA;Molecule type: DNA
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A;Reference number: 219842
    Score 36; DB
Pred. No. 63;
2; Mismatches
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A, Introns: 23/3; 56/3; 113/3; 257/2
    69.2%;
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ilarity 54.5%;
Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
                                                                                      Conservative
                                                                                                                                                                                                                                              1276 EQKIPMGMSY 1285
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                                                                                                                                                                    1 EEVVPXGMSY 10
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les 6; Conserv
    Query Match
Best Local Similarity
Matches 6; Conserv
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R)Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R)Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R)Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R)Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R)Morris, B.A.
R)Morris, B.A.
R)Morris, MID: 92188538; PMID: 1546458
R)Morris, B.A.
R)Morris, B.A.
R)Morris, MID: 9335283; PIDN: AA47947.1; PID: 9335284
R)Morris, MID: 9335283; PIDN: AA47947.1; PID: 9335284
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                                                                                                                                                                                                                                         C,Accession: T40413

C,Accession: T40413

Submitted to the EMBL Data Library, August 1998

A,Reference number: 221926

A,Recference number: 221926

A,Recference number: DNA

A,Recference number: DNA

A,Residuae: 1-877 < LNN

A,Residuae: 1-877 < L
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A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-1498 «KUR»
A, Cross-references: GB: AE001437; PIDN: AAK81629.1; PID: g15026814; GSPDB: GN00168
A, Experimental source: Clostridium acetobutylicum ATCC824
A, Genetics: CAC3709
                                                                                                                    sulfate permease - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VI protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Score 36; DB 2; Pred. No. 3.5; 3; Mismatches

n Similarity 60.0%; 6; Conservative 3

Query Match Best Local Similarity Matches 6; Conserv

à

Query Match Best Local Similarity 77.5-

C,Genetics: A,Gene: SPDB:SPBC3H7.02 A,Map position: 2

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hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein O2612; hypothetical protein YOL303.3
C;Species: Saccharomyces cerevisiae
C;Accession: S54619; S66819 of Section O1-Sep-1995 #text_change 19-Apr-2002
C;Accession: S54619; S66819 of Section S54617
A;Accession: S54619
A;Accession: S54619
A;Accession: S54619
A;Accession: S54617
A;Residues: 1-156 <DEH;Accession: S68877
A;Residues: 1-156 <DEH;Accession: S68877
A;Residues: 1-156 <DEM;Accession: S68878
A;Residues: 1-156 <DEM;Accession: S68888
A;Residues: 1-156 <DEM;Accession: S68878
A;Re
                                                                                                                                                                       A;Status: preliminary
A;Notestion: A371 or FANA
A;Notestion: A371 or FANA
A;Notestion: A271 or FANA
A;Residues: 1-271 or FANA
A;Residues: 1-271 or FANA
A;Cross-references: EMBL:X51435; NID:g38017; PIDN:CAA35798.1; PID:g38018
B;Baldwin Jr., A.S.; LeClair, K.P.; Singh, H.; Sharp, P.A.
B;D. Cell. Biol.: 10, 1406-1414, 1990
A;Title: A large protein containing zinc finger domains binds to related sequence elementally. Richerence number: A34779; MUID:90205817; PMID:2108316
A;Reference number: A34779
A;Accession: A44779
A;Accession: A44779
A;Residues: 801-1072, N', 1074-1168, 'K', 1170-1225, 'V', 1227-1434, 'N', 1436-1607, 'I', 1609-16'
A;Residues: 801-1072, N', 1074-1168, 'K', 1170-1225, 'V', 1227-1434, 'N', 1436-1607, 'I', 1609-16'
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Keywords: DNA binding; transcription regulation; zinc finger
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H69491

cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus

ci) division inhibitor (minD-2) homolog - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999

C;Accession: H69491

R;Xlenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R;Xlenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F., Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
A,Title: A DNA-binding protein containing two widely separated zinc finger motifs that A,Reference number: A34203; MUID:90169514; PMID:2106471
A,Accession: A34203
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Pred. No. 14;
1; Mismatches
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A;Map position: 15R
C;Superfamily: hypothetical protein YOR013w
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Best Local Similarity 66.7%;
Matches 6; Conservative
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2405 WPAGLTYS 2413
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bubmitted to GenBank, June 2000

Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm, J. Authors: Marchia, M.D.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh hado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E., Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. odrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, Authors: da Silva, A.C.R.; da Silva, A.M.; Verioveki-Almeida, S.; Vettore, A.L.; Z.; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Xylella fastidiosa
,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
,Accession: H82601
,anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen ature 406, 151-157, 2000
,Title: The genome sequence of the plant pathogen Xylella fastidiosa.
,Reference number: A82515, NUID:20365717; PMID:10910347
,Note: for a complete list of authors see reference number A59328 below
                                                   Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-3. Reference number: 158280; MUID:91187610; PMID:1901405
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Molecule type: DNA
;Residues: 1.749 <SIM>
;Cross-references: GB:AE003967; GB:AE003849; NID:g9106347; PIDN:AAF84162.1; GSPDB:GN001
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134203

134203

13. Alternate names: major histocompatibility complex enhancer-binding protein 1

13. Alternate names: major histocompatibility complex enhancer-binding protein 1

13. Species: Homo sapiens (man)

13. Species: 22-041-1990 #sequence_revision 22-041-1990 #text_change 20-Sep-1999

13. Accession: A34203; A34779

13. Fan, C.M.; Maniatis, T.

14. 29-42, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opoisomerase IV subunit XF1353 [imported] - Xylella fastidiosa (strain 9a5c)
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                                                                                                                                                                                                                      "Motecule type: mRNA; Residues: 1-670 cMIT>; Rouse: the authors did not translate the codon for residue 1; Superfamily: HIV-BP2 enhancer-binding protein; Reywords: DNA binding; transcription regulation; zinc finger
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48;
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Pred. No. 48;
0; Mismatches
                                                                                                                                  Accession: S22293
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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                      A, Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A, Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A, Feference number: A69250; MUID:98049343; PMID:9389475
A, Accession: H69491
A, Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: 16-Aug-1996
C;Accession: 140758; 847317
B;Hani, E.K.; Chan, V.L.
J. Bacteriol. 177, 2396-2402, 1995
A;Title: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd
A;Reference number: 140758; MUD:95247673; PMID:7730270
                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-252 <KLE>
A;Cross-references: GB:AE000970; GB:AE000782; NID:g2689293; PIDN:AAB89318.1; PID:g264860
C;Superfamily: cell division inhibitor minD
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                                                                                                                                                                                                                                                                                                                                                    65.4%; Score 34; DB 2; Length 252; 75.0%; Pred. No. 24; vative 1; Mismatches 1; Indels
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A;Molecule type: DNA
A;Residues: 1-94 <RES>
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Best Local Similarity 75.0
Matches 6; Conservative
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81 EVIPAGMS 88
Nature 390, 364-370, 1997
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Best Local Similarity
Matches 7; Conserv
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A,Gene: ABCsbp-5; UU359
A,Genetic code: SGC3
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C;Accession: B90544
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.,
Nucleic Acids Res. 29. 2145-2153, 2001
A;fifter The complete genome sequence of the murine respiratory pathogen Mycoplasma puln
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: E90544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA.
A;Resdicus: 1.116 < KUR>.
A;Cross-references: GB:A1445566; PID:g14089674; PIDN:CAC13434.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
508 ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
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Pred. No. 17;
0; Mismatches 2; Indels
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A)Genetic code: SGC3
C)Superfamily: Escherichia coli ribosomal protein L20
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Best Local Similarity 77.8%;
Matches 7; Conservative
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 25586;

MEDINES-1886394; PubMed=11889109;

MEDINES-1886394; PubMed=11889109;

Mapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Rapatral V., Anderson I., Gardner W., Grechkin G., Zhu L.,

Nasieva O., Chu Li., Kogan Y., Chaga O., Goltsman B., Bernal A.,

Larsen N., D'Souza M., Walumas T., Pusch G., Haselkorn R.,

Ronstein M., Kyrpides N., Overbeek R.;

Larsen N., D'Souza M., Overbeek R.;

Ronstein M., Kyrpides N., Overbeek R.;

Toucleatum strain ATCC 25566.;

U. Bacteriol. 184:2005-2018(2002).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its west by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                homo sapien
crithidia f
human herpe
human herpe
                                                                                                                                          escherichia
escherichia
escherichia
                                                                                              saccharomyc
                                                                                                             rattus norv
                                                                                                                          tomato
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
244677 | P44677 | P44677 | P075355 | P90516 | P905381 | P52544 | P52544 | P32784 | P08931 | P28931 | P16916 | P16916 | P16917 | P
                                                                                                                                                                                                                                                                                                                                                                                                                              Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
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                ENP3_HUMAN
S216_HUMAN
GSP_CRIFA
PRTP_HSV6U
PRTP_HSV6Z
SCT1_YEAST
EDD_RAT
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RHSA_ECOLI
RHSC_ECOLI
RHSB_ECOLI
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InterPro; IPR006475; CarA L glu.

InterPro; IPR006493; CPase L.

InterPro; IPR005499; CPase L. D2.

InterPro; IPR005480; CPase L. D3.

InterPro; IPR005481; CPase L. N.

InterPro; IPR004362; MGS IIRe.

Pfam; PF00289; CPSase L. Chain; 2.

Pfam; PF00289; CPSase L. Chain; 2.
     01.B
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   427
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117.693 Million cell updates/sec
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                                                                                                             June 3, 2004, 11:32:06 ; Search time 4.86667 Seconds
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Q04351
P15822
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P50755
P49706
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P25322
P39948
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P55169
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                       141681 segs, 52070155 residues
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                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
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X1A9_CLOAB
ZEP1_HUMAN
CY14_NEUCR
A10A_HUMAN
A10A_HUMAN
X120_MYCPU
YJ49_ARCFU
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RAT
MOUSE
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MOUSE
RAT
                                                                             M protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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LTBS 1
RPOC 7
LTBL F
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GSR2]]
BCN5]
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52
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"The genome sequence of Schizosaccharomyces pombe.";
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Matches
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RY SEQUENCE FROM N.A.

RY SEQUENCE FROM N.A.

RY MEDLINE=21848401; PubMed=11859360;

RY MEDLINE=21848401; PubMed=11859360;

RY MEDLINE=21848401; PubMed=11859360;

RA MEDLINE=21848401; PubMed=11859360;

RA SQUICOS U., Peat N., Hayles J., Bakham D., Bowman S.,

RA Gentles S., Gonnor R., Cronin A., Davis P., Felvenl T., Fraser A.,

RA Gentles S., Gonnor R., Cronin A., Davis P., Felvenl T., Fraser A.,

RA Gentles S., Gonnor R., Cronin A., Muchle B.J., Hunt S., Jagels K.,

RA Gentles S., Gonnor M., Leather S., McDonald S., McGean J.,

RA Moncey P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,

RA Moncey P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,

RA Moncey P., Moule S., Mangall M.A., Rabbinowitsch E.,

RA Riberford K., Rutter S., Saunderes R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Weltjens I., Vanstreels B., Rieger M., Schaefer M., Maeller-Auer S.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Gentles I., Wanstreels B., Rieger M., Schaefer M., Mottier S.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert B.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., More S.,

RA Gabel C., Fuchs M., Stang Z., Hunt C., More K., Hurs E.,

RA Galibert F., Aves S.J., Lehrach H., Reinhardt R., Pohl T.M.,

RA Galibert F., Aves S.J., Lehrach M., Garzon A., Thode G.,

RA Galibert R., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,

RA Doga R.R., Cruzado L., Jimenez J., Sanchez M., Garzon A., Forsburg S.L.,

RA Cerrutti L., Lowe T., Morconbis W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                          Gaps
Pfam; PF02142; MGS; 1.

TIGREAMS; TIGRO1346; CPSASE.

TIGREAMS; TIGRO1346; CPSASE 1; 2.

PROSITE; PS00866; CPSASE 1; 2.

PROSITE; PS00867; CPSASE 2; 2.

PROSITE; PS00867; CPSASE 2; 2.

PATITUTE Diosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete proceome.

DOMAIN 402 546 OLIGOMENIZATION DOMAIN.

DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

DOMAIN 920 GARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

TEPERT 1 546
                                                                                                                                                                                  ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE I (BY SIMILARITY).

MANGANESE I AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                           Score 38; DB 1; Length 1058; Pred. No. 7; 1; Indels 3; Mismatches 1; Indels
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-JUL-2003 (Rel. 42, Last annotation update)
Probable sulfate permease C3H7.02.
                                                                                                                                                                                                                                                                                                               73.1%;
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60..
Best Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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190 EIVPNGLNYS 199
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302
302
308
309
300
820
832
1058 AA;
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NCBI_TaxID=4896;
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METAL
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Nature 415:871-880 (2002).
-!- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY SIMILARITY).
-!- SUBCELLUTAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92188538; PubMed-1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
"The nucleotide sequence of the infectious cloned DNA component tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants.";
Virology 187:633-642(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-CT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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                                                                                                                             family.
-!- SIMILARITY: Contains 1 STAS domain.
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POTENTIAL.
POTENTIAL.
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PIR; T40413; T40413.
PIR; T40413; T40413.
InterPro; PR001902; Sulph_transpt.
InterPro; PR001902; Sulph_transpt.
Pfam; PP00140; Sulfate_transpt.
Pfam; PP00916; Sulfate_transp; I.
TIGREAM; TIGREOBLS; Sullp. 1.
PROSITE; PS01130; SIC26A; I.
PROSITE; PS010130; SIAS; I.
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TRANSMEM 133 153
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P31619;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8D-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sauer U., Duerre'P.;
"Sequence and molecular characterization of a DNA region encoding a
"Sequence and molecular characterization of a DNA region encoding a
small heat shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
-!- SIMILARITY: Contains 2 FtsK domains.
-!- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
in positions 76 and 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium acetobutylicum.
Bacteria, Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                            69.2%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 1.6; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                      01-FBB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein CAC3709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1498 AA
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; Pubmed=8501044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE007866; AAK81629.1; -.
EMBL, X65276; CAA46379.1; ALT_FRAME.
PIR; B97355; B97355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002543; FtsK_SpoiliE.
                                                                                                                                                                                                               InterPro; IPR002621; Gemini mov. Pfam; PF01708; Gemini mov; 1.
                                                                                                                                                                        EMBL; M81103; AAA47947.1; -.
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7 QVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                                                                                         2 EVVPXGMSYS 11
                                                                                                                                                                                              PIR; A42452; A42452.
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                                                                                                                                                                                                                                                  Hypothetical
SEQUENCE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14). Last sequence update)
10-CCT-2003 (Rel. 42, Last sequence update)
Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-binding protein 1) (HIV-RP1) (Major histocompatibility complex binding protein 1) (POSITIVE regulatory domain II binding factor 1) (PRDII-BF1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1.";
Biochemistry 31:3907-3917(1992).
-!- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE -!- FUNCTION: THE PROMOTERS STORE AS THOSE OF SV40, CRV, OR HIVI. IN VWERCUS VIRAL PROMOTERS STORE AS THOSE OF SV40, CRV, OR HIVI. IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS! I MC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Biochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDUCTION: By mitogens and phorbol ester,
DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fan C.M., Maniatis T.;
"A DNA-binding protein containing two widely separated zinc finger
motifs that recognize he same DNA sequence.";
Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR OF 2087-2142.
MEDILINE-92232684; PubMed=1567844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
Gronenborn A.M.;
                                                                                                                                                                                         ó.
Pfam; PF01580; FtsK_Spoliff; 2.
PROSITE; PS50901; FTSK; 2.
DOMAIN 655 857 FTSK 1.
DOMAIN 1001 1188 FTSK 1.
DOM IND BIND 675 682 ATP (POTENTIAL).
SEQUENCE 1498 AA; 168968 MW; FF42037A335A9649 CRC64;
                                                                                                                                                  69.2%; Score 36; DB 1; Length 1498; 60.0%; Pred. No. 27; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91064333; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                            PRT; 2717 AA
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-!- SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IN T-CELL ACTIVATION. SUBCELLULAR LOCATION: Nuclear.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 2113-2142
                                                                                                                                                                       Local Similarity 60.0
nes 6; Conservative
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ID ZEP1 HU
AC P15822;
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A10A_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDLINE-94188926; PubMed-8140616;
Sandal N.N., Marcker K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
MEDLINE=91129256; PubMed=1825178;
MEDLINE=91129256; FubMed=1825178;
Ketter J.S., Jaral G., Fu Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recognition "Nucleotide sof cys-14, the structural gene for sulfate permease II in elements of cys-14, the structural gene for sulfate permease II in
                                                                                                                  GO; GO:0005634; C:nucleus; TAS.
GO; GO:000567; F:DNA binding; TAS.
InterPro; IPR007087; Znf C2H2.
Pfam; PF00096; zf-C2H2; 5.
SMART; SM00355; ZnF C2H2; 4.
PROSITE; PS50127; ZINC FINGER C2H2 1; 4.
PROSITE; PS50127; ZINC FINGER C2H2 2; 4.
Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
Nuclear protein; Repeat; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 1; Length 2717;
Pred. No. 80;
2; Mismatches 1; Indels
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C2H2-TYPE.
POLY-SER.
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sulfate permease II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                           EMBL; X51435; CAA35798.1; -.
PIR; A34203; A34203.
PDB; 3ZNF; 15-JAN-92.
PDB; 4ZNF; 15-JAN-92.
PDB; 1BBO; 31-OCT-93.
TRANSPAC; T00497; -.
Genew; HGNC, 4920; HIVEP1.
                                                                                                                                                                                                                                                                                                                                                   67.3%;
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2123 212
2127 213
2717 AA;
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Best Local Similarity
Matches 6; Conserv
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Neurospora crassa.
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P23622;
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permease II and a putative human tumour suppressor.";
Trends Biochem. Sci. 19:19-19(1994).
-!- FUNCTION: UPTAKE OF SULFATE INTO THE CELL.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- INDUCTION: Highly expressed, but only in cells subject to sulfur limitation, and it is turned on by the positive-acting Cys-3 sulfur regulatory protein.
-!- MISCELLANEOUS: SULFATE PERVEASE II IS MAINLY FOUND IN MYCELIA.
-!- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
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MEDLINE=21225279; PubMed=11326269;
Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S.,
Oshimura M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome."; Nat. Genet. 28:19-20(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EC 3.6.3.1) (ATPVA)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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060312; 096914;
30-MAY-2000 (Rel. 39, Created)
10-OCT-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Potential phospholipid-transporting Arpase VA
ATP10A OR ATP10C OR ATPVC OR KIAA0566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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Pfam; PF00916; Sulfate transp; 1.
TGRPAMS; TIGR00815; SulP; 1.
PROSITE; PS01130; SLC26A; 1.
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les 6; Conser
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SEQUENCE FROM N.A.
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PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                           65.4%; Score 34; DB 1; Length 1499; 72.7%; Pred. No. 70; 11ve 0; Mismatches 3; Indels
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1499 AA; 167687 MW; D4996A4D0635A6BD CRC64;
                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                            POTENTIAL.
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    Local Similarity 72.7
ses 8; Conservative
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RL20 MYCPU
ID RL20 MYCPU
AC Q98QV0;
DT 28-FEB-2003 (C)
DT 28-FEB-2003 (C)
DT 28-FEB-2003 (C)
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EMBL;
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Matches
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Y990 CAMJE STANDARD; PRT; 253 AA. B45489; Q9FNVO; CHONOV-1995 (Rel. 32, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000968; AAB89307.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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TIGR; AF1949; -.
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Y990_CAMJE
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MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
"The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRANIE-20(16) DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9388475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey EK., Peresson J.D.,
Richardson D.L., Karlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
508 ribosomal protein 120.
RPLT OR MYPU_2610.
Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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C59C748901B18F14 CRC64;
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4Ppothetical protein AF1949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL445563; CAC13434.1; -.
PIR; E90544; E90544.
Mypulist; MYPU 2610; -.
HAMAP; MP 00382; -!).
INTERPRO; IPR005813; Ribosomal L20.
INTERPRO; IPR005812; Ribosomal L20.
PERM; PP00453; Ribosomal L20; TRRNTS; PR00062; RIBOSOMALL20.
PRINTS; PR00062; RIBOSOMALL20.
ProDom; PD02389; L20; 1.
PROSITE; PS0937; RIBOSOMALL20; 1.
PROSITE; PS0937; RIBOSOMALL20; 1.
Ribosomal protein; FRNA-binding; Complet SEQUENCE 116 AA; 13565 MW; C59C74890
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                                                                                     NCBI_TaxID=2107;
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Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McMeil L.K., Badger J.H., Glodek A., Zhou L., Coverbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Wasson T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Basham D., Chillingworth T., Davies R.M., Fellwell T., Holroyd S.,

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

Whitehead S., Barrell B.G.;

"The genome sequence of the food-borne pathogen Campylobacter jejuni

reveals hypervariable sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                                                        "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 160-253 FROM N.A.
STRAIN=ARCC 43431 / TGH 9011;
MEDLINE=95247673; PubMed=7730270;
MEDLINE Chan V.L.;
Mani E.K., Chan V.L.;
"Expression and characterization of Campylobacter jejuni benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 7 27 POTENTIAL.
TRANSMEM 141 161 POTENTIAL.
SEQUENCE 165 AA; 17588 MW; BEC17054910ADBF8 CRC64;
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VIBCH
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CONFLICT
CONFLICT
SEQUENCE
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O9KRE0;
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AROA_VIBCH
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-C57B/60; TISSUB-Embryonic head;

MEDLINE-21085660; PubMed=11217851;

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alaxawa T., Tawa M., Nishia K., Kiyosawa H., Kondo S., Yamanaka I.,

Alaxawa T., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

Asato T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Maching L., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Satuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaya-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshav-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshav-Rocka K., Wang K.H., Hasegawa Y., Kawaji H., Nathure D.M.,

Mynshav-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshav-Rocka K., Wang K.H., Hasegawa Y., Kawaji H., Mataki Y.,

Mynshav-Rocka K., Wang K.H., Hasegawa Y., Kawaji H., Nathure D.M.,

Mynshav-Rocka K., Wang K.H., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshav-Rocka R., Wang K.H., Hasegawa Y., Kawaji H., Mataka Y.,

Mynshav-Rocka R., Wang K.H., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshav-Rocka R., Wang K.H., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshav-Rocka R., Wang K.H., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Mammary fibroblast;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jorden H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                        63.5%; Score 33; DB 1; Length 253; 55.6%; Pred. No. 18; 2; Indels iive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete proteome.
SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9D3<u>B7;</u> Q9CxQ4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein C20orf103 homolog precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 AA
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                                                                                                                                                                            EMBL; AL139076; CAB73246.1; -. EMBL; 236940; CAA85392.1; -. PIR; C81374; C81374.
                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.5
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 DIFPSGMSY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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CTX3_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=09D387-2; Sequence=VSP 003820;
-!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts in positions 174 and 239.
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Externed Y.S., Schmutz J., Myers R.M., Farzwinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-i. SUBCELLULAR LOCATION: Type I membrane protein (Potential).
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(EPSPS).
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PROTENTIAL.
PROPERTIAL.
PROPERTIAL.
CYTOPLASHIC (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
MISSING (GLCNAC...) (POTENTIAL).
MISSING (IN 180FORM 2).
/FIId=VSP 003820.
E -> V (IM REF. 1; BAB31124).
P -> P (IN REF. 1; BAB31124).
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Vibrionaceae; Vibrio.
NCBI TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.5%; Score 33; DB 1; Length 280; 75.0%; Pred. No. 20; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31721 MW; FA11D7BF9FD5CCEF CRC64;
                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ransmembrane; Signal; Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9D387-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK014127; BAB29169.1; -.
EMBL; AK018222; BAB31124.1; ALT_FRAME.
EMBL; BC004791; AAH04791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1920368; 3110035N03Rik.
MGD; MGI:1923411; 6330527006Rik.
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Best Local Similarity 75.0
Matches 6; Conservative
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280
280
280
350
1102
1103
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230 2
238 2
280 AA;
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SEQUENCE FROM N.A.
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                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alack step.

-1- SUBGNIT: Monomer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-1- SIMILARITY: Belongs to the RPSP synthase family.

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SEQUENCE FROM N.A.

SERVINES 1 TOT N16961 / Serotype O1;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hreky E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R EMBL, AE004251, AAF94882.1; -.
R PIR; D82163.
R TIGR, VC1732, -.
R HAMAP, ME_00210; -; 1.
R HAMAP, ME_00210; -; 1.
R InterPro; IPR006264, Arch.
R InterPro; IPR001966; ESSP_synthase; 1.
R Pfam; PF00275; EBSP_synthase; 1.
R PRODIM; PD001867; EBSP_synthase; 1.
R PROSITE; PS00104; EBSP_SYNTHASE_1; 1.
R PROSITE; PS00104; EBSP_SYNTHASE_1; 1.
R PROSITE; PS00104; EBSP_SYNTHASE_1; 1.
R PROSITE; PS00104; ERSP_SYNTHASE_1; 1.
R PROSITE; PS00104; ERSP_SYNTHASE_2; 1.
R PROSITE; PS00104; ERSP_SYNTHASE_3; 1.
R PROSITE; PS00104; ERSP_S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
10-6CT-2003 (Rel. 42, Last annotation update)
Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
CDC37 OR SPBC9B6.10.
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 406:477-483(2000)
-1- CATANTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyviny1)-3-phosphoshikimate.
-1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                        "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 31;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
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Best Local Similarity
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094740;
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CC37_SCHPO
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MEDLINE=88336297; PubMed=2901768;
                                                                                                                                                          EMBL, AF182076, AAF62873.1, --
EMBL, BC004229, AAH04229.1, --
EMBL, BC006311, AAH06311.1, --
EMBL, BC20624, AAH10095.1, --
EMBL, AC29624, AAG3413.1, --
EMBL, AL359335, CAB94786.1, --
EMBL, AL359336, CAB94786.1, --
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                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL122063; CABS9242.1;
SWISS-2DPAGE; O9NZMS; HUMAN.
Genew; HGNC:4333; GLTSCR2.
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P08696;
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BCNS_CLOPE
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosax S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,

Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Ryilalon D.K., Madan A., Nodergren E.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Generation and mouse cDNA sequences.",

Human and mouse cDNA sequences.",

Human and mouse cDNA sequences.",

Lydon R. L. Allender Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S., Submitted (OCT-1999) to the EMBL/Genbank/DDBJ databases.
-!- SUBGNIT: Interacts with HSV-1 early proteins ICP22 and ICP0.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Expressed at high levels in heart and pancreas, moderate levels in placenta, liver, skeletal muscle, and kidney, and low levels in brain and lung.
-!- SIMILARITY: Belongs to the GITSCR2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=99214318; PubMed=10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins ICP22 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                 GSR2_HUMAN STANDARD; PRT; 478 AA.
Q9NZM5; Q9BTC6; Q9HXK6; Q9NPP1; Q9NPR4; Q9UF12;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60).
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J. Virol. 73:3810-3817(1999).
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REIQ -> VLTVSCRGAPCPVMTPSLLPVPPRGYGRHHGCP
WAGPVGPMPRG (IN REF. 5).
SGILRDRFKSFQRANNIEPREAKFKRKYKVKLVEKRAFR
EIQL -> RGQHSPETGSRAFRGGI (IN REF. 3).
7F189238348CB52B CRC64;
is in no
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MEDLLINE=87055/020; PubMed=2877971;
Garnler I., Cole S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pIP404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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D -> H (IN REF. 3).
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Pred. No. 35;
1; Mismatches 3; Indels
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01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Bacteriocin BCN5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005622; C:intracellular; NAS.
Nuclear protein; Polymorphism.
VARIANT 389
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                                                                      SEQUENCE OF 1-14 FROM N.A.
STRAIN=CPNSO;
MEDLINE=8039249; PubMed=2460717;
Garnier T., Cole S.T.;
"Studies of UV-inducible promoters from Clostridium perfringens in vitro and in vitro.";
vivo and in vitro.";
will microbiol. 2:607-614(1988).
-i- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
-i- INDUCTION: BY UV irradiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN 815 869 HYDROPHOBIC.
SEQUENCE 890 AA; 96699 MW; P4E5E8971C31C6C6 CRC64;
perfringens and molecular genetic analysis of the bacteriocin-encoding gene."; J. Bacteriol. 168:1189-1196 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M14481; AAA98248.1;
EMBL; M32882; AAA98249.1;
PIR; A30481; A30481.
InterPro; IRR000834; Peptidase_M14.
InterPro; IPR000834; Peptidase_M14.
InterPro; IPR000846; SH3 bac.
Pfam; PR00246; Zn carbopept; 1.
SWART; SM00287; SH3b; 3.
Antibiotic; Bacteriocin; Plasmid.
DOWAIN
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Query Match 63.5%; Score 33; DB 1; Length 890; Best Local Similarity 66.7%; Pred. No. 67; Matches 6; Conservative 1; Mismatches 2; Indels

Search completed: June 3, 2004, 11:49:50 Job time: 6.86667 secs

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Query Match 75.0%; Score 39; DB 16; Length 1044; Best Local Similarity 63.6%; Pred. No. 28; Astches 7; Conservative 2; Mismatches 2; Indels (
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TIGREPAMS; TIGR06915; ZA0602; 1.
Complete proteome.
SEQUENCE 1044 AA; 113205 WW; 00E9C13F0F636D2F CRC64;
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Q815a7 bacillus ce
Q98fx1 rhizobium 1
O74056 cenarchaeum
Q9ury8 schizosacch
Q8ewd4 mycoplasma
Q8r126 mus musculu
Q8btx4 mus musculu
Q8btx4 mus musculu
Q8btx5 mus musculu
Q8btx7 pseudomonas
Q40129 lycopersico
Q9xv4 caenorhabdi
Q8ctd7 mus musculu
Q88y7 pseudomonas
Q40129 lycopersico
Q9xv4 caenorhabdi
                                                                                                                                                                         June 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_mammal:*
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sp_fungi:*
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Match Length DB
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Q726r0 homo sapien Q9bha5 plasmodium Q9bha5 plasmodium Q1587 plasmodium Q01587 plasmodium Q01487 rattus ratt Q8pmi6 xanthomonas Q8pmi6 xanthomonas Q8pmi6 xanthomonas Q14122 homo sapien Q1473 sarchaeoglob Q28412 archaeoglob Q96mu1 homo sapien Q98mu1 rhodopirell Q9urr4 penicillium Q88tys rhizobium 1 Q98tys rhizobium 2 Q8xtos ralstonia s	S.	4 AA.	ce update) tion update)	(Thermosynechococcus elongatus). Chroococcales; Synechococcus.		MEDLINE=22225144; PLOMEG=12240834; Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C. Kohara M. Martemnoto M., Makazaki N.,	da M., Tabata S.; nilic cyanobacteriu		IEA. IEA.		
070 00000 700 00007	ALIGNMENTS	1044	ed) seguence up annotation	echoc ales;		keuch a K.,	, Ya therm	·- • .	rane; vitv:	•	
Q7Z6R0 Q9BH83 Q9BH83 Q81557 Q01487 Q01487 Q9PDM6 Q12479 Q97182 Q97182 Q97182 Q97182 Q96MU1 Q98BP5 Q9CMU4 Q9BP5 Q9CMU4 Q9C	ALI	PRT;	reat ast ast	rmosyn		40834; S., II washim	uchi C	8 BP-1	o membor	IBA.	
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\$555 \$833		PRELIMINARY;	(TrEMBLrel. (TrEMBLrel. (TrEMBLrel. :flux transpo	ngatus cteria,		Pubmed ko T., uchi M.	to M., structu	us elon 0(2002) AC09170	integr	transp	64, HAE R tran; ACRIFLA
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		17 1 10 Q8DIH0 Q8DIH0;	01-MAR-2003 01-MAR-2003 01-JUN-2003 Multidrug ef TLL1618.	Synechococcus elongatus (Bacteria; Cyanobacteria; NCBI TaxID=32046;	SEQUENCE FROM N.A STRAIN=BP-1;	SDLINE=22 kamura % tanabe A	impo S.,	Nermosyne NA Res. S	60:001	0, GO:000	InterPro; IPR004764; HAEI. Pfam; PF00873; ACR tran; 1. PRINTS; PR00702; ACRIFLAVINRP.
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The factor of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";

of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";

of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";

D. Bacteriol. 180:5003-5009(1998).

BREL, AF083072; AAC62699.1;

PR, T31308; T31308.

OG. GO:0006215; A. Canembrane; IEA.

CO; GO:0006215; Firansporter activity; IEA.

RO; GO:0006215; Firansporter activity; IEA.

RO; GO:0006810; Firansporter activity; IEA.

RO; GO:0006810; Firansporter activity; IEA.

RO; GO:0006810; PRO000215; BPD_transp.

RICEPRO; PRO004021; BPD_transp.

ROSSORTE; PSO0402; BPD_TRANSP_INN_MEMBR; 1.

ROSSORTE; PSO0402; BPD_TRANSP_INN_MEMBR; 1.

RESQUENCE 3472 AA; 367058 MW; 37F80707030P9355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical procedin.
Cenarchaeum symbiosum.
Archaea; Crenarchaeota; Thermoprotei; Cenarchaeales; Cenarchaeae;
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SEQUENCE FROM N.A.
STRAIN=972h-;
Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJINE=98422450; PubMed=9748430;
Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 1; Length 3472;
Pred. No. 1.7e+02;
4; Mismatches 1; Indels
                                                                                                             73.1%; Score 38; DB 16; Length 387; 60.0%; Pred. No. 15; ive 2; Mismatches 2; Indels
Pfam; PF01546; Peptidase M20; 1.
Hydrolase; Complete proteome.
SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
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Eukaryota; Pungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
Probable sulfate permease.
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54.5%;
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Best Local Similarity 54...
6; Conservative
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2294 EDVIPRGISFS 2304
                                                                                                                 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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NCBI_TaxID=4896;
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MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Raneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Matanabe A., Idosawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuoti C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22608415; PubMed=12721630; Ivanova N., Candelon B., Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Raparral V., Bhatracharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Gollsman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Ponstein M., Ehrlich S.D., Overbeek R., Kyrpides N.,
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaeae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.1%; Score 38; DB 16; Length 344; 60.0%; Pred. No. 13; 2; Indels tive 2; Mismatches 2; Indels
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Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 AA; 38539 MW; C55268ACB7225995 CRC64;
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EMBL, AP003002; BABS0445.1; -

GO; GO:00016787; F:Mydrolase activity; IEA.

GO; GO:0006237; F:metallopeptidase activity; IEA.

GO; GO:0006508; P:mctallopeptidase activity; IEA.

InterPro; IPR002933; Peptidase_M20.
                                                                                                                                                                                                     0815A7 PRELIMINARY, PRT; 344 AA. 0815A7, 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) ABC transporter substrate-binding protein.
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Last sequence update)
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Q98FX1;
01-0CT-2001 (TEMBLrel. 18,
01-0CT-2001 (TEMBLrel. 18,
01-JUN-2003 (TEMBLrel. 24,
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Best Local Similarity 60.0
Matches 6; Conservative
                                      843 EEVLPNGIGYS 853
   1 EEVVPXGMSYS 11
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MLR3583.
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SEQUENCE 344 AA
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RESULT 3 **098FX1**

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SEQUENCE FROM N.A.
STRAIN=NOD; IISSUE=Thymus;
MEDLINE=223546813; PubMed=12466851;
The FANTOM CONSOLIUM,
the FANTOM Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I annotation of
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
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08VD18;
01-WAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
81milar to glioma tumor suppressor candidate region gene 2.
GLTSCR2 OR AM536441.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia_Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
) NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                             69.2%; Score 36; DB 11; Length 471; 60.0%; Pred. No. 51; 2; Indels ive 2; Mismatches 2; Indels
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                                                                                  Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC055810, AAH55810.1; - MGD; MGI:2154441; Gltscr2. Hypothetical protein. NON TER SEQUENCE 471 AA; 54506 MW; E0DA685C374A9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017637; AAH17637.1; -.
MGD; MGI:2154441; G15857.2;
SEQUENCE 484 AA; 55835 WW; BBB45F3B4BE02A36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
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Best Local Similarity 60.0
Matches 6; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              226 EVIPAGAŠÝN 235
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239 EVIPAGASYN 248
                                                                                                                                                                                                                                                                                                                                                      2 EVVPXGMSYS 11
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TISSUE=Salivary gland;
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                                       SEQUENCE FROM N.A. TISSUE=Liver;
  NCBI_TaxID=10090;
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Q8VD18
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Q8BTX4
  STARBERS
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MEDLINE=22334719; PubMed=12466555;

Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
Sasaki Y., Ishikawa J., Xamashita A., Oshima K., Kenri T., Furuya K.,
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an
intracellular bacterial pathogen in humans.";

BMBL; AP004171; BAC44662.1; -.
InterPro; IPR007326; Lipoprotein. T.
InterPro; IPR007326; Lipoprotein. T.
Ffam; PF04200; Lipoprotein. T.; 3.
Complete proteome.

SEQUENCE 1123 AA; 123636 MW; A4D707330B3DB4AC CRC64;
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OBR126
OBR126
OBR126
OBR126
OBR126
OL-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 25, Last annotation update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
OINGREAL
OINGRAPHORE
OINGRAPHORE
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi,
Musmmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
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                                                                                                                                                                                                                                                                                                                             Query Match 71.2%; Score 37; DB 3; Length 840; Best Local Similarity 77.8%; Pred. No. 59; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                     840 AA; 93517 MW; ED4833E162B69077 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MYPE 2560 paralog, 57%.
                                                      Geneba Spende; SPAC86.05c; -.
Geneba Spende; SPAC86.05c; -.
GO; GO:0008271; F:sulfate porter activity; IEA.
GO; GO:0008271; F:sulfate porter activity; IEA.
GO; GO:0008272; F:sulfate transport; IEA.
InterPro; IPR002645; STAS.
InterPro; IPR002902; Sulph_transpt.
Pfam; PF00416; STAS; 1.
Pfam; PF00416; Sulfate_transp; 1.
PROSTINS; TIGR00815; Sulp; 1.
PROSTINS; TIGR00815; Sulp; 1.
SEQUENCE 840 AA; 93517 MW; ED48332162B69077 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1123 AA
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                  EMBL; AL132779; CAB60015.1; -. PIR; T39116; T39116.
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Best Local Similarity 70.0
Matches 7; Conservative
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RESULT 7

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RESULT 6

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Q8BK35; Q8BK35 RESULT 10

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STRAIN=DC3000;
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Bearan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.,
"Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AR016858; AA054162.1;
TIGR: PSPT00620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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# GO; GO: 0003571; F: DNA bindleng; IEA.

# GO; GO: 0003571; F: DNA directed RNA polymerase activity; IEA.

# GO; GO: 0003399; F: DNA-directed RNA polymerase activity; IEA.

# GO; GO: 0003399; F: DNA-directed RNA polymerase activity; IEA.

# InterPro; IPR007089; RNA_pol_Rpbl_1.

# InterPro; IPR007089; RNA_pol_Rpbl_1.

# InterPro; IPR007081; RNA_pol_Rpbl_3.

# InterPro; IPR007081; RNA_pol_Rpbl_5.

# Ffam; PF004997; RNA_pol_Rpbl_5.

# Ffam; PF004997; RNA_pol_Rpbl_5.

# Ffam; PF004993; RNA_pol_Rpbl_5.

# Ffam; PF004993; RNA_pol_Rpbl_3.

# R Ffam; PF004993; RNA_pol_Rpbl_3.

# R Ffam; PF004993; RNA_pol_Rpbl_3.

# R Ffam; PF004998; RNA_pol_Rpbl_3.

# R Ffam; PF004998; RNA_pol_Rpbl_3.

# R Ffam; PF004998; RNA_pol_Rpbl_3.

# R Ffam; PF049998; RNA_pol_Rpbl_3.

# R Ffam; PF04998; RNA_pol_Rpbl_3.

# R Ffam; PF04998
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   "Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.2%; Score 36; DB 16; Length 559; 66.7%; Pred. No. 62; 1; Indels tive 2; Mismatches 1; Indels
                           Enterococcus faecalis.";
Science 299:2071-2074(2003).
RMBL; ABGD16947; AA079943.1; -.
TIGR; BF0063; -.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IFR00044; SPP bac.5.
InterPro; IFR00044; SPP bac.5.
Fam; PF00466; SBP bac.5.
Fam; PF00466; SBP bac.5.
Formile processes.
SEQUENCE 559 AA; 61476 MW; CC15418D33D53DE7 CRC64;
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66.7%; Pred. No. 1.7e+02;
tive 2; Mismatches 1; Indels
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01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-07T-2003 (TrEMBLrel. 25, Last annotation update)
DNA-directed RNA polymerase, beta' subunit.
RPOC OR PSFTO0620.
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Les 6; Conservative
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Matches
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Q889X7
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MEDLINE=22354683; PubMed=12466831;
The PANTOM Consortum,
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:553-573 (2002).
MSTRAIN AKO77341; BAC35760.1; -.
MGD; MGI:2154441; Gltscr2.
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STRAIN=VS83 / ATCC 700802;
STRAIN=VS83 / ATCC 700802;
MEDLINE=22550857; PubMed=12663927;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson M.T., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolomay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
                                                                                                                                                                                                                                                                                                   Gaps
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Bacteria, Firmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
VEBI_TaxID=1351;
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Eukaruscuta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Pred. No. 53;
2; Mismatches 2; Indels
                                                                                                                                                                                                                     69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 53; vative 2; Mismatches 2; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MIN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
           50,770 tut. 20153-573(2002).
EMBL; AKO88461; BAC40367.1; -. MMD; MMI:2154441; GItscr2.
mmp; MAI:2154441; GItscr2.
mmy; B3056425B5EECAD8 CRC64;
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Q839T9.
Q1-JUN-2003 (TrEMBLrel. 24, Created)
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pheromone binding protein, putative.
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60,770 full-length cDNAs.";
                                                                                                                                                                                 Query Match
Best Local Similarity 60.0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 60...
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          239 EVIPAGASYN 248
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RESULT 11

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Indels

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Pred. No. 41; 2; Mismatches

60.08;

us-09-909-164-5.rspt

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Best Local Similarity 60.0
Matches 6; Conservative
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Q9XVK4
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipid and glycerol acyltransferase (From 'motifs_6.msf').
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Bacteria, Cyanobacteria, Prochlorophytes, Prochlorococcaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 225 UNKNOWN.
225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
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EMBL; BX572098; CAE21267.1; -.
Acyltransferase; Transferase; Complete proteome.
SEQUENCE 245 AA, 26907 WW; 106F7C4CBE2C6427 CRC64;
                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein precursor.
Lycopersicon esculentum (Tomato).
                                                                                                                                              225 AA
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                                                                                                                                              PRT;
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TRAIN-EPF36, TISSUE=Pistil;
MEDIINE=95375233; PubMed=7647301;
Milligan S.B., Gasser C.S.;
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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32 DEVVPNGKTYA 42
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                                     ESULT 13
140129
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67.3%; Score 35; DB 16; Length 245;

Query Match

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Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein Kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_Kinase.
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50.0%; Pred. No. 75;
ive 3; Mismatches 2; Indels
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                      425 AA
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ProDom, PD000001, Prot kinase, 1.
PROSITE, PSS0011, PROTEIN KINASE_DOM; 1.
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                                                                                                                                                                      PRT;
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology.";
Science 282:2012-2018(1998).
EMBL, 281109; CAB03241.1; --
PIR; T24111, T24111.
                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCCT-2003 (TrEMBLrel. 25, RIDDIZ-10, protein.
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nes 5, Conservative
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                               335 ÉQIVÉGELQY 344
2 EVVPXGMSYS 11
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tun on:

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                         Novel
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                 Abb86553 Rbb86652 Abb866552 Abb866552 Abb866552 Abb866542 Abb866542 Abb866542 Abb86654 Abb86655 Abb866557 Abb866557 Abb866551 Abb86651 Abb866651 Abb866651 Abb866651 Abb866651 Abb86667 Abb86667 Abb86667 Abb86667 Abb86667 Abb86667 Abb86667 Abb86
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Misc-difference
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Modified-site
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Listing first 45 summaries
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52
1 EEVVPXGMSYS 11
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Result No.

41

Gaps

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Indels

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Mismatches

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11; Conservative

Matches

us-09-909-164-6.rag

EEVVPXGMSYS EEVVPXGMSYS

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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
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                                                                                                 Score 50; DB 5; Length 11,
Pred. No. 0.002;
                                                                                                    96.2%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                            11; Conservative
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Best Local Similarity
                                                                                      Sequence 11 AA;
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Modified-site
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activity usefu
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                       virucide.
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"

/note= "C-terminal amide" note= "D-form residue"

WO200208251-A2

31-JAN-2002

Misc-difference

Modified-site

note= "N-terminal acetyl"

Location/Qualifiers

Key Modified-site

Synthetic.

virucide.

Modified-site

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide

(first entry)

08-OCT-2002

ABB80522;

ABB80522 standard; peptide; 11 AA.

#2

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Gaps
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                                                                                                                                                         96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels
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Best Local
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pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture a medicament to treat disorders associated with HCV protease. A

Claim 17; Page 64; 69pp; English.

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ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus

Brunck TK;

Levy OE,

Lim-Wilby M,

WPI; 2002-361643/39.

Novel peptide activity usefu

protease

21-JUL-2000; 2000US-0220101P. 19-JUL-2001; 2001WO-US023169

(CORV-) CORVAS INT INC

RESULT 4

Length 11;

DB 5;

96.2%; Score 50; 100.0%; Pred. No.

Query Match Best Local Similarity Sequence 11 AA;

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11; Conservative
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
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100.0%; Pred. No. ...
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          ABB80566 standard; peptide; 11 AA.
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Matches 11; Conservative
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Modified-site
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                                                            08-OCT-2002
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                                    ABB80566
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                                                                                     /note= "Valyl carbonyl forming keto-amide linkage with residue 7"
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                                                        'note= "N-terminal acetyl"
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                                                                                                                                                                                                                /note= "C-terminal amide"
Location/Qualifiers
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RESULT 8
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-amide linkage with residue 7"
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                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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/note= "C-terminal amide"
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Pred. No.
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96.2%; Sox
Best Local Similarity 100.0%; Pi
Matches 11; Conservative 0;
                                                                                                               Brunck
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                                                                                              (CORV-) CORVAS INT INC
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ABB80567
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                                                                                                                            ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
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                                         Brunck TK;
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                                                                                                                                                                                                                         Claim 17; Page 65; 69pp; English.
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Best Local Similarity 100.0%; Promatches 11; Conservative 0;
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(CORV-) CORVAS INT INC
                                         Levy OE,
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                                                                                     WPI; 2002-361643/39.
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                                         Lim-Wilby M,
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                                                                                                                                                          activity protease.
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The sequence represents a peptide compound of the invention having the peptides of the invepatities C virue (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
                  peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
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                                                                                                        English.
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                                                                                                        Claim 17; Page 65; 69pp;
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Best Local Similarity
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                  Novel pep
activity
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Claim 17; Page 64; 69pp; English.

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          The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with NGV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating and in the sequince of the pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.
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                                                                                                                                                                     96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels
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                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                          Sequence 11 AA;
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Modified-site
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
                  ABB80561 standard; peptide; 11 AA.
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                                      ABB80561;
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                                                                                                                                                                                                                                                                               note= "Alpha-propynyl-glycinyl-carbonyl residue forming
teco-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                              Gaps
                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48.
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Score 50; DB 5; Length 11;
Pred. No. 0.002;
                                                                                                                                                                                                                                                              'note= "N-terminal acetyl"
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   96.2%; Scor.
100.0%; Pre
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                                                                                                                ABB80568 standard; peptide; 11
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                           11; Conservative
                                                              1 EEVVPXGMSYS 11
                                               1 REVVPXGMSYS 11
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                   Best Local Similarity
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Best Local Simi
Matches 11;
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                                                                                                                                   ABB80568;
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          Query Match
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                                                                                                                                                                                                                   'note= "Norvaly1 carbony1 forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide compound having hepatitis C virus protease inhibitory
ty useful for treating disorders associated with hepatitis C virus
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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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Pred. No. 0.013;
0; Mismatches 1; Indels
                                                                                                                                                                       note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                           /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                          'note= "D-form residue"
                                                                                                                                                                                                                                                                                           'note= "Oxymethionine"
                                                                                                                    Location/Qualifiers
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Best Local Similarity 90.9%;

Matches 10; Conservative (
                                                                                                                                                                                                                                             residue 7"
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Gaps

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EEVVPXGMSYS 11

EEVVPXGMSYS 11

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Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide,

Synthetic

virucide

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4

08-OCT-2002

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketomaide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                             note= "Norvaly1 carbony1 forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
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                                               'note= "N-terminal acetyl"
                                                                                                                                                                                                                 /note= "C-terminal amide"
                                                                                                                                                                   note= "D-form residue"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brunck TK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2000; 2000US-0220101P.
                                                                                                                                                                                                                                                                                                                                                         19-JUL-2001; 2001WO-US023169
                                                                                                                 residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
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Best Local Similarity
                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                              WO200208251-A2
Key
Modified-site
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                                                      "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have viruside activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Norvaly1 carbony1 forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8
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Pred. No. 0.013;
0; Mismatches
                                  'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "N-terminal acetyl"
                                                                                                                                                  "C-terminal amide"
                                                                                                                          note= "D-form residue"
                                                                                                 note= "D-form residue"
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            Location/Qualifiers
                                                                                                                                                                                                                                                                                                        Brunck TK;
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                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                              19-JUL-2001; 2001WO-US023169.
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90.9%;
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                                                                          residue
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                                                                                                                                                    /note=
                                                             /note=
                                                                                                                                                                                                                                                                               (CORV-) CORVAS INT INC
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Best Local Similarity
                                                                                     Misc-difference
                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11 AA;
                                                                                                                                                                            WO200208251-A2
            Key
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/note= "C-terminal amide" /note= "D-form residue"

residue 7"

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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                  19-JUL-2001; 2001WO-US023169.
                                                                               21-JUL-2000; 2000US-0220101P.
                                                                                                           Lim-Wilby M, Levy OE,
                                                                                            (CORV-) CORVAS INT INC.
                                                                                                                        WPI; 2002-361643/39.
     Misc-difference
                                       WO200208251-A2
                  Modified-site
                                                    31-JAN-2002.
                                                                                                                                                     protease.
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Brunck TK;

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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha ketoanide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.5%; Score 46; DB 5; Length 11; Best Local Similarity 90.9%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 1; Indels
Claim 17; Page 64; 69pp; English.
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Search completed: June 3, 2004, 11:48:22 Job time: 45.9333 secs

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Sequence 3738, Application US/09134000C
Sequence 3738, Application US/09134000C
Patent No. 6617156
GENERAL INPORMATION:
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
FRIOR RILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARRE: Patentin version 3.1
SEQ ID NO 3738
LENGTH: 382
TYPE: FRT
CREATER STATES CONTRACTOR TO SECONTRACTOR TO SECONTRAC
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WESULY 6. 6632937

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Pred. No. 1.1e+02;
4; Mismatches 1;
US-08-463-772-22
PCT-US93-05000-22
US-08-464-517-6
US-08-464-517-6
US-08-246-361A-4
PCT-US93-05000-4
PCT-US93-05000-6
US-08-246-361A-6
US-08-246-361A-6
US-08-246-361A-2
US-08-463-772-23
US-08-461-517-19
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54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
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Sequence 338, Ap
Sequence 2902, Ap
Sequence 2902, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 236, App
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1. /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

3. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

1. /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-328-352-7885
US-09-346-3
US-09-760-946-3
US-08-637-759B-236
US-09-201-945-236
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US-09-357-952-66
US-09-521-650-66
US-09-168-888-66
US-08-580-988A-23
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US-08-460-714-4

US-08-607-7118-4

US-08-193-977-7

US-08-464-517-21

US-08-463-772-21
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US-08-464-517-22
US-08-246-361A-22
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 EEVVPXGMSYS 11
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Perfect score:
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Result

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Gaps

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Patent No. 6562958
GENERAL INPORMATION
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES-RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-01PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Faucher, Anne-Marie
APPLICANT: Faucher, Anne-Marie
APPLICANT: Ghiro, Elise
APPLICANT: Ghiro, Elise
APPLICANT: Ghiro, Elise
APPLICANT: Ghiro, Elise
APPLICANT: Halmos, Teddy
APPLICANT: Halmos, Teddy
APPLICANT: Lilmas-Brunet, Montse
TITLE OF INVENTION: Macrocyclic Peptides Active Against the Hepatitis C Virus
FILE REPERENCE: 13/076-1-C1
CURRENT APPLICATION NUMBER: US/09/760,946
CURRENT APPLICATION NUMBER: US 09/542,675
PRIOR APPLICATION NUMBER: US 60/128,011
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Substrate for recombinant HCV NS3 protease radiometric assay
US-09-760-946-2
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                                                                                                                                                                                                                                                                                                                                                               Query Match 65.4%; Score 34; DB 4; Length 140
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels
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45.5%; Pred. No. 1.7;
tive 4; Mismatches 2; Indels
       Application US/09328352
                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09760946
Patent No. 6608027
GENERAL INFORMATION:
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Patent No. 6608021
GENERAL INFORMATION:
APPLICANT: TSANCTIZOS, Youla S.
APPLICANT: Cameron, Dale R.
APPLICANT: Faucher, Anne-Marie
APPLICANT: Ghiro, Elise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Teantrizos, Youla S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMSYS 11
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596 EVVPEGLSF 604
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       Sequence 7885,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 12
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Patent No. 6673910

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: SON DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: SON DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
SEQ ID NO 2902
LENGTH: 1191
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION VUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SEQ ID NO 73
LENGTH: 947
; FEATURE:
NAME/KEY: MISC FEATURE
; LOCATION: (327)...(328)
; OTHER INFORMATION: Amino acids 327 & 328 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-3738
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Pred. No. 2e+02;
                                                                                                                                    69.2%; Score 36; DB 4; Length 382; 66.7%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 947;
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                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 4;
Pred. No. 1.6e+02;
                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                        5-09-228-986-73
Sequence 73, Application US/09228986
Patent No. 6359198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.4%;
55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                  Conservative
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Matches 5, Conservative
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ORGANISM: M.catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| |:||
686 VMPSGISYS 694
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783 EILPVGMAY 791
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                                                                                                                                                       Best Local Similarity
Matches 6; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-540-236-2902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-540-236-2902
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US-09-328-352-7885
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                                                                                                                                       Query Match
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Gaps

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Score 33; DB 2; Length 45;
Pred. No. 7.8;
1; Mismatches 3; Indels
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60.0%;
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                             45 amino acids
                                                                                                                                                                                                                  Query Match 63.5
Best Local Similarity 60.0
Matches 6; Conservative
  SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acide
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                          : protein
NO
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                                                                                                                                                                                                                                                                                                                                         1 EEISPLGWSY 10
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                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                ; TOPOLOGY: line; MOLECULE TYPE: ; HYPOTHETICAL: NC US-08-637-759B-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , HYPOTHETICAL:
US-08-871-355A-236
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APPLICANT: Goudreau, Nathalie
APPLICANT: Halmos, Teddy
APPLICANT: Halmos, Teddy
APPLICANT: Lilinas-Brunet, Montse
TITLE OF INVERTION: Macrocyclic Peptides Active Against the Hepatitis C Virus
FILE REFERENCE: 13/076-1-C1
CURRENT APPLICATION NUMBER: US/09/760,946
CURRENT FILING DATE: 2001-08-23
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.5%; Score 33; DB 4; Length 12; Best Local Similarity 45.5%; Pred. No. 1.7; Matches 5; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-637-759B-236

Sequence 236, Application US/08637759B

Patent No. 5876931

GENERAL INFORMATION:

Patent No. 5876931

GENERAL INFORMATION:

ITILE OF INVENTION:

INUMERS OF SEQUENCES:

ADDRESSEE: Patrea L. Pabst

STREET: 2800 One Atlantic Center

STREET: 1201 West Peachtree Street

CITY: Atlanta

STREET: 4800 One Atlantic Center

STREET: 4800 One Atlantic Center

STREET: 201 West Peachtree Street

CITY: Atlanta

STREET: BOO ONE Atlantic Center

STREET: BOO ONE Atlantic Center

STREET: 201 West Peachtree Street

CITY: Atlanta

STREET: 200 One Atlantic Center

STREET: 30309-3450

CONPUTER: DetertIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/GE95/02875

PILING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATCORDEY/AGENT INFORMATION:

NAME: PABSE, PETREE L.

RESTERENCE/DOCKET NUMBER: 31,284

REFERENCE/DOCKET NUMBER: RPMS 101

TELEPHONE: (404) 873-8720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1) OTHER INFORMATION: Asp at position 1 is biotinylated NAME/KEY: MOD RES LOCATION: (10)
                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Tracer for NS3 protease assay
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236
                                                                                                                                                                                                                                                                                                         SEQ ID NO 3
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 BEVVPXGMSYS 11
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Pred. No. 7.8;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1201 West Peachtree Street
CITY: Atlanta
STREET: 2001 West Peachtree Street
CITY: Atlanta
COUNTR: Georgia
COUNTR: Georgia
COMPUTER: Georgia
COMPUTER: EACHDINE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/71,355A
FILING DATE: 09-UUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION WHERE: PCT/GB95/02875
FILING DATE: 11-DBC-1995
CLASSIFICATION WHERE: 13,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
TELEPHONE: (404) 873-8795
INFORMATION POR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE AMINO acids
WENTER AND ACIDS ACID
US-08-871-355A-236

Sequence 236, Application US/08871355A

Patent No. 6015669

GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEB: Patrea L. Pabet
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
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Gaps

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Indels
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3; Mismatches
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Patent No. 6248904
GENERAL INFORMATION:
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Best Local Similarity 45.5
Matches 5; Conservative
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Best Local Similarity 45.5
Matches 5; Conservative
 5; Conservative
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52 KBICPGGMGYT 62
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                                 1 EEVVPXGMSYS 11
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LENGTH: 1394
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US-09-357-952-66
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 Matches
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LITHLE OF INVENTION: ISOLATED NUCLECTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORMING GROWTH PACTOR-BETAL-BINDING PROTEIN
CURREN OF SEQUENCES: 53
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 4; Length 45; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                            Sequence 236, Application US/09201945

Sequence 236, Application US/09201945

Setent No. 6342215

GENERAL INFORMATION:

APPLICANT: David William Holden

TITLE OF INVENTION: Identification of Genes

NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:

ADDRESSE: Patrea L. Pabst

STREET: 2800 One Atlantic Center

STREET: 2800 One Atlantic Center

STREET: 1201 West Peachtree Street

CITY: Atlanta

STREET: 33039-3450

COUNTRY: USA

ZIP: 33039-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/ACENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTATION UNDRER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEFONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 amino acids
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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5177197-51
;Patent No. 5177197
                   JS-09-201-945-236
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DB 6; Length 65; 12;

Score 33; Pred. No.

63.5%; 45.5%;

Query Match Best Local Similarity

; LENGTH: 65 5177197-51

SEQ ID NO:51

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APPLICANT: Zhang, Han-Zhong
APPLICANT: Zhang, Han-Zhong
APPLICANT: Zhang, Han-Zhong
APPLICANT: Drewe, John A.
APPLICANT: Drewe, John A.
APPLICANT: Drewe, John A.
APPLICANT: Drewe, John A.
TITLE OF INVENTION: Tang, Wh.
TITLE OF INVENTION: Thurescence Screening Assays for Caspases, Peptidases, Protease
TITLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735.003001
CURRENT APPLICATION NUMBER: US/09/357,952
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
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FACTOR NO. 5177197

FACTOR NO. 5177197

FAPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;

MENASTEDT, CHRISTER; HELLMAN, ULF, MIYAZONO, KOHEI; CLAESSON-WELSH,

LENA; HELDIN, CARL-HENRIK

TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING

HUMAN TRANSFORMING GROWHF FACTOR-BETAL-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA;

APPLICATION NUMBER: US/07/487,343

FILING DATE: 27-FEB-1990
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517197-13
5177197-13
FACELE NO. 5177197
FACELE NO. 5177197
FAPLICANT: KANZAKI, TETSUTO,OLOFSSON, ANDERS,MOREN, ANITA,
FERNSTEDT, CHRISTER,HELLMAN, ULF,MIYAZONO, KOHEI;CLAESSON-WELSH,
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
HUMAN TRANSPORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
NUMBER OF SEQUENCES: 33
CURRENT APPLICATION DATA:
FILING DATE: 27-FEB-1990
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45.5%; Pred. No. 3.9e+02;
ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 6; Length 410;
Pred. No. 97;
3; Mismatches 3; Indels
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RESULT 15
Sequence 66, Application US/09521650
Patent No. 6335429
Patent No. 6335429
GENERAL INFORMATION:
APPLICANT: Cai, Sui Xiong
TITLE OF INVENTION: Their Applications for Whole-Ceil Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
FILE PERERENCE: 1735. 029002
CURRENT APPLICATION NUMBER: 09/168,888
EARLIER FILING DATE: 1998-10-0
EARLIER PILING DATE: 1998-10-0
EARLIER PILING DATE: 1998-10-10
EARLIER PILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SOUTHWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 10
TANDER OF SEQ ID NOS: 142
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                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
JS-09-357-952-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.5%; Score 32; DB 4; Length 10; Best Local Similarity 50.0%; Pred. No. 2.3; Matches 5; Conservative 3; Mismatches 2; Indels
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EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 10
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ORGANISM: Artificial Sequence
FEATURE:
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Search completed: June 3, 2004, 12:03:06 Job time: 11.8 secs

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NAME/KEY:
NAME/KEY:
NOTHIN: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: artificial sequence
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FEATURE:
NAMEY KEY: MOD RES
LOCATION: (11)
OTHER INFORMATION: AMIDATION
-09-909-164-5
 Query Match
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3: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

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8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-909-164-6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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No.
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Sequence 1 Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lewy, Odile E

APPLICANT: Lewy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: INJUSTICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 5

MANDER OF SEQ ID NOS: 62

MANDER OF SEQ ID NOS: 62
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US-09-909-164-20
US-09-909-164-24
US-09-909-164-28
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US-09-909-164-45
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
URRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 10
LENGTH: 11
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thes 0;
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96.2%; Score 50; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 11; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (8)...(8)
CTHER INFORMATION: D-amino acid
US-09-909-164-9
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LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
PEATURE:
NUMBER OF SEQ ID NOS: 62
SOFWARE: Patentin version 3.1
SEQ ID NO L
ENGTH: 11
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                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD RES
LOCATION: (11), (11)
OTHER INFORMATION: AMIDATION
FEATURE:
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC FEATURE
LOCATION: (8)...(9)
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                                                                                                    TYPE: PRT
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Publication No. US20020068702A1
CENDERAL INFORMATION:
CENDERAL INFORMATION:
CENDERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TILLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-03
PRIOR PILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                     APPLICANT: Corvae International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Calie E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO SEG ID NOS: 62
LENGTH: 11
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                             0; Gaps
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     Pred. No. 0.0014;
; Mismatches 0; Indels
                                                                                                                                                                                                                                        Sequence 6, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
     Best Local Similarity 100.0%; P
Matches 11; Conservative 0;
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OTHER INFORMATION: D-amino acid
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NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
US-09-909-164-6
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Sequence 49, Application US/09909164
; Sequence 49, Application US/09909164
; Publication No. US20020068702A1
; GENERAL INFORMATION:
; APPLICANT: Coryas International, Inc.
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Brunck, Terence X
; TITLE OF INVENTION NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; FILE REFERENCE: IN01192-US
; CURRENT APPLICATION NUMBER: US/09/909,164
; CURRENT FILING DATE: 2000-07-21
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 62
; SEQ ID NO 49
; LENGTH: 11
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                                                                                           TYPE: PRT
GRANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 96.2%; Score 50; DB 12; Length 11; I Similarity 100.0%; Pred. No. 0.0014; 11; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: 11-mer synthesized according to example
FEATURE:
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NAME/KEY: MISC FEATURE

LOCATION: (6)._(6)

OTHER INFORMATION: norleucine-(CO)
US-09-909-164-49
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LOCATION: (6)...(6)
CTHER INFORMATION: leucine-(CO)
US-09-909-164-48
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                      FEATURE:
NAME/FEX: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 82
EBNGTH: 11
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ORGANISM: artificial sequence
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NAME/KEY: WOD RES
LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
FEATURE:
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity
Matches 11; Conserva
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Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Levy. Gaile E
APPLICANT: Levy. Gaile E
APPLICANT: Levy. Gaile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IND.1192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN OF SEQ ID NOS: 62
SOFTWARE: PATENTIN OF SEQ ID NOS: 62
LENGTH: 11
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Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Novel Pertibes AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-03-03
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
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                                                                    Length 11;
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                                                                                                                  0; Indels
                                                               Query Match 96.2%; Score 50; DB 12; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0
OTHER INFORMATION: D-amino acids IS-09-909-164-10
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (6). (6)
OTHER INFORMATION: valine-(CO)
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ORGANISM: artificial sequence
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OTHER INFORMATION: AMIDATION
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LOCATION: (11)..(:
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96.2%; Score 50; DB 12;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0;
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j OTHER INFORMATION: (8,8)-allothreonine-(CO)
documents.organia.
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COCATION: (6)..(6)
COTHER INFORMATION: propynyl glycine-(CO)
US-09-909-164-52
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OTHER INFORMATION: ACETYLATION
PEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEXY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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                                                                                                               NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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NAME/KEY: MOD RES
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                                                               US-09-909-164-50

Sequence 50, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Enuck, Terence K

TITE OF INVENTION: NOVED PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01199-US
CURRENT RILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: 6/220,101
PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PatentIn version 3.1

SEQ ID NO 50

LENGTH: III
TURNO 50

LENGTH: III
TURNO 50
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Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TITLE OF INVENTION NOVEER: US/09/909,164

CURRENT APPLICATION NUMBER: (0/220,101

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATEMENT NO SI

SEQ ID NO 51

LENGTH: 11

MARGUERIT NO 51
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OTHER INFORMATION: 11-mer synthesized according to example 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (6). T(6); OTHER INFORMATION: 2-amino-butyric acid-(CO) US-09-909-164-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11) (11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: artificial sequence
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Matches 11; Conservative
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US-09-909-164-51
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US-09-909-164-52

i Sequence 52, Application US/09909164

j Sequence 52, Application US/09909164

j Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 52

Lundoff: Ill

MARGUERITANT: Lim-Wilby, Marguerita

MARGUERITANT: Lim-Wilby, Marguerita

MARGUERITANT: Lim-Wilby, Marguerita

SEQ ID NO 52

Lundoff: Ill

MARGUERITANT: Lim-Wilby, Marguerita

MARGUERITANT: Lim-Wilby, Margueritant

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Length 11;
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US-09-09-01-18

Sequence 13, Application US/09909164

Sequence 13, Application US/09909164

Publication No. US2020068702A1

GENERAL IMPORMATION:

APPLICANT: Lim-wilby, Marguerita

APPLICANT: Lim-wilby, Marguerita

APPLICANT: Levy, Odile B

APPLICANT: Evy, Odile B

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TITLE OF INVENTION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 13

LEMSTH: 11

MANTH: 11
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                                                                                                NAME/KEX: MISC FEATURE
COCATION: (6)...(6)
COCATION: (6)...(6)
PEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (9)...(6)
COTHER INFORMATION: D-amino acid
US-09-909-164-12
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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; LOCATION: (8). (9)
; OTHER INFORMATION: D-amino acids
US-09-909-164-13
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
          NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FRATURE:
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NAMEJ/KEX: MOD RES
LOCATION: (11)
OTHER INFORMATION: AMIDATION
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Matches 10; Conservative
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Matches 10; Conservative
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Oddle E
APPLICANT: Levy, Oddle E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: IND139-108
CURRENT APPLICATION NUMBER: US/09/909,164
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTHARE: PATCHIN VERSION 3.1
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
IITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENDE: INJ192-02
CURRENT APPLICATION NUMBER: US/09/909,164
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
LENGTH: 11
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NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
PERATURE:
NAME/KEY: MISC_FEATURE
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Pred. No. 0.0091;
0; Mismatches 1;
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Publication No. US20020068702A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: D-amino acid
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LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
1S-09-909-164-8
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NAME/KEY: MISC_FEATURE
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IS-09-909-164-12
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LENGTH: 11
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Query Match 86.5%; Score 45; DB 12; Length 11; Best Local Similarity 90.9%; Pred. No. 0.015; Matches 10; Conservative 0; Mismatches 1; Indels
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Job time : 34.7333 secs
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NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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) LOCATION: (8)...(8)
) OTHER INFORMATION: D-amino acid
US-09-909-164-11
                                                                                            LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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US-09-909-164-7
US-09-909-164-7
US-09-909-164-7
Sequence 7, Application US/09909164
Publication No. US20020068702A1
Sequence 7, Application No. US20020068702A1
Septembra International
APPLICANT: Corvas International
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FREENT APPLICATION NUMBER: 12003-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LUMBICT PATENT APPLICATION NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
LUMBICT PATENT APPLICATION NUMBER OF SEQ ID NO 7
LUMBICT PATENT APPLICATION NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
LUMBICT PATENT APPLICATION NUMBER OF SEQ ID NO 7
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LUMBICT PAT
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
ITILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IND192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTHARE: Patentin version 3.1
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6) ... (6)
OTHER INFORMATION: norvaline-(CO)
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ORGANISM: artificial sequence
PEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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Pred. No. 0.01
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
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ORGANISM: artificial sequence
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Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)...(11)
CIBER INFORMATION: AMIDATION
US-09-909-164-7
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US-09-909-164-11
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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)M protein - protein search, using sw model

June 3, 2004, 11:35:47; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec tun on:

US-09-909-164-6 52 1 EEVVPXGMSYS 11 litle:

scoring table: sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues searched:

283366 otal number of hits satisfying chosen parameters:

finimum DB seq length: 0 faximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

)atabase :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ription	i e		permease	V1 protein - tobac	DNA segregation AT	hypothetical prote	$\overline{}$	ρ	topoisomerase IV s	DNA-binding protei	hypothetical prote	cell division inhi	probable ABC subst	hypothetical prote	_	hypothetical prote	_		hypothetical prote	beta-ketoacyl-ACP	hypothetical prote	3-phosphoshikimate	cdc37 protein - fi	iron(III) ABC tran	bacteriocin BCN5 -	ATP-dependent DNA	conserved hypothet	1	DNA-directed RNA p
SUMMARIES	e e	T31308	T39116	T40413	A42452	B97355	S57810	T24111	\$22293	H82691	A34203	854619	H69491	C82900	140758	E90544	D69493	C81374	T34536	S75817	T47670	F72281	D82163	T43653	D82352	A30481	AF3286	D87046	3	33
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	Score	. "	37		36	36	35	35	35	33	35	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
	esult No.		7	ო	4	ហ	9	7	80	6		11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	26	27	28	29

hypothetical prote masking protein pr	hypothetical prote transport protein	rho protein GDP-di hypothetical prote	cyclin D2 - rat cyclin D2 - rat	cyclin D2 - mouse cyclin D2 - human	cyclin D1 - Africa cyclin D2 - Africa	cyclin D2 - chicke	cyclin Dl - zebra cyclin D3 - human	cyclin D1 - human
T04456 A38261	E97333 PQ0616	T01457 B72481	JC4011 I58372	A41984 A42822	S57922 S57925	JC4579	562/30 B42822	A38977
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فأف	66	6 6	9 6	9 6	9 6	6	<i>6</i> 6	6
33	32	32	32	333	32	32	328	32
30 31	332	34 35	36 37	8 6 8 8	4 4 1 1	24.	4 4 2 4	45

ALIGNMENTS

T31308

hypothetical 367K protein - Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Accession: T31308
R;Schleper, C; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
Bacteriol. 180, 5003-5009, 1998
A;Title: Genomic analysis reveals chromosomal variation in natural populations of the un-A;Cession: T31308
A;Accession: T31308
A;Accession: T31308
A;Accession: T31308
A;Residues preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-3472 <SCH>
A;Choss-references: EMBL;AF083072; NID:93599393; PID:93599394; PIDN:AAC62699.1
C;Superfamily: Cenarchaeum symbiosum hypothetical 367K protein

ö Gaps ö Query Match 73.1%; Score 38; DB 2; Length 3472; Best Local Similarity 54.5%; Pred. No. 60; Matches 6; Conservative 4; Mismatches 1; Indels

|:|:| |:|:| 2294 EDVIPRGISFS 2304 1 EEVVPXGMSYS 11 ઠે 셤

RESULT 2

probable sulfate permease - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T39116
R;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, November 1999
A;Reference number: Z21829
A;Reference number: Z21829
A;Reference number: Z21829
A;Reference number: Z31829
A;Rocession: T39116
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T494 or MAA
A;Residues: 1-440 cfHUNA
A;Residues: L-440 cfHUNA
A;Residues: Leferences: EMBL:AL132779; PIDN:CABG0015.1; GSPDB:GN00066; SPDB:SPAC869.05c
A;Experimental source: strain 972h-; cosmid c869

C;Genetics: A;Gene: SPDB:SPAC869.05c

A; Map position: 1

Query Match 71.2%; Score 37; DB 2; Length 840; Best Local Similarity 77.8%; Pred. No. 21; Matches 7; Conservative 1; Mismatches 1; Indels

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Gaps

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A;Experimental source: clone R10D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Lycopersicon esculentum (tomato)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Accession: S57810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein R10D12.10 - Caenorhabditis elegans
C.ppecies Caenorhabditis elegans
C.pate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24111
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Reb-1998 #text_change 20-Sep-1999
C;Accession: S22393; I7862
R;Mitchelmore, C; Traboni, C; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: EMBL:U20592, NID:9924625, PIDN:AAA80497.1, PID:9924626
C,Superfamily: plant Kunitz-type proteinase inhibitor
                                                                           Gaps
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Plant Mol. Biol. 28, 691-711, 1995
A;Title: Nature and regulation of pistil-expressed genes in tomato.
A;Reference number: S57808; MUID:95375233; PMID:7647301
A;Accession: S57810
A;Status: preliminary; nucleic acid sequence not shown
    2; Length 1498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%; Score 35; DB 2; Length 225; 54.5%; Pred. No. 13; ive 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RiPercy, C.

Submitted to the EMBL Data Library, October 1996

A;Reference number: Z19842

A;Recession: T24111

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-425 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
Score 36; DB
Pred. No. 63;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB;
Pred. No. 26;
3; Mismatches
    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                        lypothetical protein precursor (clone TPP11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 5
A;Introns: 23/3; 56/3; 113/3; 257/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.3%;
    69.24;
Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 50.0
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1276 EQKIPMGMSY 1285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 DEVVPNGKTYA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 EQIVPGGLQY 344
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                                                                                                                                                           1 EEVVPXGMSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: mRNA
A, Residues: 1-225 < MI
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Best Local S
Matches 5
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                                                                                                                                                                                                                              셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VI protein - tobacco yellow dwarf virus (Sirain Australia)
Cispecies: tobacco yellow dwarf virus
Cispecies: tobacco yellow dwarf virus
Cidate: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
Cidate: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
Riborris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Riborris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - Clos
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                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-877 cLYN-
A;Residues: 1-877 cLYN-
A;Cross-references: EMBL:AL031261; PIDN:CAA20298.1; GSPDB:GN00067; SPDB:SPBC3H7.02
A;Experimental source: strain 972h-; cosmid c3H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA segregation ATPase, FtsK/SpoIIIE family, YUKA B. subtilis ortholog [imported] C.Species: Clostridium acetobutylicum C.Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
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A,Molecule type: DNA
A,Residues: 1-1498 «KUR»
A,Residues: 1-1498 «KUR»
A,Cross-references: GB:AE001437; PIDN:AAK81629.1; PID:g15026814; GSPDB:GN00168
A,Experimental source: Clostridium acetobutylicum ATCC824
C,Genetics:
                                                                                                                                              C;Species: Schizosaccharomyces pombe
C;Date: 0.3-Dec.1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40413
R;Lyne, M; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
A;Reference number: Z21926
A;Accession: T40413
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Pred. No. 22;
1; Mismatches 1; Indels
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                                                                                                                 - fission yeast (Schizosaccharomyces pombe)
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71.2%; 77.8%;

Query Match 71.2 Best Local Similarity 77.6 Matches 7; Conservative

A, Gene: SPDB:SPBC3H7.02 A, Map position: 2

ઠે ద Score 36; DB 2; Pred. No. 3.5; 3; Mismatches

69.2%;

Query Match
Best Local Similarity 60...

A/Accession: A42452 A/Molecule type: DNA A/Residues: 1-102 <MOR>

2 EVVPXGMSYS 11 : | | | | :: | | 7 QVVPSGINYS 16

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Niternate names: Nypothetical protein 02612; hypothetical protein Y01303.3

C.Species: Saccharomyces crevisiae

C.Species: Saccharomyces crevisiae

C.Species: Saccharomyces crevisiae

C.Species: Saccharomyces crevision 01-Sep-1995 #text_change 19-Apr-2002

C.Accession: S54619; S66879

R.de Haan, M., Maares, A.C.; Grivell, L.A.

submitted to the EMBL Data Library, May 1995

A.Reference number: S54617

A.Residues: 1-156 < DEH>
A.Residues: BMBL: 274920; NID:g1420109; PIDN: CAAS9201.1; PID:g1420111; MIPS:YOR01

A.Residues: L.I.Source: strain S288C
                                                                                                     Title: A DNA-binding protein containing two widely separated zinc finger motifs that r
Reference number: A34203, MUID:90169514; PMID:2106471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Residues: 801-1072,'N', 1074-1168,'K', 1170-1225,'V',1227-1434,'N',1436-1607,'I',1609-16
A, Cross-references: GB:WA3019
C,Superfamily: HIV-RP2 enhancer-binding protein
C;Keywords: DNA binding; transcription regulation; zinc finger
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#169491

cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus

C;Spedies: Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999

C;Accession: #66491

R;Xlank, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

F; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
N/Alternate_names: hypothetical protein 02612; hypothetical protein YOL303.3
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Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 1;
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A;Map position: 15R
C;Superfamily: hypothetical protein YOR013w
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2405 WPAGLTYS 2413
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**Molecule type: DNA
**Molecu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chacession: #82691
3.anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
4.Title: The genome sequence of the plant pathogen Xylella fastidiosa.
4.Reference number: A82515; MUID:20365717; PMID:10910347
4.Note: for a complete list of authors see reference number A59328 below
A,Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha A,Reference number: IS8280; MUID:91187610; PMID:1901405
A,Accession: S22293
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; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1.670 cMIT>
A; Residues: 1.670 cMIT>
A; Cresidues: 1.670 cMIT>
A; Cresidues: 1.670 cMIT>
Cresidues: 1.670 cMIT>
Cresidue: 1.670 cMIT>
Cresidu
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Pred. No. 48;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Gaps

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Search completed: June 3, 2004, 11:59:58 Job time: 9 secs
Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Simith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID: 98049343; PMID: 9389475

A;Accession: H69491

A;Refatus: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-252 < KLE>

A;Residues: 1-252 < KLE>

A;Cross-references: GB: AE000970; GB: ABC000782; NID: G2689293; PIDN: AAB899318.1; PID: G264866

C;Superfamily: cell division inhibitor minD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: C82900
A;Status: preliminary
A;Molecule type: DNA
A;Resional 1-54 GLAA
A;Resional Source: GB:AE002133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein 1 - Campylobacter jejuni (fragment)
C.Species: Campylobacter jejuni
C.Species: Gampylobacter jejuni
C.Species: 16-Aug-1996 #text_change 08-Oct-1999
C.Accession: 140788; 847317
R.Hani, E.K.; Chan, V.L.
T.77, 2398-2402, 1995
A.Fitle: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd
A.Fitle: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd
A.Feference number: 140758; MUID:95247673; PMID:7730270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Date: 18-Aug-2000
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a shieference number: A82870
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14;
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55;
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A;Molecule type: DNA
A;Residues: 1-94 <RES>
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Pred. No. 14;
2; Mismatches
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Pred. No. 55;
1; Mismatches
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Best Local Similarity 55.6%;
Matches 5; Conservative
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Best Local Similarity 70.0.
Best Ar 7; Conservative
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26 DIFPSGMSY 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: ABCsbp-5; UU359
A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: 140758
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505 ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C.Species: Mycoplasma pulmonis
A.Stateme number: A99512; MUD:2167165; PMID:11353084
A.Stateme number: A99512; MUD:21267165; PMID:11353084
A.Status: preliminary
A.Status: Preliminary
A.Status: DNA
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homo sapien homo sapien crithidia f human herpe human herpe

saccharomyc rattus norv tomato aspe

tomato aspe escherichia escherichia escherichia

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or.send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=ATCC 25586;

MEDINE=21886394; PubMed=11889109;

MEDINE=21886394; PubMed=11889109;

Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

N. Masleva O., Chu L., Kogan Y., Chaga O., Goltsman B., Bernal A.,

N. Jassen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

Larsen M., Kyrpides N., Overbeek R.;

Romene sequence and analysis of the oral bacterium Pusobacterium

The connem sequence and analysis of the oral bacterium Pusobacterium

The nucleatum strain ATCC 25586.";

U. Bacteriol. 184:2005-2018(2002).

U. CATALYTTC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + 1005phate + L-glutamate + carbamoyl phosphate.

C. - CATALYTA Arginine biosynthesis; first step.

C. - PATHWAY: Pyrimidine biosynthesis; first step.

C. - PATHWAY: Pyrimidine biosynthesis; the small (or glutamine) chain

Dromctos the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).

Salmilarity)
                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
944677 P 944677 P 949616 P 999616 P 999518 P 952544 P 952544 P 952784 E 95671 P 916918 P 916918 P 916918
                                                                                                                                                                                                                                                                                      Pusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
                                                                                                                                                                                                     PRT; 1058 AA
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                                                                                                                                                 AL I GNMENTS
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HAWAP, MF 01210; -; 1.
InterPro; IPR006275; Cara L glu.
InterPro; IPR005483; CPase L.D.
InterPro; IPR005489; CPase L.D2.
InterPro; IPR005480; CPase L.D3.
InterPro; IPR005481; CPase L.D3.
InterPro; IPR005481; CPase L.D.
InterPro; IPR004362; MGS like.
Pfam; PF00289; CPase L. Chain; 2.
Pfam; PF02787; CPSase L.D3; 1.
          ENP3_HUMAN

SS16_HUMAN

SS16_HUMAN

SRIF HSV6Z

SCT1_YEAST

EDD_RAT

VIA_TAV

WHSA_ECOLI

RHSB_ECOLI
  TOLB
                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=76856;
  CARB FUSNN
QBRG86;
  RESULT 1
CARB_FUSNN
  xenopus lae
gallus gall
homo sapien
homo sapien
mus musculu
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clostridium
homo sapien
neurospora
homo sapien
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archaeoglob
campylobact
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clostridium
mus musculu
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vibrio chol
homo sapien
rattus norv
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                                                                       June 3, 2004, 11:32:06; Search time 4.86667 Seconds (without alignments) 117.693 Million cell updates/sec
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P49706
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                          141681 seqs, 52070155 residues
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RL20 MYCPU
YJ49 ARCFU
Y990 CAMJE
CTX3 MOUSE
AROA VIBCH
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CLOPE
MOUSE
HUMAN
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Listing first 45 summaries
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Y1A9_CLOAB
ZEP1_HUMAN
CY14_NEUCR
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                                                     M protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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52
1 EEVVPXGMSYS 11
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Match Length DB
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MOGO V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
BOOLING W., Feat N., Hayles J., Basham D., Bowman S.,
Brocks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Brocks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalyo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
Nutherford K., Rutter S., Sanders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Schoefer M., Mulbert H.,
Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mulbert H.,
A. Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Ber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
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Gaps
                                                                                                                                                                                                                                                                                                                           ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE I (BY SIMILARITY).
MANGANESE I AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.1%; Score 38; DB 1; Length 1058; 60.0%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117451 MW; ED7037AF77C1E39F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
10-CUT-2003 (Rel. 42, Last annotation update)
Probable sulfate permease C3H7.02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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1058
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352
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NCBI_TaxID=4896;
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Best Local Similarity
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ID SULH SCHPO
AC 074377;
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-- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-- SIMILARIIY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
                                                      -1- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.2%; Score 37; DB 1; Length 877; 77.8%; Pred. No. 9.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses, ssDNA viruses, Geminiviridae, Mastrevirus.
NCBI_TaxID=31599;
enome sequence of Schizosaccharomyces pombe."; 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JTL-1993 (Rel. 26, Created)
01-JTL-1993 (Rel. 26, Last sequence update)
01-OTT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 102 AA.
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PIR; T40413; T40413.
GeneDB SPOMDe, SPECIAT, 0.2; --
InterPro; IRR002645; STAS.
InterPro; IRR001902; Sulph_transpt.
PFam; PF01916; Silfate transp; 1.
PFam; PR00916; Silfate transp; 1.
TIGRFAMS; TIGR00815; Silfate transp; 1.
PROSITE; PS0130; SLC26A; 1.
PROSITE; PS0801; STAS; 1.
Transport; Transmembrane.
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es 7; Conserv
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TRANSMEM 1
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AC 211619;
DT 01-JUL-1993
DT 01-JUL-1993
DE 4PDOTH-1993
DE 4PDOTH-1993
DE 7DD-CC 1993
DE 7DD-CC 1993
OC VILLSES; SEL
OC VILLSES; SEL
OC VILLSES; SEL
NX NEBLINE-221
RY SEQUENCE FRC
RY SEQUENCE FRC
RY MEDLINE-221
RA MOTTIS B.A.L
RT 116-CC 941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  small heat shock protein of Closridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
--- SIMILARITY: Contains 2 PtsK domains.
--- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts in positions 76 and 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21359325; PubMed=11466286; MEDLINE=21359325; PubMed=11466286; MeDLINE=21359325; PubMed=11466286; MeDLINE=21359325; PubMed=11466286; MeDLINE=21359325; PubMed=11466286; Medling J., Breton R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.M., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acercbutylicum.";
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sauer U., Duerre P., "-------""Sequence and molecular characterization of a DNA region encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                             Score 36; DB 1; Length 102;
Pred. No. 1.6;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                              102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein CAC3709.
CAC3709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1498 AA
                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE OF 1-108 FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; PubMed=8501044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE007866; AAK81629.1; -.
EMBL; X65276; CAA46379.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                              -..; A42452; A42452.
InterPro; IPR002621; Gemini mov.
Pfam; PF01708; Gemini mov.
Hypothetical protein
                                                                                                                                                                                                                                                                                                   69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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7 QVVPSGINYS 16
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PIR; B97355; B97355. InterPro; IPR002543; FtsK_SpoIIIE.

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01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
2inc finger protein 40 (Human immunodeficiency virus type I enhancer-
binding protein 1) (HIV-EP) (Major histocompatibility complex binding
protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1."; Biochemistry 31:3907-3917(1992).

Biochemistry 31:3907-3917(1992).

FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE 5'-GGGACTTTCG-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SY40, CWY, OR HIV1. IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MAC, INTERPEBEINIA SECRETOR, AND INTERFERON-BETA GENES: IT MAY ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 2113-2142.
MEDITME-SUGG4333; PubMed=2248949;
MEDITME-SUGG4333; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
Gronenborn A.M.;
"High-resolution three-dimensional structure of a single zinc finger
"High-resolution three-dimensional protein in solution.";
Biochemistry 29:9324-9334(1990).
                                                                                                                                                                                                   Gaps
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- SUBGRIGHTA.

- SUBGRIGHTA.

- INDUCTION: By mitogens and phorbol ester.

- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH ZINC-FINGER IN-BETWEEN.

- SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=90169514; PubMed=2106471;
Fan C.M., Maniatis T.;
"A DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92222684; PubMed=1567844; Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E., Gronenborn A.M.;
                                                                                                                                                                                                   ö
                                       Complete proteome; Repeat
                                                                                                                                                       Score 36; DB 1; Length 1498;
Pred. No. 27;
2; Mismatches 2; Indels
Pfam, PF01580; Ft8K_SpoIIIE; 2.
PROSITE; PS50901; FTSK; 2.
Hypothetical protein; ATP-binding; Complete proteome; Rep DOMAIN 655 857 FTSK 1.
POMAIN 1001 1188 FTSK 2.
NP BIND 675 682 ATP (POTENTIAL) .
SEQUENCE 1498 AA, 168968 MW; FF42037A335A9649 CRC64;
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                                                                                                                                                         69.2%;
                                                                                                                                                         Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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1276 EQKIPMGMSY 1285
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HIVEP1 OR ZNF40.
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P15822;
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SEQUENCE FROM N.A.
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TRANSMEM
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A10A_HA
A10A_HA
A10A_HA
DT 30-MAY
DT 28-FBB
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SEQUENCE FROM N.A.
MEDLINE=91129256; PubMed=1825178;
Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recognition
"Nucleotide sequence, the structural gene for sulfate permease II in
elements of cys-14, the structural gene for sulfate permease II in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROBABLE REVISIONS.
MEDIINE-S4188926. Pubmed-8140616;
Sandal N.N., Marcker K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
                                                                                                                                                                                                             MIM, 194540; -.

GO; GO:0005634; C:nucleus; TAS.

GO; GO:0003677; F:DNA binding; TAS.

InterPro; IPRO07087; ZIC (2H2.

Ffam; PF00036; zf-C2H2; S.

SMART; SM00355; ZnF (2H2; 4.

PROSITE; PS00028; ZINC FINGER (2H2.1; 4.

PROSITE; PS00028; ZinC FINGER (2H2.2; 4.

Transcription regulation; ZinC-finger; Metal-binding; DNA-binding;

Nuclear protein; Repart; 3D-structure.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%; Score 35; DB 1; Length 2717; 66.7%; Pred. No. 80; ive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          C2H2-TYPE.
C2H2-TYPE (POTENTIAL).
C2H2-TYPE.
C2H2-TYPE.
POLY-SER.
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01-NOV-1995 (Rel. 32, Last sequence update)
11-OCT-2003 (Rel. 42, Last annotation update)
Sulfate permease II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                      EMBL; X51435; CAA35798.1; -.
PIR; A34203; A34203.
PDB; 3ZNF; 15-7AN-92.
PDB; 4ZNF; 15-7AN-92.
PDB; 1BBO; 31-0CT-93.
TRANSFAC; T00497; -.
Genew; HGNN:4920; HIVEP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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2405 VVPAGLTYS 2413
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Matches 6; Conserv
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P23622;
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permease II and a putative human tumour suppressor.";
Trends Biochem. Sci. 19:19-19[1994].
-!- FUNCTION: UPTAKE OF SULFATE INTO THE CELL.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- INDUCTION: Highly expressed, but only in cells subject to sulfur limitation, and it is turned on by the positive-acting Cys-3 sulfur regulatory protein.
-!- MISCELLANBOUS: SULFATE PERMEASE II IS MAINLY FOUND IN MYCELIA.
-!- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDILINE-1225279; Pubmed=11326269;

Meguro M., Kaehiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S., Oshimura M.;

Mitsuya M.,

Mitsuya M.
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N-LINKED (GLCNAC. ..) (POTENTIAL).
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 36;
2; Mismatches 1; Indels
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4FC604B60798CE77 CRC64;
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Edan, PR00916; Sulfate transp; 1.
TICRPAMS: TICR00815; BILP; 1.
PROSITE; PS01130; SLC26A; 1.
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PIR; A37956; A37956.
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788 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY029564, ARX33100.1;
AY029487; ARX33100.1; JOINED.
L; AY029489; ARX33100.1; JOINED.
L; AY029489; ARX33100.1; JOINED.
L; AY029491; ARX33100.1; JOINED.
L; AY029491; ARX33100.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB051358; BAB47392.1; -.
                                                                                                                                                                                                                                         SEQUENCE OF 337-1499 FROM N.A.
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EMBL;
EMBL;
EMBL;
EMBL;
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PERNTS; PRO0702; Hydrolary L. PRINTS; PRO0119; CATATPASE.
PRINTS; PR00119; CATATPASE.
TIGRRAMs; TIGRO1652; ATPASE P-type; 6.
PROSITE; PS00154; ATPASE EL E2; 1.
Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding; Multigene family.

1 86 CYTOPLASMIC (POTENTIAL).
TRANSMEM 87 106 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004012; F:phospholipid-translocating ATPase activity; NAS.
GO; GO:0008360; P:regulation of cell shape; NAS.
InterPro; IPRO0539; AIPase E1-E2.
InterPro; IPRO0539; AIpase.
InterPro; IPRO05834; Hydrolase.
                                         MIM; 605855; -.
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           EMBL;
EMBL;
EMBL;
              OD RANGO DE 
                                                                                                                                                                                                                                                                                                      Straubberg R.L., Feingrald E.A., Grouse L.H., Derge J.G.,

Klausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Babat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F. S.

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheferz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Du X., Gibbs R.A.,

Kachards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and mouse cDNA sequences",

Ill Mman and mouse cDNA sequences",

Ly Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
MEDLINE=21313119; PubMed=11353404;
Herzing L.B.K., Kim S.-J., Cook B.H. Jr., Ledbetter D.H.;
"The human aminophospholipid-transporting ATPase gene ATPIOC maps adjacent to UBE3A and exhibits similar imprinted expression.";
Am. J. Hum. Genet. 68:1501-1505(2001).
                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932;
                                                                                                                                          Am. J. Hum. Genet.
[3]
SEQUENCE FROM N.A.
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HGNC:13542; ATP10A

. 0 Score 34; DB 1; Length 1499; Pred. No. 70; 0; Mismatches 3; Indels (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update) PRT; 116 AA 65.4%; Local Similarity 72.7 les 8; Conservative 469 EEVVPRGGSVS 479 STANDARD; 1 EEVVPXGMSYS 11 RESULT 8
RL20 MYCPU
ID RL20 MYCPU
AC Q98QV0;
DT 28-FEB-2003 (0)
DT 28-FEB-2003 (0)
DT 28-FEB-2003 (0) Query Match Best Loca Matches g

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Gaps

CYTOPLASMIC (POTENTIAL).
PHOSEPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).

EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASTIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).

POTENTIAL. CYTOPLASMIC (POTENTIAL).

POTENTIAL

POTENTIAL. PYTRACELLULAR (POTENTIAL).

86 106 110 128 309 332 362 1108

DOMAIN TRANSMEM DOMAIN TRANSMEM

TRANSMEM

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EXTRACELLULAR (POTENTIAL)

POTENTIAL. CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.

POTENTIAL.

388 Q -> R (IN RBF. 4). AA; 167687 MW; D4996A4D0635A6BD CRC64;

388 1499

CONFLICT

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us-09-909-164-6.rsp

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  Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McKell L.K., Badger J.H., Glodek A., Zhou L., Coverbeek R., Gocarne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Wenson T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=NCTC 11168;
MEDLINE=20150912; PubMed=10688204;
Parkhill J., Wen B.W., Mungall K., Ketley J.M., Churcher C.,
Parkhill J., Wen B.W., Mungall K.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rafandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
                                                                                                                                                                           "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 160-253 FROM N.A.
STRAIN=ATCC 43431 / TGH 9011;
MEDLINE=95247673; PubMed=7730270;
Mail E.K., Chan V.L.,
"Expression and characterization of Campylobacter jejuni
benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%; Score 33; DB 1; Length 165; 60.0%; Pred. No. 12; tive 1; Mismatches 3; Indels
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BMEL; AEONOS68; AAB89307.1; -.
FIRS; D69493; D69493.
TIGR; A71949; -.
Hypothetical protein; Transmembrane; Complete proteome.
Typothetical protein; Transmembrane; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 403:665-668(2000)
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Y990_CAMJE
ID Y990_C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                            Mycoplasma pulmonis.",

Nucleic Acids Res. 29:2145-2153(2001).

-!- FUNCTION: This protein binds directly to 23s ribosomal RNA and is necessary for the in vitro assembly process of the 50s ribosomal subunit. It is not involved in the protein synthesizing functions of that subunit (By similarity).

-!- SIMILARITY: Belongs to the L20P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                        STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
Chamband I., Heilig R., Ferris S., Barbe V., Samson D., Galisson Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
                                                                                                                                                                                                                                                                                                The complete genome sequence of the murine respiratory pathogen
508 ribosomal protein L20.
RPLT OR MYPU-2610.
Wycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
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PIR; E90544; B90544.

MypuList; MYPU 2610; -

HAMAP; MP 00382; -1 1.

InterPro; IPR005813; Ribosomal_L20.

InterPro; IPR005812; Ribosomal_L20.

Profin; PP00453; Ribosomal_L20, 1.

PRINTS; PR00062; RIBOSOMALL20.

Profin; PR00062; RIBOSOMALL20.

Profin; PR0001389; L20; 1.

RIBOSOMAL L20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
8.1;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein AF1949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%; Score 33; DB 77.8%; Pred. No. 8.1; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMSYS 11
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                    NCBI_TaxID=2107;
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ID YJ49 ARCFU
AC O28330;
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Query Match

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Gaps

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AROA VIBCH
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VARSPLIC
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
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AROA_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOTALINGE TROWN (ISOPORMS 1 AND 2).

ENGURNEE FROM M.A. (ISOPORMS 1 AND 2).

STRAIN=C57BL/6J; TISOPORMS 1 AND 2).

STRAIN=C57BL/6J; TISOPORMS 1 AND 2).

KRAWAI J., Shinagawa A., Shibata K., Yoohino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Kondo B., Yamanaka I., Arakawa T., Grazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Asdota K., Matsuda H., Kondo S., Yamanaka I., Radota K., Matsuda H., Rabulama W., Gasaferland T., Gasaic C., King B., Kochiwa H., Fleischmann W., Gasaferland T., Gissi C., King B., Kochiwa H., Rubil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner I., Washio T., Sakai K., Okido T., Furuno W., Aono H., Baldarelli R., Barsh G., Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H. Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Ratch B., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Havsahizaki W., Kawaji H., Kohtsuki S., Havsaki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Mammary fibroblast;
MEDLINE-22188257; PubMed=12477932;
Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,
Altschul S.E., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jorden H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                     63.5%; Score 33; DB 1; Length 253; 55.6%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                           Hypothetical protein, Complete proteome.
SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTX3_MOUSE STANDARD; PRT; 280 AA. Q9D387; Q9CXQ4; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT_2003 (Rel. 42, Last annotation update) C200RF103.
                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                     EMBL; AL139076; CAB73246.1; -. EMBL; Z36940; CAA85392.1; -. PIR; C81374; C81374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: | ||||
185 DIFPSGMSY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.
                                                                                                                                                                                                                                                                                                                                          Query Match
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CTX3 MOUSE

CTX3 MOUSE

CTX3 MOUSE

TX 28-FEB

TX 10-OCT

TX 10-OC
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=09D387-2; Sequence=VSP 003820;
-!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
in positions 174 and 239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
29-FEB-2003 (Rel. 41, Last annotation update)
29-Phosphoshikimate 1-carboxyvinyltransferase (BC 2.5.1.19) (5-enclpyruvylshikimate-3-phosphate synthase) (BPSP synthase) (BPSP).
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Mithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.

YOTOPLASHIC (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL)
N-LINKED (GLCNAC. ...) (POTENTIAL)
N-LINKED (GLCNAC. ...) (POTENTIAL)
N-LINKED (GLCNAC. ...) (POTENTIAL)
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Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E -> V (IN REF. 1; BAB31124).

Q -> P (IN REF. 1; BAB31124).

P -> A (IN REF. 1; BAB31124).

F FALID/BF9FDSCCEF CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN C200RF103 HOMOLOG.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform 2). /FTId=VSP 003820.
                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fransmembrane; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 20;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isold=Q9D387-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AK014127; BAB29169.1; -.
EMBL; AK018222; BAB31124.1; ALT_FRAME.
EMBL; BC004791; AAH04791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1920368; 3110035N03Rik.
MGD; MGI:1923411; 6330527006Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 230 Q
238 238 P
280 AA; 31721 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n 63.5%;
Similarity 75.0%;
6; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 VTPAGMSY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMSY 10
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholerae.
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[1]
SEQUENCE FROM N.A.
SECRINE SI TOX N16961 / SETOTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gall S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
MCDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HSP90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 406:477-483 (2000).
-!- CATALVIIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.
-!- PATHWAY: Arcmatic amino acids biosynthesis; shikimate pathway; sixth step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGN, VC172; -...
HAWAP; MF 00210; -; 1.
InterPro; IPR000264; AroA.
InterPro; IPR000266; EPSP synth.
Pfam; PF00275; EPSP synthase; 1.
ProDom; P0010467; EPSP-syntase; 1.
TIGRFAMS; TIGR01365, AroA; 1.
PROSTITE; PS00085; EPSP SYNTHASE 1; 1.
PROSTITE; PS00885; EPSP SYNTHASE 2; 1.
Aromatic and biosynthasis; Transferase; Complete proteome. SEQUENCE 426 AA; 46101 MW; 38852D6483BFEIG3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Westwood P.K., Preston N.C., Fantes P.A.; "Schizosaccharomyces pombe cdc37 gene."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBMIT: Monomer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-1- SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
MCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE004251; AAF94882.1; -. PIR; D82163; D82163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 60.0
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CC37 SCHPO
ID CC37 SCHPO
AC 094740;
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                                     EXUANDE FROM N.A.

REALINE-1948,

REALINE-1948,

REALINE-1948,

REALINE-1948,

ROOD V., GWILLIAM R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,

RA SGOURO J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA SGOURO J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA GOLLINE M., COMNOR S., COMILIANGWORTH T., CHURCHAR C.M.,

RA HOLYONG S., HORTHADIA N., Harris D., Hidalgo J., Hodgson G.,

RA HOLYONG S., HORTHADY J., HOWSTER E.J., Hunt S., Jagels K.,

A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA MOONEY P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA JOHVER K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Relton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Skelton J., Volckaert G., Aert R., Robben J., Grymonprez B.,

ROOGWARD J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Reltjens I., Volckaert G., Aert R., Robben J., Grymonprez B.,

Reltjens I., Volckaert G., Herrs C., Holzer E., Meetl D., Hilbert H.,

RA Gorge M., Firze C., Holzer E., Meetl D., Hilbert S.,

RA Golfean A., Cadieu B., Dreano S., Gloux S., Lelaure V., Motter S.,

RA Golfean A., Revuelta J.L., Moreno S., Armetrong J., Foreburg S.L.,

RA Lucas M., Rochet M., Gaillardin C., Rancer M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armetrong J., Foreburg S.L.,

RA Dominguez A., Revuelta J.L., Moreno S., Armetrong J., Foreburg S.L.,

RA Depakowski G.V. Ussery D., Barrell B.G., Nurse P.,

RA Shpakovski G.V. Ussery D., Barrell B.G., Nurse P.,

RA The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.

MEDLINE=22745456; PubMed=12861001;
Tatebe H., Shlozaki K.;

"Identification of cdc37 as a novel regulator of the stress-responsive mitogen-activated protein kinase.";

Mol. Cell. Biol. 23:5132-5142(2003).

-! FUNCTION: Co-chaperone that binds to numerous kinases and promotes their interaction with the Hsp90 complex, resulting in stabilization and promotion of their activity.

-! SUBUNIT: Forms a complex with Hsp90. Interacts with sty1.

-! SUBCELLULAR LOCATION: Unclear, and cytoplasmic. When in the nucleus associated with chromatin.

-! SIMILARITY: Belongs to the CDC37 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gарв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ132377; CAB38758.1; -.
EMBL; AJ132376; CAB38757.1; -.
EMBL; AJ132376; CAB38757.1; -.
EMBL; AJ132376; CAB38757.1; -.
EMBL; AJ132376; CAB42371.2; -.
GeneDB SPombe; SPBC9B6.10; -.
InterPro; IPR004918; Cdc37.
Pfam, PF03234; Cdc37.
CABPECODE, Cell dision; Cell cycle; Nuclear protein.
SEQUENCE 466 AA; 52554 MW; 647238B34CABB3C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 50.0
Matches 5; Conservative
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[2]
SEQUENCE FROM N.A.
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RESULT 14

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BCNS_CI
P08696;
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BCNS_CLOPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Straubberg R.L., Feingrold E.A., Grouse L.H., Derge J.G.,
Riduaner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Babat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Raplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Moorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Generch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S., Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: Interacts with HSV-1 early proteins ICP22 and ICP0.
-!- SUBCELLUIAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Expressed at high levels in heart and pancreas, moderate levels in placenta, liver, skeletal muscle, and kidney, and low levels in brain and lung.
-!- SIMILARITY: Belongs to the GITSCR2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99214318; PubMed=10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins IC22 and IC70 is modified in a cell-type-specific manner and is recruited to the nucleus after
                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE-20174430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanaxajasingam U.,
Portier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.;
A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
GSR2_HUMAN STANDARD; PRT; 478 AA.
QSNZMS; QSBTC6; QSHAX6; QSNPP1; QSNRR4; Q9UF12;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glicma tumor suppressor candidate region gene 2 protein (p60).
GLTSCR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 12-478 FROM N.A.
Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                       Genomics 64:44-50(2000).
                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                      R -> Q.

(FTIG=VAR. 011486.

GGS -> HEG (IN REF. 2; AAH04229).

G -> R (IN REF. 3).

RRKEGLWEKTAKOGELPREVRRAQARLINDSATRAKPGPQD

RYERD -> SGRSSYGRSWPERASPGGAQGPSPVAQPFCN

KGPNTAPGHALAA (IN REF. 3).

SDNPLDRPLVGQDEFFLE -> INNPDKPVVWPGCLFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                             (IN REF. 3).

- S (IN REF. 2; AAH04229).

D - H (IN REF. 3).

PEGNILRDRFKSFQRRNMIEPRERAKFKRYKVKLVEKRAF

REQ - VLTVSCRGAPCPVMTPSLLPVPPRGYGRHHGCP

WAGPVGPMPG (IN REF. 5).

EGNILRDRFKSFQRRNMIEPRERAKFKKYKVKLVEKRAFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garnier T., Cole S.T.; "Complete and genetic organization of the "Complete nucleotide sequence and genetic organization of the bacteriorinogenic plasmid, plP404, from Clostridium perfringens."; plasmid 19:134-150(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CPN50;
MEDLINE-87055/020; PubMed=2877971;
Garrier I., Cole S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIQL -> RGQHSFETGSRAFRGGI (IN REF. 7F18923E348CB52B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid p1P404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 1; Length 478;
Pred. No. 35;
1; Mismatches 3; Indels
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(Rel. 06, Last sequence update)
(Rel. 30, Last annotation update)
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                                                                                                                                                                                                                                                                     30; GO:0005622; C:intracellular; NAS.
                                                                              EMBL, AF182076, AAF62873.1, --
EMBL, BC004229; AAH04229.1, --
EMBL, BC0100951, AAH06311.1, --
EMBL, BC010095, AAH10095.1, --
EMBL, AF256124, AAG30413.1, --
EMBL, AL359335, CAB94786.1, --
EMBL, AL329336, CAB94786.1, --
EMBL, AL122063; CAB59422.1; --
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MEDLINE=88336297; PubMed=2901768;
                                                                                                                                                                                                                                                                                      Nuclear protein; Polymorphism.
VARIANT 389 389 R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478 AA; 54417 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%;
                                                                                                                                                                                                                      Q9NZMS; HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.00,
                                                                                                                                                                                                                                   Genew; HGNC:4333; GLTSCR2
MIM; 605691; -.
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417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel.
01-OCT-1994 (Rel.
Bacteriocin BCN5.
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417
433
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                                                                   SEQUENCE OF 1-14 FROM N.A.
STRAIN=CPNSO;
MEDLINE=89039249, PubMed=2460717;
Garnier T., Cole S.T.;
"Studies of UV-inducible promoters from Clostridium perfringens in viro.";
Mol. Microbiol. 2:607-614(1988).
-!- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
-!- INDUCTION: By UV irradiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.5%; Score 33; DB 1; Length 890; 66.7%; Pred. No. 67; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN 815 869 HYDROPHOBIC.
SEQUENCE 890 AA, 96699 MW; F4E5E8971C31C6C6 CRC64;
perfringens and molecular genetic analysis of the bacteriocin-encoding gene. ", J. Bacteriol. 168:1189-1196 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M14481; AAA98248.1; -
EMBL; M32882; AAA98249.1; -
PIR; A30481; A30481.
Interpro; IPR000834; Peptidase M14.
Interpro; IPR003646; SH3 bac.
Pfam; PF00046; Zn carbopept; 1.
SMART; SM00287; SH3b; 3.
Antibiotic; Bacteriocin; Plasmid, DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 66.7
Matches 6, Conservative
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Search completed: June 3, 2004, 11:49:50 Job time : 4.86667 Becs

2 EVVPXGMSY 10 |||| :| 170 EVVPGGPTY 178

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Q9bh83 plasmodium Q9bh83 plasmodium Q9bh85 plasmodium Q81587 plasmodium Q81587 plasmodium Q81587 plasmodium Q01487 rattus ratt Q01487 rattus ratt G01487 rattus ratt G01472 homo sapien Q1479 saccharomyc Q97182 sulfolobus Q28md rhizobium Q95mul homo sapien Q96my homo sapien Q98my homo sapien Q87kg candidatus Q87kg candidatus Q88kg candidatus Q786m homo sapien Q98my homo sapien Q98my homo sapien Q87kg candidatus Q88kg candidatus Q88kg candidatus Q88kg candidatus lae Q7852 synechococc
homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-2225144; PubMed=12240834;
A MEDLINE-22255144; PubMed=12240834;
A Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., A Matanabe A., Iriguothi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
T. Complete genome structure of the thermophilic cyanobacterium DNA Res. 9:123-130(2002).
E. EMBL, APPOS374; BAGO9170.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
R GO; GO:0005476; F:transporter activity; IEA.
R InterPro; IPR0014764; HALI.
R InterPro; IPR0014764; HALI.
R Pfam; PF00873; ACR_tran; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113205 MW; 00E9C13F0F636D2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria: Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                      Q81587
Q01487
Q8PMI6
Q8PAT2
Q9PDM6
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Q8G415
Q8XT05
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Q9PQD2
Q7UWU7
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Q8TX62
Q8PPP5
Q8VUA8
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O28342
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Q8IYM3
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QBRE56
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Q7U552
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TIGREAMS; TIGR00915; 2A0602; 1.
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TLL1618.
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Best Local Similarity 63.6
Matches 7; Conservative
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SEQUENCE 1044 AP
01-MAR-2003
01-MAR-2003
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QBDIHO
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QBDIH0
ACT THE TENT OF TH
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Q815a7 bacillus ce
Q98fx1 rhizobium 1
O74056 cenarchaeum
Q9ury8 schizcaacch
Q8ewd4 mycoplasma
Q81126 mus musculu
Q8btx4 mus musculu
Q8btx4 mus musculu
Q8btx9 mus musculu
Q8btx9 peudomonas
Q40129 lycopersico
Q7v6q4 prochloroco
Q7v6q4 prochloroco
Q7v6q4 prochloroco
Q9vx4 caenorhabdi
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116.206 Million cell updates/sec
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                                                                                                    June 3, 2004, 11:35:06 ; Search time 29.8667 Seconds
                                                                                                                                                                                                                                                                                                  1017041
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Q815A7
Q98FX1
Q7056
Q9URY8
Q8EWD4
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Q7V6Q4
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Gapop 10.0 , Gapext 0.5
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sp_phage:*
sp_plant:*
sp_rodent:*
sp_vront:*
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sp_unclassified:*
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9p_archea:*

9p_bacteria:*

9p_fungi:*

8p_human:*

9p_nmmmal:*

9p_mammal:*
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1 EEVVPXGMSYS 11
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Match 1
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Maximum DB seq
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Perfect score:
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SEQUENCE FROM N.A.
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Q9URY8
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MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Kanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22608415; PubMed=12721630; Rapleron N., Candelon B., Raplare N., Sorokin A., Anderson I., Galleron N., Candelon B., Raplaral V., Bhatcacharya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Maur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N.; Grechkin Y., Kyrpides N.; Gereus and comparative analysis with Bacillus anthracis."; Mature 423:87-91(2003).

BMEL, AB017015; AAP12123.1; -.. BMEL, AB017015; AAP12123.1; -.. BMEL, PS00011; PROMAR_LIPOPROTEIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriacae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                          Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=226900;
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EMBL, AP003002; BAB50445.1; -.

GO; GO:0016787; F:hYdrolase activity; IEA.

GO; GO:0008237; F:metallopeptidase activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR002933; Peptidase_M20.
                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter substrate-binding protein.
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Last annotation update)
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01-0CT-2001 (TrEMBLrel. 18,
01-JUN-2003 (TrEMBLrel. 24,
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Matches 6; Conservative
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843 EEVLPNGIGYS 853
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152 EEIAPLGLSY 161
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1 EEVVPXGMSYS
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Q98FX1;
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"Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";

J. Bacteriol. 180:5003-5009(1998).

EMBL; AF083072; AAC62699.1; -.

EMBL; AF08307; AAC62699.1; -.

EMBL; AF08307; Firmansporter activity; IEA.

GO; GO:0005215; Firmansporter activity; IEA.

GO; GO:0005810; Pransport; IEA.

InterPro; IPR000515; BPD_transp.
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Cenarchaeum.
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STRAIN=972h-;
Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
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                                                                                              / Match 13.1%; Score 38; DB 16; Length 387; Local Similarity 60.0%; Pred. No. 15; Local Similarity 60.0%; Pred. No. 15; Indel8 6; Conservative 2; Mismatches 2; Indel8
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54.5%; Pred. No. 1.7e+02;
ive 4; Mismatches 1; Indels
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Pfam; PF01546; Peptidase M20; 1.
Hydrolase; Complete proteome.
SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
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Bukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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SMART; SM00320; WD40; 2.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
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01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein.
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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2294 EDVIPRGISFS 2304
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hes 6; Conservative
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367 DEAIPHGMSY 376
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Gaps

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SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
THe FANNE Consortium,
the RINEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I annotation of
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                         Score 36; DB 11; Length 471;
Pred. No. 51; 2; Indels
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 20, Last sequence update) Similar to glioma tumor suppressor candidate region gene 2. GLISCR2 OR AWS36441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 53;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                              Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025810; AAH25810.1; -.
MGD; MGI:2154441; G1tscr2.
Hypothetical protein.
NON TER
SEQUENCE 471 AA; 54506 MW; E0DA685C374A9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
EMBL, BC017637, AAH17637.1; -.
MGD, MGI:215441, G116622.
SEQUENCE 464 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             484 AA.
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Q8VD18 PRELIMINARY; PRT; Q8VD18; 01-MAR-2002 (TrEMBLrel. 20, Created)
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                                                                                                                                                                                                69.2%;
                                                                                                                                                                                Query Match
Best Local Similarity 60.0°
-hag 6; Conservative
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Best Local Similarity 60.0°
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226 EVIPAGASYN 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Salivary gland,
Strausberg R.;
                                                                                                                                                                                                                                                              2 EVVPXGMSYS 11
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                                SEQUENCE FROM N.A.
TISSUE=Liver;
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     NCBI_TaxID=10090;
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GLTSCR2.
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Q8BTX4
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Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an
intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
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                                                                                                                                                                                                                                               Score 37; DB 3; Length 840;
Pred. No. 59;
                                                                                                                                                                                                                                                                              1; Indels
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132779; CAB60015.1; -.
                                                                                                                                                                                                               93517 MW; ED4833E162B69077 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 21, Last sequence update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                             PRT; 1123 AA
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                                                                                                                                                                                                                                                                              1; Mismatches
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InterPro; IPR009895; ConA.like_lec_gl.
InterPro; IPR00136; Lipoprotein_17.
Pfam; PF04200; Lipoprotein_17; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TEMBLEEL 23,
01-OCT-2003 (TEMBLEEL 25,
MYPE 2560 paralog, 57%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.0.
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SEQUENCE 1123 A
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"Role of mobile DNA in the evolution of vancomycin-resistant
                                                            EMBL; AE016947; AA079943.1; -.
TIGR; EF0063; -.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000437; Prok lipoprot_S.
InterPro; IPR00914; SEP_bac_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1399 AA
                                                                                                                                                                                                Pfam, PF00496; SBP_bac_5; 1.—
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
COMPLETE PROCEOME.
SEQUENCE 559 AA; 61476 MW; CC15418D3:
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                        Enterococcus faecalis.";
Science 299:2071-2074(2003).
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Best Local Similarity 66.,
6, Conservative
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581 QVVPAGLSY 589
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SEQUENCE FROM N.A.
MEDLINE=25354681, TISSUE=Pituitary;
MEDLINE=25354681, PubMed=1246681;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analyze of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
BMBL; AK077741; BA256760.1; -.
SEQUENCE 484 AA; 55792 MW; EB67949BCBE92D44 CRC64;
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STRAIN=V583 / ATCC 700802;
MEDLINE=22550657; PubMed=12663927;
MEDLINE=22550657; PubMed=12663927;
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kôlonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
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Enterococcus faecalis (Streptococcus faecalis).

Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

NCBL TaxID=1351;
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                                                                                                                                   69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 24, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
                                                                                                                                                                                    2; Indels
                     Nature 420:563-573 (2002).

EMBL, AR088461; BAC40357.1; -.

MGD; MGI 2154441; G1tscr2.

SEQUENCE 484 AA; 55806 MW; B3056425B5EECAD8 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                              484 AA
                                                                                                                                                                                 2; Mismatches
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  60,770 full-length cDNAs.";
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                           Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                             239 EVIPAGASYN 248
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                                                                                                                                                                                                                               2 EVVPXGMSYS 11
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                                                                                                                                        Query Match
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Q839T9
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STRAIN=DC3000;

AB Buell R. Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,

Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,

Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,

Berry K., Utterback T., Van Aken S., Kolonay J., Madupu R., Daugherty S.,

Brinkac L., Beanan M., Haff D., Selengut J., Nelson W., Davidsen T.,

Mhite O., Fraser C., Collmer A., Kolonay J., Madupu R., Davidsen T.,

White O., Fraser C., Collmer A., Kolonay J., Nelson W., Davidsen T.,

White O., Fraser C., Collmer A., Kolonay J., Nelson W., Davidsen T.,

White O., Fraser C., Collmer A., Kolonay J., Nelson W., Davidsen T.,

Brinkac L., Beanan M., Haff D., Selengut J., Nelson W., Davidsen T.,

Micoplete sequence of Pseudomonas syringae.";

EMBL, AEO16858; AAO54162.1;

BREJ, AEO16858; AAO54162.1;

CO, GO:000530; P: Transcription; IEA.

GO, GO:000530; P: Transcription; IEA.

GO, GO:000530; P: Transcription; IEA.

GO, GO:000530; P: Transcription; IEA.

CO, GO:000530; P: Transcription; IEA.

BRITERPRO; IPRO0706; RNA_DOL_Rpbl. 3.

InterPro; IPRO07081; RNA_DO
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01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OTN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DNA-directed RNA polymerase, beta' subunit.
RPOC OR PSPTOGE20.
Pseudomonas syringae (pv. tomato).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales;
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Pred. No. 1.7e+02;
2; Mismatches 1; Indels
                                                                                                  Query Match
69.2%; Score 36; DB 16; Length 559;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 1; Indels
559 AA; 61476 MW; CC15418D33D53DE7 CRC64;
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Best Local Similarity
Matches 6; Conserva
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Q9XVK4
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                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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MEDLINE-22825698; PubMed=12917642;
MEDLINE-22825698; PubMed=12917642;
Macoap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Sreglich C., Sullivan M.B., Ting C.S., Tolonen A.,
"Genome divergence in R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-007-2003 (TrEMBLrel. 25, Created)
01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLRel. 25, Last smotation update)
Phospholipid and glycerol acyltransferase (From 'motifs_6.msf').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                      Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.3%; Score 35; DB 10; Length 225; 54.5%; Pred. No. 37;
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EMBL; BX572098; CAE21267.1,.
ACYLtransferase; Transferase; Complete proteome.
SEQUENCE 245 AA; 26907 NW; 106F7C4CBE2C6427 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN 21 225 UNKNOWN.
SEQUENCE 225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein precursor.
Lycopersicon esculentum (Tomato)
                                                                      225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 AA
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PROSITE; PS00283; SOYBEAN KUNITZ; 1.
Hypothetical protein; Signal.
1 20
SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=V876; TISSUB=Pistil;
MINISHS=95375233; PubMed=7647301;
Milligan S.B., Gasser C.S.;
"Nature and regulation of pistil-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 54.5.
Thes 6; Conservative
                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                        NCBI_TaxID=4081;
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Caemorhabditis elegans.
Bukaryota, Matazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caemorhabditis.
NCBI_TaxID=6239;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR00019; Prot kinase.
Probom; PF00069; pkinase; 1.
Probom; PF00061; Prot kinase; 1.
Probom; ES50011; Prot kinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0%; Pred. No. 75;
Matches 5; Conservative 3; Mismatches 2; Indels
                            2; Indels
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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60.0%; Pred. No. 41;
tive 2; Mismatches
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology,";
Science 282:2012-2018(1998).
EMBL; Z81109; CAE03241.1; -.
PIR; T24111; T24111.
                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25, R10D12.10 protein.
                         6; Conservative
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                                                                    2 EVVPXGMSYS 11
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
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                                                          Abb80542 Abb80543 Abb80538 Abb80538 Abb80539 Abb80540 Abb80549 Abb80549 Abb80544 Abb80544 Abb80556 Abb80556 Abb80557 Abb80556 Abb80557 Abb
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Abb80553 B
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ABB80552
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ABB80536
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   Misc-difference
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ABB80523
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Abb80527 Hepatitis
Abb80537 Hepatitis
Abb80541 Hepatitis
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Abb80559 Hepatitis
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67.664 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Result No.

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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                  Score 54; DB 5; Length 11;
Pred. No. 0.00071;
0; Mismatches 0; Indels
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                                                                                                                  96.4%; Scillarity 100.0%; P. Conservative 0;
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Best Local Similarity
Matches 11; Conserv
                                                                                       Sequence 11 AA;
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96.4%; Score 54; DB 100.0%; Pred. No. 0.0 ive 0; Mismatches
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Query Match
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                                                                                                                                                                                                                                                                                  Synthetic.
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Best Local Si
Matches 11;
                                                                                                                                                                  ABB80560;
                                                                                                                                                                                                                                                        virucide
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                                                                                                               RESULT 3
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RESULT 4

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue ?"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #21.
                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 5;
Pred. No. 0.0069;
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                                                                                                                                                                                                                                      'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                           /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                           'note= "D-form residue"
                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brunck TK;
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90.9%;
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                                                  (first entry)
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Best Local Similarity 90.9
Matches 10; Conservative
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Modified-site
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                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                  08-OCT-2002
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                                                                                                                                                                     Synthetic.
                   ABB80537;
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                                                                                                                                                                                                                                                                                                                                                                                                            note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
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0.00071;
hes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                          note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                 ABB80527 standard; peptide; 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                residue 7"
                                                                                                                                                                                     (first entry)
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                         EEVVPXGMHYS 11
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EEVVPXGMHYS 11
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Best Local Similarity
Matches 11; Conserv
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Modified-site
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activity usefu
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                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                       ABB80527;
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RESULT 5 ABB80537 ID ABB80

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Length 11; 1; Indels

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have invincide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
/note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                    peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis {\sf C}
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Pred. No. 0.011;
0; Mismatches
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                                                        /note= "C-terminal amide'
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                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.7%;
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                                                                                                                                                       19-JUL-2001; 2001WO-US023169
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10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 65; 69pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EBVVPXGMHYS 11
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                                                                                                                                                                                                                     (CORV-) CORVAS INT
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Modified-site
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Local St.
10;
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activity
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ABB80554
ID ABB80554
XX ABB80504
XX ABB80504
DD 08-0
DT 08-0
XX Hepa
XX Modil
FT Misc
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                                                                                                                                     /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus
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virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C ^{\gamma}
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.. 0.0069;
1; Indels
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Pred. No. 0.006
0; Mismatches
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                                                                                                           'note= "N-terminal acetyl"
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                                                                                                                                                                                          'note= "D-form residue"
                                                                             Location/Qualifiers
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90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMHYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                            Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                          (CORV-) CORVAS INT INC
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                                                                                                                                                                         Misc-difference
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Modified-site
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                                            Synthetic.
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            virucide
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprrising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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                                                                                                                             Brunck TK;
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                   19-JUL-2001; 2001WO-US023169.
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ilarity 90.9%;
Conservative (
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                                                                                                                             Levy OE,
                                                                                        (CORV-) CORVAS INT INC.
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Best Local Similarity
Matches 10; Conserv
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Modified-site
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                                                                                                                         Lim-Wilby M,
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                                                                                                                The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                 virus
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                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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Pred. No. 0.011;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 ABB80555 standard; peptide; 11 AA.
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                                                                                       Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                 85.7%;
90.9%;
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         WPI; 2002-361643/39
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Gaps

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Score 48; DB 5; Length 11; Pred. No. 0.011; 0; Mismatches 1; Indels

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Gaps

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Length 11; 1; Indels

Score 48; DB 5; Pred. No. 0.011; 0; Mismatches 1

85.7%;

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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              Claim 17; Page 65; 69pp; English
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Best Local Similarity 90.9
Matches 10; Conservative
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'note= "N-terminal acetyl"

Location/Qualifiers

(first entry)

/note= "C-terminal amide" 'note= "D-form residue"

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Brunck

Levy OE,

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pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11.
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                                                                  Length 11;
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                                                                   Score 46; DB 5;
Pred. No. 0.027;
                                                                                               Mismatches
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                                                                  82.1%;
nilarity 90.9%;
Conservative 0
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Best Local Simi:
Matches 10;
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Matches
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ABB80531
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WPI; 2002-361643/39.
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                                                                                                             Synthetic
   ABB80561;
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Matches
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residue 7"
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                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
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Pred. No. 0.042
0; Mismatches
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BB80561
D ABB80561 standard; peptide; 11 AA.
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                                                                       ABB80525 standard; peptide; 11 AA.
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90.9%;
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Modified-site
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Best Local S:
Matches 10
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                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
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Pred. No. 0.042;
0; Mismatches
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC
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Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.

'note= "N-terminal acetyl"

'note= "C-terminal amide"

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/note= "Norvaly1 carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
                                  Location/Qualifiers
                                                                                                                                                                                                                                Claim 17; Page 64; 69pp; English.
                                                                                                                                           21-JUL-2000; 2000US-0220101P.
                                                                                                                             19-JUL-2001; 2001WO-US023169.
                                                                                                                                                                        Levy OE,
                                                                                                                                                         (CORV-) CORVAS INT INC
                                                                                                                                                                                     WPI; 2002-361643/39.
                                                                                                 WO200208251-A2
                                  Key
Modified-site
                                                       Modified-site
                                                                            Modified-site
                                                                                                                                                                        Lim-Wilby M,
                                                                                                               31-JAN-2002.
                    Synthetic
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Brunck TK;

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus ö Query Match 80.4%; Score 45; DB 5; Length 11; Best Local Similarity 90.9%; Pred. No. 0.042; Matches 10; Conservative 0; Mismatches 1; Indels Sequence 11 AA;

1 EEVVPXGMHYS 11 ઠે g

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Gaps

Search completed: June 3, 2004, 11:48:22 Job time: 45.9333 secs

Appli Appli

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Sequence 4794, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/064, 964
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4794

LENGTH: 1037
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEARER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21444
LENGTH: 856
TYPE: PRI
                         Sequence 6 Sequence 6 Sequence 6 Sequence 6 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 1 Sequence 1 Sequence 2 
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                                                                                           US-08-26-517-23

US-08-246-361A-6

US-08-246-361A-23

US-08-246-361A-23

US-08-246-361A-23

US-08-477-120-8

US-08-460-694-2

US-08-460-694-2

US-08-464-517-19

US-08-246-361A-19

US-08-246-361A-19

US-08-246-361A-19

US-08-246-361A-19

US-08-246-361A-19

US-08-246-361A-19

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10-00-252-991A-21444
1 Sequence 21444, Application US/09252991A
1 Patent No. 6551795
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ORGANISM: Staphylococcus epidermidis
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Matches 7, Conservative
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1 REVVPXGMHYS 11
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Sequence 2, Appli
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Sequence 36, Appl
Sequence 36, Appli
Sequence 3950, Ap
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Sequence 21444, A
Sequence 7304, Ap
                                                                                                                                                                        June 3, 2004, 11:36:47; Search time 11.7333 Seconds (without alignments) 48.399 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-464-517-21
US-08-246-361A-21
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Maximum Match 100%
Listing first 45 summaries
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Sequence 2, Application US/08821118

Patent No. 598989

Patent No. 598989

Patent No. 598989

Patent No. 5989890

APPLICANT: Rey, Michael

APPLICANT: Rey, Michael

APPLICANT: Rey, Michael

APPLICANT: Golightly, Elizabeth

TITLE OF INVENTION: HAVING TRIPEPTIDE AMINOPEPTIDASE

TITLE OF INVENTION: ACTIVITY

NUMBER OF SEQUENCES: ACTIVITY

NUMBER OF SEQUENCES: CORRESPONDING POLYPEPTIDASE

STREET: 405 Lexington Avenue

GITY: New York

CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 600;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compartible
OMPUTER: IBM Compartible
OMPRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMB: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 33,728
REPERENCE/DOCKET NUMBER: 4107.400-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 212-067-0123
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.7%; Score 34; DB 2; Best Local Similarity 75.0%; Pred. No. 1.2e+02; Matches 6; Conservative 0; Mismatches 2
                                                                                INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein ; FRAGMENT TYPE: internal US-08-821-119-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GARY BRETON
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7304
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08821119
; Sequence 19, Application US/08821119
; Patent No. 5821104
; GENERAL INFORMATION:
APPLICANT: Halm, Kaj Andre
APPLICANT: Halkier, Torben
APPLICANT: Lehnbeck, Jan
TITLE OF INVENTIONS: Tripoptidyl Aminopeptidase
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSES:
AD
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60.7%; Score 34; DB 4; Length 323;
Best Local Similarity 55.6%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                     DB 4; Length 856;
48;
                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ for Windows Version 2.0
CURRENT APPLICATION NAME: US/08/821,119
                                                                                                 Score 37; DB 4
Pred. No. 48;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107.204-US
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
18-09-543-681A-7304
18-09-ence 7304, Application US/09543681A
18-08-ent No. 6605709
   ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21444
                                                                                                     66.1%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7304
                                                                                              Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                      1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                              64 EAVVPGGEHY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | |:||
75 DVCPAGVHY 83
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US-08-821-119-19
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| Sequence 3950, Application US/09134001C | Sequence 3950, Application US/09134001C | Sequence 3950, Application US/09134001C | Patent NO. 6380370 | GENERAL INFORMATION: | APPLICANT: Lynn Doucette-Stamm et al APPLICANTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS | TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS | TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS | TITLE OF INVENTION NUMBER: US 60/064,964 | PRIOR APPLICATION NUMBER: US 60/064,964 | PRIOR APPLICATION NUMBER: US 60/065,779 | PRIOR PILING DATE: 1997-08-14 | NUMBER OF SEQ ID NOS: 5674 | SEQ ID NO 3950 | LENGTH: 70 | TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
APPLICANT: Schleper, Christa
TILE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR PILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FESSES FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
TITLE OF INVENTION: by the polymucleotides and methods for their use. PILE REFERENCE: 11000.105601
CURRENT PPLICATION NUMBER: 02/09/724,864
CURRENT FILING DATE: 2000-11.28
PRIOR PLING APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR PLING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3 6
LENGTH: 747
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.9%; Score 33; DB 4; Length 747; Best Local Similarity 71.4%; Pred. No. 2.5e+02; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-408-020-4
; Sequence 4, Application US/09408020
; Patent No. 653937
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3472
TYPE: PRT
ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|:| |: :|
2294 EDVIPRGISFS 2304
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Best Local Similarity 45.5
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PXGMHYS 11
                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Rat
US-09-724-864-36
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABENGAINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27834
LENGTH: 1895
                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US, 09/252, 991A

CURRENT FILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

EROGIH: 277
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1S-09-724-864-36
Sequence 36, Application US/09724864
Sequent No. 638036
GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Murison, James G
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 385;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 4
Pred. No. 83;
0; Mismatches
                                                                                                                                       Sequence 26615, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 EETVPGGGHTS 58
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     31 VPKGWHYS 38
                                                                                                                   IS-09-252-991A-26615
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US-08-580-988A-23
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Sequence 23, Application US/08580988A

Patent No. 5866161

GENERAL INFORMATION:
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-1-Associated Protein Kinase And Methods
TITLE OF INVENTION: A Adder
STREET: 8011 Candle Lane
CITY: Houston
STREET: 8011 Candle Lane
CITY: Houston
STREET: 8011 Candle Lane
CONFUTEY: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
CURRENT APPLICATION DATA:
STREET: US/08/580,988A
FILING DATE: US/08/580,988A
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CTHER INFORMATION: Xaa = * ,Ala,Glu,Gly,Ile,Lys,Leu,Arg,Ser,Thr,Val US-09-621-976-6096
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Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 1; Indels
                                                                         Query Match 57.1%; Score 32; DB 4; Length 70; Best Local Similarity 62.5%; Pred. No. 29; Matches 5; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                          RESULT 11
US-09-621-976-6096

Sequence 6096, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Obcert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET:054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: NO0-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 6096
LENGTH: 101
LENGTH: 101
; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                36 MPKGFHYS 43
                                                                                                                                                                              4 VPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 PXGMHY 10
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ATTOMORY IN THE PROPERATION:

NEGISTRATION WITHOUS ASSETT THE PROPERATION:

NEGISTRATION WITHOUS ASSETT THE PROPERATION:

TELEBROWN: 173-77-221

TELEBROWN: 173-
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                                                                                                          Score 32; DB 2; Length 126;
Pred. No. 55;
1; Mismatches 2; Indels
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Pred. No. 55;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                             GENERAL INPORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Mathew R.
TILLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STREET: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONTUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM COmpatible
COMPUTER: 1BM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEM for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0326 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFCATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-845-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09215096 Patent No. 6008194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                            57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative :
                                                                                                      Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                         28 EQVVPGGGH 36
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 163590
JS-08-879-995A-3
                                                                                                                                                                                  1 EEVVPXGMH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: GenBa
                                                                                                                                                                                                                                                                         RESULT 14
JS-09-215-096-3
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28 EQVVPGGGH 36

RESULT 15

1 EEVVPXGMH 9

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USERVALENCE OF INTERPOLATION US/08460694

SEQUENCE:

GENERAL No. 585655

COMPRESSOURCES:

STREET: 1100 New York Avenue, N.W., Suite 600

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

Z.PP: COMPATING NEW YORK AVENUE, N.W., Suite 600

COUNTRY: USA

Z.PP: COMPATING NEW YORK AVENUE, N.W., Suite 600

COUNTRY: USA

Z.PP: COMPATING NEW YORK AVENUE, N.W., Suite 600

COUNTRY: USA

Z.PP: COMPATING NEW YORK AVENUE, N.W., Suite 600

COUNTRY: USA

Z.PP: COMPATING NEW YORK AVENUE, N.W., Suite 600

COMPATING NEW YORK AVENUE, N.W., SUITE 600

COMPATING NEW YORK AVENUE, N.W., SUITE 800

COMPATING NEW YORK AVENUE, SUITE 800

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GenCore version 5.1.6
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M protein - protein search, using sw model

June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec

tun on:

US-09-909-164-7 56 1 EEVVPXGMHYS 11 fitle:
Perfect score:
Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1155919 segs, 281338677 residues Searched:

Total number of hits satisfying chosen parameters:

1155919

Winimum DB seq length: 0 Waximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/PCT_TRAF_PUB_Dep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_TRAF_PUB_Dep:*

3: /cgn2_6/ptodata/1/pubpaa/PCT_TRAF_PUB_Dep:*

4: /cgn2_6/ptodata/1/pubpaa/USOG_NEW_PUB_Dep:*

5: /cgn2_6/ptodata/1/pubpaa/USOG_NEW_PUB_Dep:*

6: /cgn2_6/ptodata/1/pubpaa/USOG_NEW_PUB_Dep:*

7: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB_Dep:*

8: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Dep:*

9: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Dep:*

10: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Dep:*

11: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Dep:*

12: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Dep:*

13: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Dep:*

14: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Dep:*

15: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Dep:*

16: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Dep:*

17: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Dep:*

18: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Dep:*

18: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Dep:*

18: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB_Dep:*

18: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB_Dep:* Jatabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	quence 7,	Sequence 11, Appl	Sequence 21, Appl	Sequence 25, Appl	Sequence 30, Appl	Sequence 34, Appl	Sequence 38, Appl	Sequence 39, Appl	Seguence 42, Appl	Sequence 44, Appl	•	Sequence 16, Appl	Sequence 5, Appli	Sequence 6, Appli	Sequence 8, Appli	
SUMMAKIES	QI	US-09-909-164-7	US-09-909-164-11	US-09-909-164-21	US-09-909-164-25	US-09-909-164-30	US-09-909-164-34	US-09-909-164-38	US-09-909-164-39	US-09-909-164-42	US-09-909-164-44	US-09-909-164-15	US-09-909-164-16	US-09-909-164-5	US-09-909-164-6	US-09-909-164-8	
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	Len	1 1 1 1	11	11	11	11	11	11	11	11	11	11	11	11	11	11	
de	Query Match	96.4	96.4	87.5	87.5	85.7	85.7	85.7	85.7	85.7	85.7	82.1	82.1	80.4	80.4	80.4	
	Ü	54	54	49	4,0	48	48	48	48	48	48	46	46	45	45	45	
	Result No.	7	2	٣	4	'n	φ	,	00	σ	10	11	12	13	14	15	

FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)

9555	equence 15, equence 47, equence 48, equence 49,	20220	222222	sequence 20, Appl. Sequence 21, Appl. Sequence 31, Appl. Sequence 32, Appl. Sequence 33, Appl. Sequence 35, Appl.	C 4 4 4 4 4 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6
12 US-09-909-164 12 US-09-909-164 12 US-09-909-164	12 US-09-909-16 12 US-09-909-16 12 US-09-909-16 12 US-09-909-16	US-09-909-16 US-09-909-16 US-09-909-16 US-09-909-16 US-09-909-16	12 US-09-909-164 12 US-09-909-164 12 US-09-909-164 12 US-09-909-164 12 US-09-909-164	1 12 US-09-909-164- 1 12 US-09-909-164- 1 12 US-09-909-164- 1 12 US-09-909-164- 1 12 US-09-909-164- 1 12 US-09-909-164-	06-60-SD 06-60-SD 06-60-SD 06-60-SD
4 4 4 7 7 7 1	4 4 4 4 ሊ የ የ የ	. 4. 4. 4. 4. 1 70 70 70 0	4 4 4 4 4 C		

ALIGNMENTS

RESULT 1 US-09-909-164-7 is 2090-164-7 sequence 7, Application US/09909164 publication No. US20020068702A1 general involvementuring general involvementuring general involvementuring APPLICANT: Lim-Wilby, Marguerita APPLICANT: Levy, Odile E APPLICANT: Levy, Odile E APPLICANT: Levy, Odile E APPLICANT: Brunck, Terence K TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C FILE REPERSENCE: IND192-08 CURRENT APPLICATION NUMBER: US/09/909,164 CURRENT FILING DATE: 2003-03-25 FRIOR APPLICATION NUMBER: 60/220,101 PRIOR FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 62 SOFTWARE: Patentin version 3.1 IERGTH: 11 IERGTH: 11	TYPE: PRT ORGANISM: artificial sequence PERATURE: FRATURE: OTHER INFORMATION: 11-mer synthesized according to example 1 FRATURE: NAME/KEY: MOD RES LOCATION: (1) (1) OTHER INFORMATION: ACETYLATION FRATURE: NAME/KEY: MISC_FRATURE COTHER INFORMATION: norvaline-(CO) FRATURE: NAME/KEY: MISC_FRATURE LOCATION: (6) (6) COTHER INFORMATION: norvaline-(CO) FRATURE: NAME/KEY: MISC_FRATURE LOCATION: (9) (9) COTHER INFORMATION: D-amino acid
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FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
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Pred. No. 0.0067;
0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTHARE: Patentin version 3.1
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (9)...(9)
; OTHER INFORMATION: D-amino acid
US-09-909-164-21
                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FRATURE:
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NAME/KRY: MOD RES
NOCATION: (1)...(1)
OTHCER INFORMATION: ACETYLATION
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                                                                                                                                                              TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMHYS 11
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NAME/KEY: MISC_FEATURE
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NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
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LOCATION: (11)...(
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Sequence 11, Application US/09909164

Sequence 11, Application US/09909164

GENERAL INFORMATION:
APPLICANT: Carvas International, Inc.
APPLICANT: Lin-Wilby, Marguerita
APPLICANT: Lin-Wilby, Date: US/09/909,164
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
FRIOR APPLICATION NUMBER: 60/220,101
FRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3:1
SEQ ID NO 11
FRIENTH: 11
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ENGINEE INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: APPLICANT: Corvas INTERNATION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
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Pred. No. 0.0007;
                                                                   Length 11;
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                                                               Score 54; DB 12;
Pred. No. 0.0007;
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                                                                 Query Match 96.4%; Score 54; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICCATION: (8). (8) OTHER INFORMATION: D-amino acid US-09-909-164-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
    ; OTHER INFORMATION: AMIDATION US-09-909-164-7
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NAME/KEY: MISC_FEATURE
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C '
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C '
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 38
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                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 11-mer synthesized according to example 1 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 12; Length 11;
Pred. No. 0.01;
0; Mismatches 1; Indels
   CURRENT APPLICATION NUMBER: US/09/909,164
                                   CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION WUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 34
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 38, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (9)...(9)

JCOPHER INFORMATION: D-amino acid
US-09-909-164-34
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NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.9%;
Matches 10; Conservative 0
                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: artificial sequence
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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OTHER INFORMATION: AMIDATION
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NAME/KEY: MOD RES
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US-09-909-164-38
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IS-SULT 5
IS-SULT 5
IS-099-164-30
Sequence 30, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lorvy, Odile E
APPLICANT: Lorvy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2000-03-25
PRAIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEGFWARE: PATENTING DATE: PATENTING DATE:
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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87.5%; Score 49; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0067;
Matches 10; Conservative 0; Mismatches 1; Indels
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Pred. No. 0.01;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
18-09-909-164-30
OTHER INFORMATION: norvaline-(CO)
                                   FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)...(8)
OTHER INFORMATION: D-amino acid
S-09-909-164-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES LOCATION: (11\overline{1})...(11) OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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JS-09-909-164-34
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US-US-US-194-44

| Sequence 44, Application US/09909164
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| Publicant: Corvas International, Inc.
| APPLICANT: Lim-Wibby, Marguerita
| APPLICANT: Levy, Odile E
| APPLICANT: Levy, Odile E
| APPLICANT: Lim-Wibby, Marguerita
| APPLICANT: Lim-Wibby, Marguerita
| APPLICANT: Lovy, Odile E
           APPLICANT: BYLICK, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: INO1192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PELING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOPTHWARE: PATENTION VERSION 3.1
SEQ ID NO 42
LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: artificial sequence PRATURE: PERTURE: OTHER INFORMATION: 11-mer synthesized according to example 1
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Pred. No. 0.01
0; Mismatches
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FRATURE: NAME/KEY: MOD_RES
LOCATION: (11)...(11)
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NAME/KEY: MOD_RES
LOCATION: (1). (1)
OTHER INPORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11). (11)
OTHER INPORMATION: AMIDATION
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Best Local Similarity 90.9%;
Matches 10; Conservative
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COTHER INFORMATION: Met(0)
US-09-909-164-42
   Levy, Odile E
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Sequence 39, Application US/09909164

Publication No. US20020068702A1

APPLICANT: Cirvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-21

SOFTWARE: Patentin version 3.1

SEQUENCE: APPLICATION NUMBER: Circum-1, Marguerita Number 0.2

SOFTWARE: Patentin version 3.1
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NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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Pred. No. 0.01;
0; Mismatches 1; Indels
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
                                                                           NAME/KEY: MISC_FEATURE
COCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
JS-09-909-164-38
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OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: D-amino acids
OTHER INFORMATION: D-amino acid PEATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative
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NAMES/KEY: MOD RES
LOCATION: (11)...(11)
GCHER INFORMATION: AMIDATION
FEATURE:
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Best Local Similarity 90.9
Matches 10; Conservative
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Sequence 5, Application US/09909164

| Sequence 5, Application US/09909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corves International, Inc.
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| FILE REFERENCE: 1001192-US
| CURRENT FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE FALENCE FALENCE OF SEQ ID NOS: 62
| SEQ ID NO S
| LENGTH: 11
| LENGTH: 11
| LENGTH: 11
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lin-Wilby, Marguerita
APPLICANT: Lin-Wilby, Marguerita
APPLICANT: Lin-Wilby, Marguerita
APPLICANT: Lin-Wilby, Marguerita
APPLICANT: Encry, Calle E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FULE REPERENCE: INOINGER: US/09/909,164
CURRENT APPLICATION NUMBER: US/09/909,164
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTING NATE: DOOR - 07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTING NATE: DATE: DAT
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NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
NAME/KEY: MOD_RES
OTHER INFORMATION: AMDATION
OTHER INFORMATION: AMDATION
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Pred. No. 0.026;
0; Mismatches 1; Indels
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (9) -- (9) OTHER INFORMATION: D-amino acid US-09-909-164-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: artificial sequence
PEATURE:
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90.9%;
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ORGANISM: artificial sequence
PEATURE:
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Best Local Similarity 90.5
Matches 10; Conservative
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NAME/KEY: MOD RES
LOCATION: (1)..(1)
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S-09-909-164-15
Sequence 15, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: USAPLICANTON: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT PILING DATE: 2003-03-25
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NOS: 62
SEQ ID NO 15
LENGTH: 11
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Pred. No. 0.01;
0; Mismatches
                     FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)..(9)
OTHER INFORMATION: D-amino acids
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)..(8)
OTHER INFORMATION: Met (0)
S-09-909-164-44
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'S-09-909-164-16
Sequence 16, Application US/09909164
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: ACETYLATION
FEATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: artificial sequence
          OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.5
Matches 10; Conservative
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GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilbly, Marguerita
APPLICANT: Lim-Wilbly, Marguerita
APPLICANT: Lim-Wilbly, Marguerita
APPLICANT: Lim-Wilbly, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENCE: IN01192-US
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 11
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ORGANISM: artificial sequence
FRATURE:
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NAME/KRY: MOD RES
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TOCATION: (1)...(1)
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OTHER INFORMATION: ACETYLATION
FRATURE:
MAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE
LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
Publication No. US20020068702A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Law.Wilby, Marguerita
APPLICANT: Law.y. Odile E
APPLICANT: Lawy, Odile E
APPLICANT: Lawy, Odile E
APPLICANT: Lawy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
PRIOR PLILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 11
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                                                                                                                                                                                                                                                          Query Match

80.4%; Score 45; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

80.4%; Score 45; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 1; Indels
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-909-164-6
Sequence 6, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
                 FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC FEATURE
LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD RES

LOCATION: (11)...(11)

CTHER INFORMATION: AMIDATION

US-09-909-164-6
                                                                                                                           ; NAME/KEY: MOD RES
; LOCATION: (11)
; OTHER INFORMATION: AMIDATION
US-09-909-164-5
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RESULT 15 US-09-909-164-8 ; Sequence 8, Application US/09909164

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein June 3, 2004, 11:35:47; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec Run on:

US-09-909-164-7 56 1 EEVVPXGMHYS 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	ftsH proteinase ac	carbamoy1-phosphat	V1 protein - tobac	hypothetical prote	_	Н	5	DNA binding protei	GMP synthetase, su	hypothetical prote	TSI8.1 protein - A	diphthine synthase	hypothetical prote	3-dehydroquinate в	probable DNA ligas		thetical p	c	14		hypothetical prote		S.	ole a	id anti	finger protein (cl		F420	hypothetical prote
Ð	A72207	F89892	A42452	AE2001	\$69046	S38143	D82618	T02590	H69194	T24111	G86430	G69117	C75538	B75478	T35025	E69086	C83903	S58132	T28717	AF3286	S54619	E83607	G82253	G71542	H81697	S65811	HODVLB	A69284	T08564
四日	~	7	N	~	0	~	~	~	~	~	7	~	N	~	~	C3	7	7	7	7	7	7	N	N	N	7	н	N	0
Length	308	S	102	252	460	743	156	233	311	425	510	264	279	350	355	360	425	426	495	1028	156	367	441	466	466	487	514	534	545
% Query Match	. 6	•	64.3	64.3	4	•	ď	ď	•	ď	ď	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	8	8	8	58.9	ω.	ω.	æ	8	58.9
Score			36			36	35	35	35	35	35	34	34	34	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33
esult No.	! !	7	m	4	ហ	G	7	ထ	σ	10	11	12	13	. 14	15	16	17	18	13	20	21	22	23	24	25	56	27	28	29

DNA mismatch repai macrophage-stimula C1489 R protein	L-shaped tail fibe hypothetical 367K tachykinin B precu	heme exporter prot hypothetical prote ribosomal protein	ribosomal protein probable ThuA prot hypothetical prote	cyclin D2 - rat cyclin D2 - rat cyclin D2 - mouse cyclin D2 - mouse
A69663 JC5061 S44754	S36851 T31308 A25905	D71640 S57810 E97120	T07215 C95881 T25737	JC4011 IS8372 A41984 A42822
210	9000	01 01 01	0 0 0	0000
627	1396 3472 126	197 225 233	267 270 283	7 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
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310	ነ ພ ພ ພ ያ ພ ፋ ኪ	36 37 88	39 0 4 4 0 1	4 4 4 4 0 6 4 0

ALIGNMENTS

RESULT 1 A72207	ftsH proteinase activity modulator HflK - Thermotoga maritima (strain MSB8) C:Species: Thermotoga maritima	C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000	R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, L	<pre>Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Ric! C.M.</pre>	
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Nature 399, 323-329, 1999
A.Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome sec
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: A72207
A,Status: praiminary
A,Status: projective rype: DNA
A,Residues: 1-308 <ARN>
A,Rocosser-references: GB:AE001819; GB:AE000512; NID:g4982396; PIDN:AAD36885.1; PID:g498248
A,Raperimental source: strain MSB8
C;Genetics: D.H.; Hicker hardson, D.

A;Gene: TM1822 C;Superfamily: erythrocyte band 7 integral membrane protein

Gaps ö Query Match
66.1%; Score 37; DB 2; Length 308;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels

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3 VVPXGMHY 10 ||| |:|| -41 VVPSGIHY 48 ઠ 셤

RESULT 2

carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N31f

C;Species: Stabhylococcus aureus
C;Species: Stabhylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F88892
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Ohta, T.; Hobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1057 «KUR» A;Cross-references: GB:BA000018; PID:g13701002; PIDN:BAB42298.1; GSPDB:GN00149 A;Experimental source: strain N315

C;Genetics: A;Gene: pyrAB C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin

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A;Status: preliminary
A;Rolecule type: DNA
A;Residues: 1-156 <SINA
A;Cross-references: GB:AED004014; GB:AED003849; NID:G9107044; PIDN:AAF84752.1; GSPDB:GN0C
A;Cross-references: GB:AED04014; GB:AED03849; NID:G9107044; PIDN:AAF84752.1; GSPDB:GN0C
A;Cross-references: GB:AED0404; F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, W.C.A.; Ferro, J.A.; Ferraga, J.S.; Franca, S.C.; Franco, M.C.; Frob
J.D.; Junqueira, M.L.; Remper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig-
chado, M.A.; Madeira, A.W.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cypecies: Xylella fastidiosa
Cypecies: Xylella fastidiosa
Cypecies: Xylella fastidiosa
Cybate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
Cybacession: D85618
Ryanonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seque
Nature 406, 151-157, 2000
Ayritle: The genome sequence of the plant pathogen Xylella fastidiosa.
Ayreference number: A82515; MUID:20365717; PMID:10910347
Ayrote: for a complete list of authors see reference number A59328 below
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A,Residues: 1-73 <VAN-
A,Crosa-references: EMBL:Z28292; NID:g486536; PIDN:CAA82146.1; PID:g486537; MIPS:YKR067
A,Experimental source: strain S288C
                                A;Accession: S69046
A;Molecule type: DNA
A;Residues: 1-460 <HAL>
A;Cross-references: EMBL:U43703; NID:g1244769; PIDN:AAB68221:1; PID:g1244776; MIPS:YPL1
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Saccharomyces cerevisiae
C;Species: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C;Accession: S3814
R;van Vliet-Reedlik, J.C.; Planta, R.J.
Submitted to the Protein Sequence Database, March 1994
A;Reference number: S38130
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                   A.Gene: SGD:UME1
A.Cross-references: SGD:S0006060; MIPS:YPL139c
A.Map position: 16L
C.Superfamily: Saccharomyces cerevisiae transcription modulator WTM1
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                                                                                                                                                                                                                                                                                                                                                       / Match 64.3%; Score 36; DB 2; Length 460; Local Similarity 62.5%; Pred. No. 25; 1; Indels nes 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Cross-references: SGD:S0001775
A)Map position: 11R
C)Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| |:||
294 VVPCGLHY 301
A; Reference number: S69040
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Matches
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C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Accession: AE2001
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Rhazazki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analy, Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C)Accession: A42452
R)Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.B.
R)Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.B.
R)Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.B.
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
A;Reference number: A42452; MUD: 92188538; PMID: 1546458
A;Accession: A42452
A;Molecule type: DNA
A;Residues: 1-102 AMOR.
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hypochetical protein YPL139c - yeast (Saccharomyces cerevisiae)

hypochetical protein YPL139c - yeast (Saccharomyces cerevisiae)

C; Species Saccharomyces cerevisiae

C; Accession: S69046

C; Accession: S69046

C; Accession: J.; Debrulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Submitted to the EMBL Data Library, December 1995

A; Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-252 «KUR>
A,Cross-references: GB:BA000019; PIDN:BAB77929.1; PID:g17135383; GSPDB:GN00179
A,Experimental source: strain PCC 7120
C,Genetics:
A,Gene: alr1563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Species: tobacco yellow dwarf virus
C,Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
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                                Length 1057;
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64.3%; Score 36; DB 2; Length 102;
Best Local Similarity 60.0%; Pred. No. 5;
Matches 6; Conservative 3; Mismatches 1; Indels
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50.0%; Pred. No. 13;
tive 3; Mismatches 2; Indels
                                                                                                     2; Indels
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                                       7
                                       39;
                                                                                                     2; Mismatches
                                       Score 37;
Pred. No.
                                       66.1%;
60.0%;
                                       Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                     190 EIVSNGLHYS 199
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Matches 5; Conserv
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Cypaces or G86430

Rytheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunder, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Liu, Z.A.; Liu, S.X.; Liu, Z.A.; Liu, Z.A.; Liu, S.X.; Liu, Z.A.; Maiti, R.; Maiti, R.; Maiziali, R.; Muthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Helestence number: A66141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: EMBL:Z81109, PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
A,Experimental source: clone R10D12
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                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSIB.1 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 25-Aug-2003
C;Accession: G69117
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diphthine synthase - Methanobacterium thermoautotrophicum (strain Delta H)
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Pred. No. 45;
2; Mismatches 2; Indels
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    Caenorhabditis elegans

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: T24111
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 <WIL>
                                                                                                                                                                                                                                                                                                                                     RiPercy, C. submitted to the EMBL Data Library, October 1996 A; Reference number: Z19842
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Pred. No. 37;
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A;Map position: 5
A;Introns: 23/3; 56/3; 113/3; 257/2
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Best Local Similarity 60.0%;
Matches 6; Conservative
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les 5; Conservative
           219 EEVVESGLHES 229
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EEVKPPGIHF 21
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A;Molecule type: DNA
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Matches
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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Ri, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Thle: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID: 98037514; PMID: 9371463
A;Accession: H65134
A;Accession: H65134
A;Accession: H65134
A;Acsession: H65134
A;Accession: H65134
A;Acsession: H65134
A;Accession: H65134
R;Obme-Takagi, M.; Shinshi, H. Plant Cell 7, 173-182, 1995
A;Title: Ethylene-inducible DNA binding proteins that interact with an ethylene responsi A;Reference number: Z14671; MUID:95276459; PMID:7756828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA binding protein EREBP-2 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-233 <OHM>
A;Cross-references: EMBL:D38126; NID:g790362; PIDN:BAA07324.1; PID:g1208498
A;Experimental source: strain BY4; tissue-type leaf
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63.6%; Pred. No. 27;
ive 1; Mismatches 3; Indels
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Pred. No. 13;
3; Mismatches 1; Indela
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A,Molecule type: mRNA
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 55.6
Matches 5, Conservative
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A;Start codon: GTG
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Search completed: June 3, 2004, 11:59:59 Job time : 10 secs
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20 IPPGMHY 26
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Oa.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: C75538
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shn, M.; Yamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Maitch, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75538
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C;Species: Deinococcus radiodurans
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: B75478
R;White, 0.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
K; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ms
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S.; Smith, H.O.; Venter J. P.; Apps
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
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A;Molecule type: DNA
A;Resides 1-279 <WHI>
A;Resides references: GB:AE001889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795
A;Experimental source: strain R1
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Oiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: G69117
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A;Residues: 1-264 <MTH>
A;Cross-references: GB:AE000940; GB:AE000666; NID:g2623011; PIDN:AAB86340.1; PID:g262301
A;Experimental source: strain Delta H
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A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DR0271
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Pred. No. 38;
0; Mismatches
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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A)Status: preliminary
A,Molecule type: DNA
A)Residues: 1-350 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene: MTH1874
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SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
PubMed=12950922;
                                                                                                                                                                                               NCBI_TaxID=1282;
                                                                                                                            Q8cpj4 staphylococ
Q8rg86 fusobacteri
Q8749 vibrio para
Q99urs staphylococ
P5840 staphylococ
P5840 staphylococ
P51619 tobacoc yel
Q03010 saccharomyc
Q3586 methanobact
Q27902 methanobact
Q27902 methanobact
Q27902 methanobact
Q27903 methanobact
Q27804 methanobact
Q2158 yarrowia li
P46231 vibrio para
P1305 desulicovibr
P49850 bacillus su
P34335 caenorhabdi
P13300 bacteriopha
P08858 bos tearus
                                                                                                                                                                                                                                                                                                                                                                                                        anopheles g
vibrio para
clostridium
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homo sapien
homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                             chlorella v
                                                                                                                                                                                                                                                                                                                                                                                                                                   rattus norv
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gallus gall
xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                        brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                              xenopus lae
                                       June 3, 2004, 11:32:06 ; Search time 4.86667 Seconds (without alignments) 117.693 Million cell updates/sec
                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                              Q878W6
Q97i66
P56351
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P24385
P25322
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P30280
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                                                                                                                                  141681
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                   141681 seqs, 52070155 residues
                                                                                                                                                                                                                                        SUMMARIES
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ANOGA
CLOAB
CHLVU
                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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MOUSE
BRARE
XENLA
CHICK
                           - protein search, using sw model
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VIBPA
DESBA
BACSU
CAEEL
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YEAST
MESAU
METTH
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Gapop 10.0 , Gapext 0.5
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UMB1
YK47
IDI1
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0902]
0901]
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Maximum DB seq length: 200000000
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                                                                  US-09-909-164-7
56
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1396
1396
126
153
212
233
267
267
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Match 1
                                                                  Title:
Perfect score:
                                                                                               Scoring table:
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                                                                                  Sequence:
                                                                                                                   Searched:
                                       Run on:
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P39946 rattus norv P40595 azotobacter P19887 bacillus an Q9vwp4 drosophila Q89a96 buchnera ap P32784 saccharomyc O74377 schizosacch Q9kv29 vibrio chol P15822 homo sapien P20273 homo sapien P20273 homo sapien P20273 homo sapien P17280 chimpanzee P97885 rattus norv
CGDI_RAT HYPE_AZOVI TIDBE_BACAR SUOX_DROME MDLB_BUCRNE SULH_SCHPO RPOC_VIBCH ZEPI HUMAN CD22_HUMAN REV_SIVCZ SZ05_RAT
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295 341 3541 573 578 759 877 1401 2711 124
0.000000000000000000000000000000000000
911.
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ALIGNMENTS

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DATE OF THE STANDARD) PRT; 1057 AA.

DE GARGEGREE GREE STANDARD) PRT; 1057 AA.

DE GARGEGREE GREE GREE GREEN GREEN
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us-09-909-164-7.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

KAPATCZ 25586;

KADELINE=21886394;

N. Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Rapatral V., Anderson I., Ivanova N., Garchkin G., Zhu L.,

Nasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

Larsen N., D'Souza M., Waluns T., Pusch G., Haselkorn R.,

Larsen N., D'Souza M., Overbeek R.;

Larsen N., D'Souza M., D'Souza M., D'Souza M., D'Souza M.,

Larsen N., D'So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
TIGRFAMS; TIGRULSOS, C.E. 1, 2. PROSITE; PSOOBGE, CPSASE 1; 2. PROSITE; PSOOBG7; CPSASE 2; 2. Arginine biosynthesis; Pytimidine biosynthesis; Pytimidine brosynthesis; Pytimidine brockene ARP-binding; Manganese; Complete proteome CARBOXPHOSPHATE SYNTHETIC DOMAIN.

DOWAIN 402 546 OLIGOMERIZATION DOMAIN.

CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSRGES;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-
                                                                                                                                                                                                                                                            153 210 ATP (POTENTIAL).
302 352 ATP (POTENTIAL).
284 284 MANGANESE 1 (BY SIMILARITY).
298 298 MANGANESE 1 AND 2 (BY SIMILARITY).
300 MANGANESE 2 (BY SIMILARITY).
820 MANGANESE 3 (BY SIMILARITY).
831 MANGANESE 3 (BY SIMILARITY).
832 MANGANESE 3 (BY SIMILARITY).
834 MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.6%; Score 39; DB 1; Length 1057; 63.6%; Pred. No. 7.3; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusobacterium nucleatum (subsp. nucleatum).
Bacteria, Fusobacteria, Fusobacterales, Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1058 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphate synthetase ammonia chain).
CARB OR FN0422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 69.6
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMHYS 11
                                                                                                                                                 NCBI_TaxID=76856;
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METAL
SEQUENCE
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NP BIND
NP BIND
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CARB_FUSNN
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Gaps
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STRAIN=RIMD 2210633 / Serctype 03:K6;
MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Putnokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. choleree.";
Lancet 361:743-749(2003).
-!- CATALYTIC ACTIVITY: Phosphoenlpyruvate + 3-phosphoshikimate = phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate pathway;
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
        EMBL; AE010554; AAL94625.1; ALT_INIT.

R HAMAR; MF 01210; --; 1.

R InterPro; IPR00543; Cara L glu.

R InterPro; IPR00543; Cara L glu.

R InterPro; IPR00549; CPase L D2.

InterPro; IPR00549; CPase L D2.

InterPro; IPR00549; CPase L D3.

R InterPro; IPR00549; CPase L D3.

R InterPro; IPR00549; CPase L D3.

R Ffam; PP02189; CPase L D3; 1.

R Pfam; PP02187; CPase L D3; 1.

R Pfam; PP02187; CPase L D3; 1.

R Pfam; PP02187; CPase L D3; 1.

R RIMTS; PR00098; CPSASE.

R RIMTS; PR00098; CPSASE.

R RIGHEAMS; TIGR01369; CPSASE.

R ROSITE; PS00867; CPSASE.

W Arginine biosynthesis; Dytmidine biosynthesis; Ligase; Repeat; DAATH, DAATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-CCT-2003 (Rel. 42, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
110-CCT-2003 (Rel. 42, Last annotation update)
13-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSP synthase)
                                                                                                                                                                                                                                                                                        CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                   ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

AMAGANESE 3 (BY SIMILARITY).

AMAGANESE 3 (BY SIMILARITY).

117451 MW; ED7037AF77CLE39F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 1; Length 1058;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio parahaemolyticus.
Bacceria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
VOSE_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sixth step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
                                                                                                                                                                                                                                                                                                                                           ALLOSTERIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 60.0
es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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1058
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1058
352
246
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Q87QX9;
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NP BIND
NP BIND
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DOMAIN
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REPEAT
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ID AROA V
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Matches
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Lancet 359:1819-1827(2002).
-!- CAPALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP
-!- CAPALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP
phosphate + L-glutamate + carbamoyl phosphate.
-!- CORACTOR: Binds 3 manganese ions per subunit (By similarity).
-!- PATHWAY: Arginine biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
CARBOXYPHOSHATE SYNTHETIC DOMAIN.
OLIGOMEIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P58940;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

ANANGANESE 3 (BY SIMILARITY).

117171 MW; E3E179EF0591F0F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00098; CPSASE.
TIGREAMS; TIGR01369; CPSASEII_lrg; 1.
TROSTE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22040717; PubMed=12044378; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.; Mimi T., Kuroda H., Cui L., andennome and virulence determinants of high virulence community-acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 1; Length 1057;
Pred. No. 19;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus (strain MM2).
Bacteria: Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1057 AA.
or send an email to license@isb-sib.ch)
                                                                                             PIR; F89892; F89892.
HAMAP; MC 01210; -:
INTERPEYO; IPRO06275; Cara L glu.
InterPro; IPR006431; Cpase L.
InterPro; IPR006431; Cpase L.
InterPro; IPR005481; Cpase L. D2.
InterPro; IPR005481; Cpase L. D2.
InterPro; IPR005481; Cpase L. D3.
InterPro; IPR005481; Cpase L. D3.
InterPro; IPR005481; Cpase L. D3.
Pfam; PP0229; CPSase L. Chain; 2.
Pfam; PP02781; CPSase L. D2; 2.
Pfam; PP02781; CPSase L. D2; 2.
Pfam; PP02781; CPSase L. D3; 1.
Pfam; PP02781; CPSase L. D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.1%;
60.0%;
                                                 EMBL; AP003361; BAB57365.1;
EMBL; AP003132; BAB42298.1;
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Best Local Similarity
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DOMAIN
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                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!-CATALYTIC ACTIVITY: 2 AIP + b-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.

-!-COFACTOR: Binds 3 manganese ions per subunit (By similarity).

-!-COFACTOR: Binds 10 manganese ions per subunit (By similarity).

-!-PATHWAY: Arginine biosynthesis.

-!-PATHWAY: Pyrimidine biosynthesis, first step.

-!-SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).

-!-SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MISO / ATCC 700699, and N315;
STRAIN=21311952; PubMed=11418146;
Cui L., Oguchi A., Aoki K.-I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Mizutami M., Matsuman H., Maruyama A., Murakami H., Hosoyama A.,
Mizutami-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Samehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba 'Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                               HAMAP, MF_00210; -; 1.
InterProf; IRPO01986; EPSP synth.
Pfam; PF00275; EPSP synthase; 1.
PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
PROSITE; PS00886; BRSP_SYNTHASE_2; 1.
Aromatic amino acid biosynthasis; Transferase; Complete proteome.
SEQUENCE 426 AA; 46094 MW; 373D39CC5BA1F70F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamcyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamcyl-phosphate synthase ammonia chain).
CARB OR PYRAB OR PAYL203 OR SA1046.
Staphylococcus aureus (strain Mu50 / ATCC 700699), and
Staphylococcus aureus (strain N315).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.1%; Score 37; DB 1; Length 426; 60.0%; Pred. No. 7.3; ive 1; Mismatches 3; Indels
-!- SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                                                                         EMBL; AP005076; BAC59283.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 EFVIPAGOHY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARB STAAM
ID CARB STAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
PATHWAY: Pyrimidine biosynthesis; first step.
SUBINIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=92188538; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0098; CPSASE.
TIGREAMS; TIGR01369; CPSASEII_Irg; 1.
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.1%; Score 37; DB 1; Length 1057; 60.0%; Pred. No. 19; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D8E3B09F9BC6F152 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL)
ATP (POTENTIAL)
                                                                                    similarity).
-!- SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                     HAMAP, MF 01210; -; 1.
InterPro; IPR006575; Cara L glu.
InterPro; IPR006575; Cara L glu.
InterPro; IPR005483; CPase L D2.
InterPro; IPR005480; CPase L D3.
InterPro; IPR005480; CPase L D3.
InterPro; IPR005481; CPase L D3.
InterPro; IPR004362; MS2 13.e.
Pfam; PP02786; CPSase L Chain; 2.
Pfam; PP02786; CPSase L D3; 1.
Pfam; PP02787; CPSase L D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117185 MW;
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nes 6; Conservative
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153 21
302 35
298 298
298 29
300 820
820 82
832 83
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SEQUENCE
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NP BIND
NP BIND
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P31619;
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DOMAIN
DOMAIN
DOMAIN
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ID XIIK TY
DT 01-JUL
DT 01-JUL
DT 01-JUL
DE HYPOCH
GN V1.
CO VICUS
OX NCBI
COX NCBI
TRN [1]
TRN SEQUEN
RX MEDLIN
RA MOTTIF
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      SOLUTION STATEMENT OF STATEMENT
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REGUENCE FROM N.A.

FOR SEQUENCE FROM N.A.

RC STRAIN=2288C / AB972;

RX MUDLINE=97313271; PubMed=9169875;

RA BUSSEY H., Storma R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Abarajo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Cherry D., Bowman S., Burckner M., Carpenter J., Cherry J.M., Araujo R., Araujo R., Coster C.M., Coster F., Davis K., Davis R.W., Albertich F.S., Delius H., Discolo T., Dubois B., Duesterhoeft A., Albertich F.S., Delius H., Discolo T., Dubois B., Duesterhoeft A., Andri J., Hebling U., Heumann K., Hilbert H., Hillier L.W., R. Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kaline K., Amarahe R., Messenguy F., Mewse H.-W., Mirtipati S., Moestl D., RA Municke-Smith S., Namath A., Namtwich U., Oefner P., Pearson D., RA Mueller-Auer S., Namath A., Namtwich U., Oefner P., Pearson D., RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Schromam S., Schroeder M., Schreub S., Vissers S., Voss H., Schrens B., Schramm S., Schroeder M., Schler H., Winnett E., Wedler E., Wedler H., Winnett E., Ra Alsh S.V., Wambutt R., Wob D.H., Hani J.;

RA Ansan S.V., Wambutt R., Wo D.H., Hani J.;

RA The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";

REGULATION AND SILENCING. NEGATIVE REGULATOR OF MEIOSIS.

C. -- FUNICARIY: Contains 4 WD TESPERIS.

-- SIMILARIY: STRONG, TO YEAST WTM1 AND WIWE.
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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   cloned DNA component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONTROL 1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Meiosis negative regulator UNE1.
UMEI OR WIM3 OR YPL139C OR LPI7C.
Saccharomyces cerevisiae (Baker's speat).
Bukaryota, Fungi; Ascomycota; Saccharomyceties; Saccharomycescharomycescharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
"The nucleotide sequence of the infectious cloned DNA compone tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants."; virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.3%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 2.7; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A364A;
Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, M81103, AA47947.1; -.
PIR, A42452, A42452.
InterPro, IPR002621, Gemini mov.
Pfam, PF01708, Gemini mov. \(\bar{1}\).
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A40ECFIEOAF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 AA
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Best Local Similarity
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Q03010; P87330;
01-NOV-1997 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
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UMB1_YEAST
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us-09-909-164-7.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    van Vliet-Reedijk J.C., Planta R.J.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBL011W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kDa protein in CCPI-MET1 intergenic region.
                                                                                                                                                                                                                                             GO, GO:0005634, C:nucleus; IDA.
GO; GO:0005634, C:nucleus; IDA.
GO; GO:0003714; F:transcription co-repressor activity; IDA.
GO; GO:0040020; P:regulation of meiosis; IGI.
Interpro; IPRO:01680; WD40.
Ffam; PF00400; WD40; WD40.
Ffam; PF00400; WD40; 4.
PROSITE; PS00629; WD REPEATS_1; FALSE NEG.
PROSITE; PS500824; WD REPEATS_2; FALSE NEG.
PROSITE; PS500834; WD REPEATS_2; FALSE NEG.
Transcription regulation; Meiosis; Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.3%; Score 36; DB 1; Length 460; 62.5%; Pred. No. 13; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51022 MW; AA6F60448B7BCBA9 CRC64;
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8 8 3 2.
4 3 .
                                                                                                                                                EMBL; U10280; AAB40937.1; -. EMBL; U43703; AAB68221.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.5.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                              PIR; S69046; S69046.
GermOnline; 144121; -.
TRANSFAC; T04309; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VVPXGMHY 10
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460 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GermOnline; 140046;
SGD; S0001775; GPT2.
                                                                                                                                                                                                               TRANSFAC; T04309;
SGD; S0006060; UME1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S288c;
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GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0004366; F:glycerol-3-phosphate O-acyltransferase acti. . .; IDA.
GO; GO:000864; P:phospholipid biosynthesis; IDA.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase.
PFam; PF01553; Acyltransferase.
Hypothetical protein; Transmebrane.
TRANSMEM 31 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-97373601; PubMed-9228075;
Paton V.G., Shackellord J.E., Krisans S.K.;
Paton V.G., Shackellord J.E., Krisans S.K.;
"Cloning and subcellular localization of hamster and rat isopentenyl
"Cloning and subcellular diphosphate isomerase. A PrS1 motif targets
the enzyme to peroxisomes.";
J. Biol. Chem. 272:18945-18950 (1997).
-I. FUNCTION: CATALYZES THE 1,3-ALLYLIC REARRANGEMENT OF THE
HOMORLIVIIC SUBSTRATE ISOPENTENYL (IPP) TO ITS HIGHLY
BIECTROPHILIC ALLYLIC ISOMER, DIMETHYLALLYL DIPHOSPHATE (DMAPP).
-I. CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
11-Gropentenyl-diphosphate delta-isomerase 1 (EC 5.3.3.2) (IPP isomerase
1) (Isopentenyl pyrophosphate isomerase 1) (IPPII).
                                                                                                                                                                                                                                                                                           Gaps
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Proflow; PB004109; I.PP. isomerase; 1.

Carotenoid biosynthesis; Cholesterol biosynthesis;

Isoprene biosynthesis; Sterol biosynthesis; Isomerase; Peroxisome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: Magnesium.
-!- COFACTOR: Magnesium.
-!- PATHWAY: Isoprenoid biosynthetic pathway whose end products include dolichols, vitamins A. D. E, and K, steroid hormones, carotenoids bile acids and cholesterol.
-!- SUBCELLUTAR LOCATION: Peroxisomal.
-!- SIMILARITY: Belongs to the IPP isomerase type 1 family.
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                 Score 36; DB 1; Length 743;
Pred. No. 21;
1; Mismatches 1; Indels
                                                                                                                                                                                                                84B9946ES6B82F15 CRC64;
                                                                                                                                     POTENTIAL. POTENTIAL.
                                                                                                                                                                          POTENTIAL. POTENTIAL.
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InterPro; IPR000086; NUDIX hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesocricetus auratus (Golden hamster)
                                                                                                                                 31 55 PG
69 85 PG
502 85 PG
539 554 PG
743 AA; 83644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF003836; AAC53283.1; -.
                                                                                                                                                                                                                                                     64.3%;
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                      294 VVPCGLHY 301
                                                                                                                                                                                                                                                                                                                                3 VVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDII MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Magnesium.
                                                                                                                                                                          TRANSMEM
TRANSMEM
SEQUENCE
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IDI1_MESAU
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1 EEVVPXGMHYS 11
                                                                                                            METTH
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                                                                                                            DPHB ME
027902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Delta H;

WEDLINE=98037514; PubMed=9371463;

MEDLINE=98037514; PubMed=9371463;

MEDLINE=98037514; PubMed=9371463;

Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Aldredge T., Bashirzadeh R., Mang Y., Wierzbowski J., Gibson R.,

A Harrison D., Hoang L., Keagle P., Luum W., Pothier B., Qiu D.,

Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

An Daniels C.J., Maco J.-I., Rice P., Noelling J., Reeve J.N.;

Complete genome sequence of Methanobacterium thermoautotrophicum

of Half Hunctional analysis and comparative genomics.";

I. GATALYTIC ACTIVITY: ATP + xanthosine S'-phosphate + L-glutamine +

H(2)O = AMP + diphosphate + GMP + L-glutamine amidotransferase

c. - CATALYTIC ACTIVITY: ATP + xanthosine S'-phosphate + L-glutamine amidotransferase

c. - STBUNIT: Heterodimer composed of a glutamine amidotransferase

c. - STBUNIT: Heterodimer composed of a glutamine amidotransferase

c. - STBUNIT: Heterodimer composed of a glutamine amidotransferase

c. - STBUNIT: Heterodimer composed of a glutamine amidotransferase

c. - STBUNIT: Heterodimer composed of a glutamine amidotransferase

c. - STBUNIT: Heterodimer composed of a glutamine amidotransferase

c. - STBUNIT: Heterodimer composed of a glutamine amidotransferase
                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (EC 6.3.5.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00958; GMP synt_C; 1. TIGREAMs; TIGRO0884; guaA_Cterm; 1.
TIGREAMs; TIGRO0884; guaA_Cterm; 1.
Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 1; Length 308;
Pred. No. 13;
1; Mismatches 3; Indels
                                                                           Score 35; DB 1; Length 227; Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMP-BINDING (BY SIMILARITY).
 96 BY SIMILARITY.
148 BY SIMILARITY.
27 MICROBODY TARGETING SIGNAL.
26317 MM; F500A6586385E803 CRC64;
                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (BY SIMILARITY) . F2DCF6ED202CAEC1 CRC64;
                                                                                                                                                                                                                                                              308 AA
                                                                                                            0; Mismatches
                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000850; AAB85215.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF_00345; -; 1.
Interpro; IPR001674; GMP_gynth_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 184 G
29 35 A
308 AA; 34403 MW;
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                                                                               62.5%;
                                                                                              Local Similarity 70.0
                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                               121 EEVDPNEMHY 130
                                                                                                                                              1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P04079; 1GPM.
   86
148
225
227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                  GUAAB OR MTH710.
                                                                                                                                                                                                                               RESULT 10
GAAB METTH
ID GAAB METTH
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SEQUENCE
 ACT_SITE
ACT_SITE
SITE
SEQUENCE
                                                                               Query Match
Best Local S
Matches 7
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Gaps

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Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dubois J.,
                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable diphthine synthase (BC 2.1.1.98) (Diphthamide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98037514; FubMed=9371463; Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois Jantedge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jannis D., Bash D., Safer H., Patvell D., Prabhakar S., McDugall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Moo J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum Complete Genomal analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biosynthesis (By similarity).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 2-(3-carboxy-3-aminopropyl)-L-histidine = 8-adenosyl-L-homocysteine + 2-[3-carboxy-3-(archylammonio)propyl]-L-histidine.
-!- PATHWAY: Diphthammide biosynthesis, second step.
-!- SAMILARITY: Belongs to the diphthine synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.7%; Score 34; DB 1; Length 264; 62.5%; Pred. No. 18; 1; Indels :ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; ABOUDSHY.

PIR; G69117; G69117.

HAWAP; MF 01084; -; 1.

INTERPRO; IPR001687; COX/DOZ METRANSf.

INTERPRO; IPR004551; Dphthn_Synthase.

Pfam; PF00590; TP methylase; 1.

TIGRRAMS; TIGR00522; dph5; 1.

Transferase; Methyltransferase; Complete proteome.

Transferase; Methyltransferase; Complete proteome.

264 AA; 28858 MW; 366BAE4E4D992C21 CRC64;
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                                                                                                                                                                                          264 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLS1_YARLI
ID SLS1_YARLI STANDARD;
AC 099158;
DT 01-NOV-1997 (Rel. 35, Created)
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Matches 5; Conservative
216 EEVVESGLHES 226
                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 VVPAGLHF 242
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                                                                                                                                                                                                                                                                                                                                                                                                   methyltransferase).
DPHB OR MTH1874.
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Lancet 361:743-749(2003).
                                                                                                                                                                                                                                                                                                                                                   363
419
441 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=899;
                                              McCarter L.L.;
                                                                                                                                                                                                                                            Hypothetical TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHSL DESBA
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SEQUENCE
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PHSL DESBA
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-RIMD 2210633 / Serotype 03:K6;
MEDLINE-22508454; PubMed-12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Oshima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Ysuunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae."
                                                                                                                                                                                                                                                                                                                                                                       SLSI PROTEIN.
PREVENT SECRETION FROM ER (POTENTIAL).
OACD7EF17540B8E2 CRC64;
                          Yarrowia lipolytica (Candida lipolytica).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                            60.7%; Score 34; DB 1; Length 426;
44.4%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                     SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) SLS1 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein VP2115 (ORF3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                      InterPro; IPR000938; ARM.
InterPro; IPR000986; ER target_S.
PROSITE; PS00014; ER TARGET; 1.
Endoplasmic reticulum; Signal.
SIGNAL 18 426 SLS1
                                                                                                                                                                                                                                                                                                                                                                                           47201 MW;
                                                                                                                                                                                                                                                                                                    EMBL; Z50154; CAA90516.1; -. PIR; S58132; S58132.
                                                                                                                                                                                                                                                                                                                                                                                                                       44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                   426
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                                                                                                                                                                                                                                                                                                                                                                                          426 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=670;
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P46231;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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01-JAN-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Periplasmic [NiFeSe] hydrogenase large subunit (EC 1.12.99.6) (NiFeSe hydrogenlyase large chain)
Desulfovibrio baculatus (Desulfomiorobium baculatus).
Bacteria, Proteobacteria, Deltaproteobacteria; Desulfovibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-B805674; PubMed=1316183; MEDLINE-B8056744; PubMed=1316183; Menon N.K., Peck H.D. Jr., le Gall J., Przybyla A.E.; Control and sequencing of the genes encoding the large and small subunits of the periplasmic (NIPeSe) hydrogenase of Desulfovibrio
                                                                                                     "MotY, a component of the sodium-type flagellar motor.";
J. Bacteriol. 176:4219-4255(194).
-!- SUBGELLUIAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: STRONG, TO H.INFLUENZAB HI0325.
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Pred. No. 50;
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451969FE307E4D46 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP005080; BAC60378.1; -.
EMBL; U06949; AAA21571.1; -.
InterPro; IPR004770; Antiport nhaC.
InterPro; IPR01991; Na/dico_Symport.
Pfan; PR03553; Na H antiporter; 1.
PRINTS; PR00173; EDTRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                     MEDLINE=94292449; PubMed=8021208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 169:5401-5407(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45961 MW;
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54.5%;
SEQUENCE OF 1-140 FROM N.A.
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Best Local Similarity 5%...
6; Conservative
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Pred. No. 58;
1; Mismatches 1; Indels
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MOTL_CT-1996 (Rel. 34, Created)

MOTL-CT-1996 (Rel. 34, Last sequence update)

MOTL-CT-2003 (Rel. 42, Last annotation update)

MUTL-CT SEQUENCE

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Best Local Similarity 71.4%;
Matches 5; Conservative 1
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513 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR EMBL; M18271; AAA23375.2; ...
DR PIR; A33101; HQDVLB.
DR PDB; ICC1, 0.10N.99
DR INTERPO; IPRO01501; Ni hdL.
DR PROSITE; PS00507; NI HGENASE L.; 1.
DR PROSITE; PS00507; NI HGENASE L.; 1.
TWO Oxidoreductase; Periplasmic; Metal-binding; Nickel; Iron; Selenium; T INTT MET 0

T MATAL 51

T MATAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ligands.
--- SUBUNIT: Heterodimer of a large and a small subunit.
--- SUBCELLULAR LOCATION: Periplasmic.
--- MISCELLANBOUS: PERHAPS THE LEADER OF THE SWALL SUBUNIT SERVES AS A TRANSPORT VEHICLE FOR BOTH SUBUNITS.
--- SIMILARITY: Belongs to the [NiFe]/[NiFeSe] hydrogenase large subunit family.
                                                                                      IRON 2.
NICKEL.
IRON 1.
NICKEL.
IRON 2 (VIA CARBONYL OXYGEN).
NICKEL.
IRON 1.
NICKEL.
IRON 2.
          Bacteriol. 170:4429-4429(1988)
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Gaps

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58.9%; Score 33; DB 1; Length 627; 54.5%; Pred. No. 71; 4; Indels iive 1; Mismatches 4; Indels

Query Match
Best Local Similarity 54.5.,
Best Local Similarity 64.5.,

Search completed: June 3, 2004, 11:49:51 Job time : 5.86667 secs

à g

DNA repair; Complete proteome. SEQUENCE 627 AA; 70431 MW; 068A0509CC265343 CRC64;

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PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
                                                                                                                                                                                                                                        EMBL; U27343; AAB19236.1; -.
EMBL; 299112; CAB13578.1; -.
EML; A6963; A66663.
HSSP; P23367; 1BKN.
Subclitat; B011402; mutc.
HAMAP; MF 00149; -; 1
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR002099; DNA mis repair.
Pfam; PP01119; DNA mis repair.
Pfam; PP02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                    TIGRFAMS;
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Minst F., Ogasawara N., Moszer P., Bolotin A.M., Alloni G., Azevedo V., Bertero M.G., Bessiers P., Bolotin A., Borchett S., Boursise T., Brans A., Braun M., Brignell S.C., Bron S., Borriss R., Boursier L., Chambar B., Capuano V., Carter N.M., Bornise R., Boursier L., Canarion I.S., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Pabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Avinta K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Naula G., Lauber J., Lazarevic V., Layidus A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Mosetl D., Nakai S., Noback M., Newlin A., Liu H., Masuda S., Mauel C., Medigue C., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Barcov D., Stelly M., Portetelle D., Porvollik S., Prescott A.M., Stonic C., Scholl T.M., Portetelle D., Porvollik S., Scoffone F., Schleich S., Schoeter F., Scoffone F., Scholl M., Takemaru K., Scollon F., Scholl M., Takemaru K., Takendhi M., Tamakoshi A., Tarancoll E., Takagi T., Takahashi H., Takemaru K., Tosanto V., Uchiyama S., Vandelber B., Wanters P., Walmoutt R., Wanters P., Walmanct R., Wanters P., Walmoutt R., Wanters P., Walmout E., Schleier E., Waller E., Walmancto H., Vanamoto K., Yasawoto K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Danchin A., Tarhen Complete genome sequence of the Gram-positive bacterium Bacillus F., Ruht I. Farmer D., Scholler E., Walmancto O., Wooller E., Walmancto O., Wool
                                                                                                                                                                                                                   MEDLINE=56349107; PubMed=8760914;
Ginetti F., Perego M., Albertini A.M., Galizzi A.;
"Bacillus subtilis mutS mutL operon: identification, nuclectide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                    sequence and mutagenesis.";
Microbiology 142:2021-2029(1996)
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                                                                                                                      SEQUENCE FROM N.A.
NCBI_TaxID=1423;
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FUNCTION: This protein is involved in the repair of mismatches in DNA. It is required for dam-dependent methyl-directed DNA mismatch repair. May act as a "molecular matchmaker", a protein that promotes the formation of a stable complex between two or more DNA-binding proteins in an ATP-dependent manner without itself being part of a final effector complex (By similarity). SIMILARITY: Belongs to the DNA mismatch repair mutl/hexB family.
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Q98A71 arabidopsis
QP8A71 arabidopsis
QFL207 methanopyru
QFL207 methanopyru
Q9FMUG rhizobium 1
Q9FWJ2 deinococcus
Q9KMJ3 streptomyce
Q9KMJ3 streptomyce
Q9KMJ3 streptomyce
Q9KMJ3 arabidopsic
Q9KMJ3 caenorhabdi
Q8CA21 mus musculu
Q8CA21 mus musculu
Q9YQ5 drosophila
Q9YQ6 drosophila
Q9YQ1 arabid herpe
Q9Y01 maind herpe
Q9Y01 maind herpe
Q9MJ1 brucella me
Q8KJ11 brucella me
Q8KJ11 brucella me
Q8KJ2 drosophila
Q8YJ1 drosophila
Q8YJ1 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                OBP598 xanthomonas
Q8ktq4 candidatus
Q9xdc1 streptomyce
Q7v6q4 prochloroco
Q8piD0 xanthomonas
Q99011 prototheca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032195; AAH32195.1; -. MGD; MGI:1915724; Tada31.
GO; GO:0030374; F:ligand-dependent nuclear receptor transcrip. . .; IDA. GO; GO:0005515; F:protein binding; IPI.
SEOUENCE 413 AA; 46621 MW; A9BBAlDC70CDA0D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OL-UCI-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence A1987856.
TADA3L OR 1110004B19RIK.
Why musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalla; Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus. (VI TAXID=10090;
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Last sequence update)
Last annotation update)
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01-00T-2002 (TrEMBLrel. 22, Last seq
01-00T-2003 (TrEMBLrel. 25, Last anno
                                                                      Q7T1G5
Q9RXN9
Q9RHU6
Q9RW92
Q9XAM3
Q27679
Q9CAL1
Q8CAL1
Q8CAL1
Q8CAL1
Q8CAL1
Q9CAL1
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Q9VQL7
Q12479
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Q8KTQ4
Q9RDC1
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Q8PIB0
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QBBNL0
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                                                                          1 EEVVPXGMHYS 11
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QBCPJ4;
01-MAR-2003
01-MAR-2003
01-OCT-2003
 Query Match
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Matches
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                                                                                                                   June 3, 2004, 11:35:06 ; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                  1017041
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                             1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                        OM protein - protein search, using sw model
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Q8C2E4
Q9K2E4
Q9K2E4
Q9K1H0
Q8KWP1
Q8KWP1
Q9KYR4
Q5A89
Q9FC35
Q87D3
Q87
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sp_mnammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteriap:*
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1 EEVVPXGMHYS 11
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156
156
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Match
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Perfect score:
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Maximum DB
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Nature 399:323-329(1999).
EMBL; AE001819; AAD36885.1;
PIR; A72207; A72207.
TIGR; TM1822; -
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Best Local Similarity 75.v.
For G, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2303;
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Best Local Si
Matches 6;
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STRAIN-MSBR / DSM 3109,
MEDLINE=99287316; PubMed=10360571;
MEDLINE=99287316; PubMed=10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
MCDONald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Exidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                                                                                                                                                                                                                    STEAIN-ATCC 12228;
Andray Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                                                                           Chen Z., Wen Y.;
Chen Z., Wen Y.;
Chen Z., Wen Y.;
Chen Z., Wen Y.;
Chen Z., Wen Y.;
Chen Z., Wen Y.;
Chen Z., Wen Y.;
Chen Z., Wen Y.;
Chen Z., Wen Y.;
Chen Z., Wen Y.;
Chen Z., Wen Y.;
Chen Z., Wen Y.;
Chen Z., Wen Y.;
Chen Z., Choologal Z., Chen EMBL/GenBank/DDBJ databases.
Chen Z., Choologal Z., Chen Z.,
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1057 AA; 117391 MW; 8944D7D8DB1CAE59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
FISH protease activity modulator HFLK.
                                               Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=1282;
           Carbamoyl-phosphate synthase large chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0099; CFSASE.
TICKFAMS; TICKR01369; CFSASE11_1rg; 1.
PROSITE; PSO0866; CPSASE_1; 2.
PROSITE; PSO0867; CPSASE_2; 2.
PROSITE; PSO0639; THIOL_PROTEASE_HIS; 1.
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nes 7; Conservative
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SEQUENCE 1057 AA
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Q9X2E2
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XX MEDLINE=20479972; PubMed=11029001;

Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Ruepp A., Graml W., Stocker S., Lupas A.N., Baumeister W.;

Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;

"The genome sequence of the thermoacidophilic scavenger Thermoplasma cradophilum.""

"The genome sequence of the thermoacidophilic scavenger Thermoplasma cradiophilum.""

"The genome sequence of the thermoacidophilic scavenger Thermoplasma cradiophilum.""

"The genome sequence of the thermoacidophilic scavenger Thermoplasma cradiophilum."

"The genome sequence of the thermoacidophilic scavenger Thermoplasma cradiophilum."

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"The genome sequence of the genome sequence 
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Thermoplasmataceae, Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrENBLrel. 23, Created)
01-MAR-2003 (TrENBLrel. 23, Last sequence update)
01-MAR-2003 (TrENBLrel. 24, Last annotation update)
Multidrug efflux transporter.
TLIG18.
Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria; Cyanobacteria; Chrococccales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease; Complete proteome.
SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNM-2003 (TrEMBLrel. 24, Last annotation update)
Glucose-fructose oxidoreductase related protein.
PIR; A72207; A72207.
TIGN: TM1822; -
GO; GO:0016020; C:nembrane; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
InterPro; IPR001107; Band 7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band 7; I.
PRINTS; PR00721; STOMATIN.
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Best Local Similarity 50.0
Matches 5; Conservative
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Matches
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MEDLINE=20194806; PubMed=10732668;
Tauch A., Krieft S., Kalinowski J., Puhler A.;
"The 51,409-bp R-plasmid prplof from the multiresistant clinical
"The 51,409-bp R-plasmid prplof from the multiresistant clinical
isolate Corynebacterium striatum M82B is composed of DNA segments
initially identified in soil bacteria and in plant, animal, and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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SPECIES=C.xerosis; STRAIN=M82B;
MEDIINE=96117603; PubMed=8559800;
MEDIINE=96117603; PubMed=8559800;
Tauch A., Kassing F., Kalinowski J., Puhler A.;
"The Corynebacterium xerosis composite transposon Tn5432 consists of two identical insertion sequences, designated IS1249, flanking the erythromycin resistance gene ermCX.";
                                                                                                                                      Sasamoto S.,
                                                                                         MEDLINE-2225144; PubMed=12240834;

A Watanabe A., Iriquchi M., Kawashima K., Kimura T., Kishida Y.,

A Watanabe A., Iriquchi M., Kawashima K., Kimura T., Kishida Y.,

Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N.,

Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.,

I "Complete genome structure of the thermophilic cyanobacterium

Intermosynachococcus elongatus BP-1.";

DNA Res. 9:123-130(2002).

R EMBL; Ap065374; BAC091701; -.

R GO; GO:0016021; Crintegral to membrane; IEA.

GO; GO:0016021; Crintegral to membrane; IEA.

R GO; GO:0016021; Priransporter activity; IEA.

R GO; GO:00160103; Acrilvin_res.

R InterPro; IPR00103; Acrilvin_res.

R InterPro; IPR00103; Acrilvin_res.
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acteria, Actinobacteridae, Actinomycetales,
Corynebacterinaes, Corynebacteriaceae,
Corynebacterines, Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64;
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, Last sequence update)
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EMBL, U21300; AAC95478.1; -.

EMBL, AF024666; AAG03390.1; -.

GO: 0646821; C:extrachromosomal DNA; IEA.

Hypothetical protein; Plasmid.

SEQUENCE 208 AA; 23012 WW; F1504BE1ECDE8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00702; ACRIFLAVINRP.
TIGREAMS; TIGRO315; 2A0602; 1.
Complete proteome.
SEQUENCE 1044 AA; 113205 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium xerosis, and
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Best Local Similarity 63.6
Matches 7; Conservative
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843 EEVLPNGIGYS 853
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                                               FROM N.A.
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NCBI_TaxID=32046;
                                            SEQUENCE FRO
STRAIN=BP-1;
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Q46486
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Length 208;

DB 2;

64.3%; Score 36;

Query Match

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STRAIN=cv. Alaska;
MEDLINE=21231727; PubMed=11333309;
ASSES N., Mateushita Y., Nakamura T., Nyunoya H.;
"The Molecular Characterization and in situ Expression Pattern of Pea
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids 1; Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21595285; PubMed=11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 8:205-213(2001).

EMBL, AP003586; BAB77929.1; -.

PIN, AE2001, AE2001.

Hypothetical protein; Complete proteome.

SEQUENCE 252 AA; 28831 NW; 925572DA5DICA519 CRC64;
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Plant Cell Physiol. 42:385-394(2001).
Bulst, ABORSIOS.1;
TRANSFAC, T05513;
GO; GO:0009288; C:flagellum (sensu Bacteria); IEA.
GO; GO:000374; F:mertor activity; IEA.
GO; GO:0005188; F:setructural molecule activity; IEA.
GO; GO:0005189; F:setructural molecule.
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Last annotation update)
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Pred. No. 36;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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50.08;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                        130 DVIPEGKHYA 139
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235 EMIVPAGLHF 244
                                                                                                             2 EVVPXGMHYS 11
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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55.6%;
                                   Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 55.6
les 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 EEILPOGVH 127
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                                                         NCBI_TaxID=2371;
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SEQUENCE 1
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087D36
1D 087D3
AC 087D3
AC 087D3
DT 01-JU
DT 01-JU
DT 01-JU
DE CODES
CON XY1e1
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COX XX1e1
COX XX1e1
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"A multiple site-specific DNA-inversion model for the control of Ompl
phase and antigenic variation in Dichelobacter nodosus.";
Mol. Microbiol. 17:183-196(1995).
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=96020672; PubMed=7476204;
Moses E.K., Good R.T., Sinistaj M., Billington S.J., Langford C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96257263; PubMed=8654969; Billington S.J., Sinistaj M., Cheetham B.F., Ayres A., Moses B.K., Katz M.E., Rood J.I.; Mart M.E., Rood J.I.; and the property of a native Dichelobacter nodosus plasmid and implications for the evolution of the vap regions."; Gene 172:111-116(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Cardiobacteriales;
Cardiobacteriaceae; Dichelobacter.
NCBI_TaxID=870;
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                                                                                                                                                                            64.3%; Score 36; DB 10; Length 819;
45.5%; Pred. No. 1.5e+02;
.ive 4; Mismatches 2; Indels
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55.6%; Pred. No. 37;
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   InterPro; IPR001444; Flag_bb_rod.
InterPro; IPR005202; GRAS.
Pfam, PF03514; GRAS, IPR0514; BRAS.
PROSTIR; PS00588; PLAGELLA BB ROD; 1.
SEQUENCE 819 AA; 90372 WW; 41B67BD6DC72ADFA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q57489;
01-NOV-1196 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
DNA ligase (Fragment).
Bacteroides nodosus (Dichelobacter nodosus).
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01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Xf1950.
XF1950:
Xylella fastidiosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                            Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
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                                                                                                                                                                                                                                                                                                                                        343 DDVVPTSLHFS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                     1 EEVVPXGMHYS 11
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21 IVPAGVHWS 29
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Best Local Similarity
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SEQUENCE
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Q9PC35;
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09PC35
ID 09PC3
DT 01-0C
DT 01-0C
DT N1-0U
DD N1-0U
DD XF1995
OS XY161.
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05748

AC 05744

AC 05744

DD 01-01

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RA MEDLINE 2036517; Pubmed=1091037;
RA MEDLINE 2036517; Pubmed=10910347;
RA Alvarenga R. Alvee L.M.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alvee L.M.C., Arruda P., Baid G.S., Baptista C.S., Bardacoreil E.D., Bordin S., Bove J.M., Briones M.R.S., Bearoo M.R., Camargo L.B.A., Cararaco D.M., Carrer H. Barroon M.R., Colombo C., Costa F.F., Cocta M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Praga J.S., Franca S.C., Franco M.C., Ferroo J.A., Farna S.C., Franco M.C., Ferroo J.A., Garnier M., Goldman M.H.S., Gomes S.L., Gruber A., Garnier M., Goldman G.H., Lopes C.R., Machado J.A., Racines E.G., Marman E.E., Marina J.F., Marchado J.A., Marches M. Wartins E.M., Marchala M.R., Marchado J.A., Marchado M.A., Marchas E.C., Martins E.M.F., Marchado J.A., Marchado M.A., Marchas B.C., Martins E.M.F., Marchado J.A., Marchado M.A., Marchado M.A., Marchado M.A., Marchas B.C., Minas L.R., Glubasis M.R., Iceite L.C.C., Marchado M.A., Marchado M.A., Marchado M.A., Marchas B.C., Minas L.R., Olivelra M.A., Marchado J.A., Paris A.M. Marchado M.A., M
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MEDLINE=22421331; PubMed=12533478;
Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xylella fastidiosa (strain Temeculal / ATCC 700964).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
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Pred. No. 42;
3; Mismatches 1; Indels
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156 AA; 17144 MW; D8358619C6671A5D CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothetical protein.
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SEQUENCE FROM N.A.
STRAIN=9a5c;
MEDLINE=20365717; PubMed=10910347;
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Q9LW50
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Takita M.A., Lemos B.G.M., Machado M.A., Ferro M.I.T., da Silva F.R., Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M., Carrer H., Carraro D.M., de Olivaira K.C., Nunes L.R., Siqueira W.J., Coutinho L.L., Kimra B.T., Ferro B.S., Harakava R., Kuramae E.E., Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M., Baia G.S., Blanco S.R., Brito M.S., Camnavan F.S., Celestino A.V., Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.I., Kishi L.T., Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.I., Sena J.A.D., Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C., Kitajima J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                               راكسيومدعتابه analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella fastidiosa.";
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transcription, DNA-dependent; IEA.
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MEDLINE=9227649; Pubmed=7756828;
MEDLINE=9227649; Pubmed=7756828;
Chme-Takagi M., Shinshi H.;
Ethylene-inducible DNA binding proteins that interact with an ethylene responsive element.";
Plant Cell 7:173-182(1999).
Plant Cell 7:173-182(1999).
Plant TO2590; TO2590.
                                                                                                                                                                                                                                                                                                                                                                                          62.5%; Score 35; DB 16; Length 156; 55.6%; Pred. No. 42; 1; Indels ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.5%; Score 35; DB 10; Length 233; larity 60.0%; Pred. No. 65; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Complete proteome.
SEQUENCE 156 AA; 17130 MW; D83583B9C6671A5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00380; AP2; 1.
SEQUENCE 233 AA; 25563 MW; 6CD16783582C0CB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
EREBP-2.
                                                                                                                                                                                                                 J. SECTEMBER 185:1018-1026(2003).

EMBL; AE012556; AAO28718 1; --
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007165; P:signal transducer activity; IEA.
GO; GO:0007165; P:signal transducer activity; IEA.
INCOTINE, P:signal transduction; IEA.
INCOTINE; PS50851; CHEW.
INCOTINE; PS50851; CHEW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicotiana tabacum (Common tobacco)
                                                                                                                                                         Kitajima J.P.;
"Comparative analyses of the
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 ÉÉILPQGVH 127
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Best Local Similarity
Matches 6; Conserv
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
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STRAIN=RBSO / ATCC BAA-588;
STRAIN=22827954; PubMed=1210271;
BARKhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Dogget J.,
Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Morberzak H., O'Neil S., Ormond D., Price C.,
Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-2039950; PubMed=10945353;

Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;

Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;

Kitazatcerization of gene expression of NeBRFs, transcription factors

of basic PR genes from Nicotiana sylvestris.";

Plant Cell Physiol. 41:817-824 (2000).

EMBL; AB016264; BA897122.1;

HSSP; 080337; 2GCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0006355; P:regalation of transcription, DNA-dependent; IEA.

InterPro; IPR001471; TF_ERP.

PRAM; PR00847; APZ-domain; 1.

PRINTS; PR00367; ETRESPELEMNT.

ProDom; PD001423; TF_ERP; 1.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.5%; Score 35; DB 10; Length 237; 60.0%; Pred. No. 66; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00380; AP2; 1.
SEQUENCE 237 AA; 26243 MW; 01BC3EBB51E46298 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative enoyl-COA hydratase.
                                                                                                                                                                           237 AA
                                                                                                                                                                                                                              Created)
                                                                                                                                                                           PRT;
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01-OCT-2000 (TIEMBLIA, 15,
01-OCT-2000 (TIEMBLIA, 15,
01-JUN-2003 (TIEMBLIA, 24,
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Best Local Similarity 60.0
Matches 6; Conservative
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94 QAVVPKGRHY 103
  10
                                             90 QAVVPKGRHY 99
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1 EEVVPXGMHY
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Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
"Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertussis and Bordetella bronchiseptica.";
Nat. Genet. 35:32-40(2003).
BMBL, BX640440; CAE31621.1; -.
CCMplete protecome.
CCMplete protecome.
262 AA; 28907 MW; B3CA29331CB776B2 CRC64;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=519;
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                                                                                                                                                                                                                                              Score 35; DB 16; Length 262;
Pred. No. 73;
1; Mismatches 2; Indels
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Q7W0Z3;
01-OCT-2003 (TYENBLE1. 25, Created)
01-OCT-2003 (TYENBLE1. 25, Last sequence update)
01-OCT-2003 (TYENBLE1. 25, Last annotation update)
Putative enoyl-CoA hydratase.
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Best Local Similarity 66.7%;
Matches 6; Conservative 1
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Best Local Similarity 66.7
Matches 6; Conservative
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182 QEVVPYGQH 190
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Search completed: June 3, 2004, 11:57:31 Job time: 30.8667 secs

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45 83.3 11 5 ABB80558 Abb80558 Hepati 45 83.3 11 5 ABB80560 Abb80527 Abb80527 Abb80527 Abb80527 Abb80527 Abb80527 Abb80534 Abb80584 Abb805	44 81.5 11 5 ABB80533 Abb80533 Hepati 41 75.9 11 5 ABB80536 Abb80536 Hepati	32 41 75.9 11 5 ABB80535 Abb80535 Heparitis 33 41 75.9 11 5 ABB80540 Abb80540 Heparitis 34 41 75.9 11 5 ABB80539 Abb80539 Heparitis 35 40 74.1 11 5 ABB80549 Abb80549 Heparitis	40 74.1 11 5 ABB80544 AD080544 Hepatic 40 74.1 11 5 ABB80537 AD0805541 Hepatic 40 74.1 11 5 ABB80541 AD0805541 Hepatic 40 74.1 11 5 ABB80553 AD080553 Hepatic 40 74.1 11 5 ABB80553 AD080553 Hepatic	40 74.1 11 5 ABB80545 ADD80032 ADD800545 Hepatic	39 /2.2 11 5 ABB80550 ADD80534 Hepati 39 72.2 11 5 ABB80550 ADD80550 Hepati 30 73 11 5 ADB80655	מיין מיין מיין מיין מיין מיין מיין מיין	ALIGNMENTS	RESULT 1 ABB80561 ID ABB80561 standard; peptide; 11 AA.	AC ABB80561;	AA DT 08-OCT-2002 (first entry)	XX DB Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.	XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; KW virucide. XX	OS Synthetic.	Key Location/Qualifiers Modified-site 1	Modified-site 6	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Modified-Site	Misc-differ	Modified-site 11 /note= "C	XX PN W0200208251-A2.	XX PD 31-JAN-2002.	AA 19-JUL-2001; 2001WO-US023169.	AA 21-JUL-2000; 2000US-0220101P.	AA (CORV-) CORVAS INT INC.	AA PI Lim-Wilby M, Levy OE, Brunck TK;	AA WPI; 2002-361643/39.	PT Novel peptide compound having hepatitis C virus protease inhibitory PT activity useful for treating disorders associated with hepatitis C virus PT protease.	XX PS Claim 17; Page 65; 69pp; English. XX
5.1.6 Compugen Ltd.		earch time 45.9333 Seconds (without alignments) 67.664 Million cell updates/sec			ង	ers: 1586107				*			4	B predicted by chance to have a concrete the result being printed, total score distribution.		4 6 7	<u> </u>	524	229	242	4 60 6	94.0	222	766	557	163	Abb80567 Hepatitis Abb80559 Hepatitis Abb80526 Hepatitis	23 23 36 4 50 50 50 50 50 50 50 50 50 50 50 50 50
GenCore version 5 Copyright (c) 1993 - 2004 C	OM protein - protein search, using sw model	Run on: June 3, 2004, 11:31:01; Sear (wi) 67.	Title: US-09-309-164-8 Perfect score: 54 Sequence: 1 BEVVPXGMDYS 11	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 1586107 seqs, 282547505 residue	Total number of hits satisfying chosen parameters	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	4			<pre>5: geneseqp2002s:* 6: geneseqp2003as:* 7: geneseqp2003bs:* 8: qeneseqp2004s:*</pre>		s the number of result er than or equal to the ved by analysis of the	SITALAMADE	Query Match Icaath DB	Score March Length DB	1 52 96.3 11 5 2 52 96.3 11 5	52 96.3 11 5 52 96.3 11 5	47 87.0 11 5	47 87.0 11 5	0 46 85.2 II 5	2 46 85.2 11 5	4 46 85.2 II S	6 46 85.2 11 5	8 46 85.2 11 5 0 46 85.2 11 5	20 46 85.2 11 5 ABB80567 21 46 85.2 11 5 ABB80559 22 46 85.2 11 5 ABB80526	3 46 85.2 11 5 4 46 85.2 11 5 5 45 83.3 11 5

Sequence 11 AA;

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
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                                                                                                                                   Length 11;
                                                                                                                                ch 96.3%; Score 52; DB 5; Length 11; Similarity 100.0%; Pred. No. 0.0024; 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                  Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                           Sequence 11 AA;
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activity usefu
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

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96.3%; Score 52; DB 5; Lei
llarity 100.0%; Pred. No. 0.0024;
Conservative 0; Mismatches 0;
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                                                                                                                                                      ABB80529 standard; peptide; 11 AA.
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                                                                                                                                                                                                     (first entry)
                                             Conservative
                                                                   1 EEVVPXGMDYS 11
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                                                                                          EEVVPXGMDYS
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Best Local Similarity
Matches 11; Conserv
                     Query Match
Best Local Similarity
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                           11;
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                                                                                                                                                                                                                                                                                          Synthetic
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"Norvalyl carbonyl forming keto-amide linkage with ? 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus protesse inhibitory activity useful for treating disorders associated with hepatitis C virus
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virucide.
                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42
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100.0%; Pred. No. 0.0024;
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                                                                                                                                                                                                                                   'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                       'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                   'note= "Oxymethionine"
                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         /note= "D-form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brunck
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                                                (first entry)
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                                                                                                                                                                                                                                                                                 residue
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                                                                                                                                                                                                      Key
Modified-site
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                                                08-OCT-2002
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                                                                                                                                                                  Synthetic.
                ABB80562;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have viucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                     note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
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                                                                                                                                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8
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                                                                                                                                                                                                                                                                                                                                                                         'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal amide"
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                                                                                                              ABB80528 standard; peptide; 11 AA
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                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       residue 7"
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11; Conservative
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                              EEVVPXGMDYS 11
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EEVVPXGMDYS
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Modified-site
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Best Local &
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Gaps

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0; Indels

(first entry)

08-OCT-2002

RESULT 5 ABB80562 ID ABB80562 standard; peptide; 11 AA.

Matches

8 셤 ABB80542

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                          "Norvaly1 carbony1 forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                           btide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                           'note= "N-terminal acetyl"
                                                                                                                                                                         /note= "C-terminal amide"
                                                                                                         note= "D-form residue"
                                                                                                                                        'note= "D-form residue"
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Location/Qualifiers
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                                                               /note= "No
residue 7"
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Best Local Similarity
                                                                                                                           Misc-difference
                                                                                            Misc-difference
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                                                                                                                                                         Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                         /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23.
                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22.
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Pred. No. 0.023;
0; Mismatches 1; Indels
                                                                                                                                                              'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                          /note= "C-terminal amide"
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                                                                                                                                 Key
Modified-site
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                                                                                                 Synthetic
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Best Local S
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                              Gaps
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                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
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Length 11;
                                Indels
Score 47; DB 5;
Pred. No. 0.023;
                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
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Modified-site
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Synthetic

virucide

Best Loca Matches

ABB80543

/note= "C-terminal amide"

Brunck TK;

Levy OE,

/note= "D-form residue"

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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virucide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 64; 69pp; English.
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Misc-difference
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Modified-site
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EEVVPXGQDYS 11

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hepatitis C virus (HCV) professe inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.036;
0; Mismatches
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                                                                                                               Brunck TK;
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                                              21-JUL-2000; 2000US-0220101P.
                19-JUL-2001; 2001WO-US023169
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Local Similarity 90.9%;
Les 10; Conservative (
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                                                                               (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                                    virus
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Gaps

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87.0%; Score 47; DB 5; Length 11; 90.9%; Pred. No. 0.023; 1; Indels ive 0; Mismatches 1; Indels

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(first entry)

'note= "N-terminal acetyl"

Location/Qualifiers

/note= "C-terminal amide"

note= "D-form residue"

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compound having hepatitis C virus protease inhibitory il for treating disorders associated with hepatitis C virus

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV procease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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          WPI; 2002-361643/39
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Best Local Similarity
Matches 10; Conserv
                                              useful
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activity usefu
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(first entry)

'note= "Norvaly1 carbony1 forming keto-amide linkage with

'note= "C-terminal amide'

residue 7"

note= "N-terminal acetyl"

Location/Qualifiers

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                               Length 11
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Pred. No. 0.036;
0; Mismatches
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Score 46; DB 5; Length 11; Pred. No. 0.036; 0; Mismatches 1; Indels

85.2%;

EEVVPXGTDYS 11

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ABB80547

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/note= "2-aminoisobutyryl carbonyl residue forming a keto-amide linkage with residue 7"
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                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
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Pred. No. 0.036;
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                             ABB80566 standard; peptide; 11
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Pred. No. 0.036;
0, Mismatches 1; Indels
               Length 11;
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Pred. No. 0.036
0; Mismatches
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           Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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Gaps

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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #36.

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7\mbox{\ensuremath{^{"}}}
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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                             'note= "N-terminal acetyl"
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/note= "C-terminal amide"
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                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC.
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Query Match 85.2%; Score 46; DB 5; Length 11; Best Local Similarity 90.9%; Pred. No. 0.036; Matches 10; Conservative 0; Mismatches 1; Indels

Search completed: June 3, 2004, 11:48:23 Job time : 46.933 Becs

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SEQ ID NO 4
LENGTH: 341
TYPE: PRT
ORGANISM: Citrus unshiu
FEATURE:
OTHER INFORMATION: Xaa at position 109 is one of Ala, Arg, OTHER INFORMATION: Cys, Gln, Glu, Gly, His, Ile, Leu, Lys,
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33. /cgn2 = 6/pcdata/2/iaa/6A_COMB.pep:*
4. /cgn2 = 6/pcdata/2/iaa/Ba_COMB.pep:*
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6: /cgn2 = 6/pcdata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-394-272-4

US-09-394-272-4

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US-09-569-147-76

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US-09-569-147-82

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Listing first 45 summaries
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No.
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Sequence 4, Appli Sequence 23, Appl Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 7, Appli Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 22, Appl	SEQUENCES RELATING TO DIAGNOSTICS AND THERAPEUTICS	Length 181; ; Indels 0; Gaps 0;	FROM CITRUS AND DNA ENCODING
883 4 US-09-667-373-4 65 5 17197-51 152 2 US-08-580-98A-23 152 2 US-08-460-694-4 152 3 US-08-460-744-4 173 1 US-08-460-771B-4 173 1 US-08-46-517-21 189 2 US-08-46-517-21 189 3 US-08-46-3772-21 189 3 US-08-46-3772-22 189 5 PCT-US93-05000-21 231 3 US-08-464-517-22 236 2 US-08-464-517-22 236 2 US-08-464-517-22 236 2 US-08-464-517-22 236 3 US-08-464-517-22 236 4 US-08-464-517-22 236 4 US-08-464-517-22 236 5 US-08-464-517-22 236 5 US-08-464-517-22 236 6 US-08-464-517-22 236 7 US-08-464-517-22 237 7 US-08-464-517-22 238 7 US-08-	ACIL FOR	7%; Score 36; DB 4; 0%; Pred. No. 11; 0; Mismatches 3	38853948B SE PHOSPHATE SYNTHASE WE - US/08/853,948B - 05-09
228 331 332 333 344 444 444 444 444 444	RESULT 1 US-09-134-000C-4848 ; Sequence 4846, Application US/09134000C ; Parent No. 6617156 ; PAPLICANT: Lynn Doucette-Stamm et al	Query Match Best Local Similarity 70. Matches 7; Conservative Qy 1 EEVVPXGMDY 10 Db 145 EEVVPTSEDY 154	RESULT 2 US-08-853-948B-4 ; Sequence 4, Application US/(; Patent No. 621043 ; GENERAL INFORMATION: ; TITLE OF INVENTION: ; TITLE OF INVENTION: ; TITLE REFERENCE: 0049-0235; ; CURRENT FILING DATE: 1997. ; NUMBER OF SEQ IN OS: 10

Asp, Phe, Asn, Met,

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TYPE: PRT
CORGANISM: Oryza sativa
US-09-394-272-10
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Sequence 5, Application US/08853948B
Patent No. 621004A;
GENERAL INFORMATION:
TITLE OF INVENTION: SUCKOSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: 199-0235-0
CURRENT FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 10
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 348
TYPE: PRT
TYPE: PRT
CORMANISM: Citrus unshiu
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Pred. No. 24;
2; Mismatches 1; Indels
                                                      Query Match 66.7%; Score 36; DB 3; Length 341; Best Local Similarity 66.7%; Pred. No. 22; Msmatches 1; Indels Matches 6; Conservative 2; Mismatches 1; Indels
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Pred. No. 22;
2; Mismatches 1; Indels
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patent No. 6323015
general information of cozoo Jr., Emil M.
APPLICANT: Cozoo Jr., Emil M.
APPLICANT: Calmi, Perry G.
APPLICANT: Calmi, Perry G.
APPLICANT: Tarczynski, Mitchell
TITE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: BB1166 US NA
CURRENT APPLICATION NUMBER: US/09/697,367
CURRENT APPLICATION NUMBER: 60/084,529
PRIOR PILING DATE: 1998-MAY-07
PRIOR PLING DATE: 1999-WAY-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENTH: 368
; OTHER INFORMATION: Pro, Ser, Thr, Trp, Tyr, or Val
US-08-853-948B-4
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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US-09-697-367-24
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US-09-697-367-24
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        435 VIPPGMDFS 443
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CITY: Palo Alto
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                          Score 36; DB 2; Length 1068;
Pred. No. 81;
                                                                                                                                                                                                                                                        1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: THEN PC -DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/128,777
FILING DATE: NOT YET ASSIGNED
CITASIFFCATION: B00
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 08/175,471
FILING DATE: 27-DEC-1933
ATTORNEY/AGENT INFORMATION:
NAME: BAIDATA RAS-VENCET
RECISTRATION NUMBER: CGNE.072.02US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Law Offices of Barbara Rae-Venter STREET: 260 Sheridan Avenue, Suite 440 CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Van Assche, C.
APPLICANT: Lando, D.
APPLICANT: Bruneau, J. M.
APPLICANT: Gervais, M.
APPLICANT: Gervais, M.
TITLE OF INVENTION: MODIFICATION OF SUCROSE TITLE OF INVENTION: PHOSPHATE
TITLE OF INVENTION: SYNTHASE IN PLANTS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSESSE: Law Offices of Barbara Rae-Venter
                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08718777
Patent No. 5981852
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068
                                                                                                                                                                                                            66.7%;
                                                                                                                                                                                                                                Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415)328-4477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 amino aci
                                                                                  TYPE: Amino acia
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                       |:| |||:|
435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                           3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VVPXGMDYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                 US-08-429-054A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Ca
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-718-777-7
                                                                                                                                                                                                               Query Match
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Gaps
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US-09-394-272-8

Sequence 8, Application US/09394272

Patent No. 6472588

GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, A. Scott
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14
Sequence 7, Application US/09051341
Patent No. 6124528
Patent No. 6124528
Patent No. 6124528
Patent No. 6124528
TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: AADRESSE:
STREET: 260 Sheridan Avenue, Suite 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                               ZULE: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 800
PRIOR PEPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17351
FILING DATE: 25-0CT-1996
APPLICATION NUMBER: US 08/549,016
FILING DATE: 27-0CT-1995
PRIOR APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-DAN-1995
APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-DAN-1995
ATOMERA/BADENT INFORMATION:
REGISTRATION NUMBER: 32,750
REGISTRATION NUMBER: 32,750
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)328-4470
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
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PA
                                                                                                                                                                                                                                                                                                                   SEQ ID NO 9
LENGTH: 1084
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Sequence 11, Application US/09394272;
Patent No. 6472589;
GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 1083
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                                                                                                                                                                                           Gaps
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Sequence 4, Application US/09394272

Patent No. 6472588

GENERAL INFORMATION:
APPLICANT: Hadigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REPERENCE: 201304/100 NUMBER: US/09/394,272

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4
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66.7%; Score 36; DB 4; Length 1081;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                            Score 36; DB 4; Length 1068; 
pred. No. 81; 
2; Mismatches 1; Indel8 ·
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; ORGANISM: Craterostigma plantagineum
US-09-394-272-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana US-09-394-272-11
                                                                                                                                                   66.7%;
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 1068
                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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483 VIPPGMDFS 491
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445 VIPPGMDFS 453
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435 VIPPGMDFS 443
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                                     ; LENGTH: 1068
; TYPE: PRT
; ORGANISM: Zea mays
US-09-394-272-8
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US-09-394-272-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Sequence 9, Application US/09394272
Sequence 9, Application US/09394272
Patent No. 6472588
GENERAL INFORMATION:
APPLICANT: Haiglar, Candace H.
APPLICANT: Haiglar, Candace H.
APPLICANT: Haiglar, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REPERENCE: 201304/100
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 66.7%; Score 36; DB 4; Length 1084;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFWWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,147

FILLING DATE: 25-March-1996

CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
TITLE OF INVENTION: HUMANISED ANTIBODIES
NUMBER OF SEQUENCES: 95
NUMBER OF SEQUENCES: 95
NUMBER OF SEQUENCES: 95
ADDRESSEE: No-GROOCK Washburn Kurtz Mackiewicz & ADDRESSEE: No-GROOCK Washburn Kurtz Mackiewicz & STREET: One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: T-U-ILO, DOTEGN YALKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: 35,719
RELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 annino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 76, Application US/08569147
Patent No. 6180377
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 VIPPGMDFS 461
                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-394-272-9
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US-09-252-991A-31637

Sequence 31637, Application US/09252991A

Sequence 31637, Application US/09252991A

Sequence 31637, Application US/09252991A

Sequence 31637

Sequence 31637

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107166-136

CURRENT PAPLICATION NUMBER: US/09/252,991A

CURRENT PAPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-17

NUMBER OF SEQ ID NOS: 33142

LENGTH: 1065
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                                                                                     RESULT 14

US-08-569-147-82

US-08-569-147-82

Sequence 82, Application US/08569147

Patent No. 6180377

GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: HUMANISED ANTIBODIES

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 61803771s, LLP

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STREET: One Liberty Place - 46th Floor
STREET: One Liberty Place - 46th Ploor
CUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: PA PECOMPUTER: DOS/MS-DOS
SOFTWARE: PAECHLIN Release #1.0, Version #1.25 (EPO)
SOFTWARE: PAECHLIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/569,147

FILMO BATE: 25-ABACH-1996
CLASSIFICATION NUMBER: US/08/569,147

TELECOMMUTICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION NUMBER: 35,719
REFERENCE/COMPUTER: SEQ.1100
TELEFAX: (215) 568-3439
INFORMATION POR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICA:

SEQUENCE CHARACTERISTICA:

SEQUENCE CHARACTERISTICA:

SEQUENCE CHARACTERISTICA:

SEQUENCE CHARACTERISTICA:
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63.0%; Score 34; DB 3; Length 140;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 VVPTGFDY 129
                                                       122 VVPTGFDY 129
VVPXGMDY 10
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
is ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31637

Query Match
Best Local Similarity 85.7%; Pred. No. 2e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PXGMDYS 11

Db 324 PGGMDYS 330

Search completed: June 3, 2004, 12:03:07
Job time : 12.8 secs
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Sequence 8, Appli
Sequence 12, Appl
Sequence 13, Appl
Sequence 22, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                      June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35,
Sequence 40,
Sequence 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6,
Sequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31
Sequence 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1155919
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-12
US-09-909-164-13
US-09-909-164-25
US-09-909-164-27
US-09-909-164-5
US-09-909-164-9
US-09-909-164-9
US-09-909-164-10
US-09-909-164-10
US-09-909-164-10
US-09-909-164-32
US-09-909-164-32
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US-09-909-164-35
US-09-909-164-35
US-09-909-164-35
US-09-909-164-35
US-09-909-164-35
                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                     1155919 segs, 281338677 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                       US-09-909-164-8
54
1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length DB
                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                     Searched:
                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
No.
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Sequence 45, Appl	equence 46,	equence 47,	48,	equence 49,	equence 50,	equence 51,	22	equence 7,	equence 11,	17	equence 18	equence 19	Sequence 20, Appl	equence 23	equence 24,	2	equence 25,	equence 28,	eguence 29,	33	36,	equence 37,	43	30	equence 34,	equence 38,	quence 39,	42	9 44,
-09-909-164-4	-09-909-16	-09-909-164-4	-09-909-164-4	-09-909-164-4	-09-909-164-	-09-909-164-5	-09-909-164-5	-09-909-164-	-09-909-164-1	-09-909-164-1	-09-909-164-1	-09-909-164-1	-16	-09-909-164-2	9-164-2	-09-909-164-2	-09-909-164-2	-09-909-164-2	-09-909-164-2	-09-909-164-3	9-909-164-3	US-09-909-164-37	-09-909-164-4	-09-909-164-3	-09-909-1	-09-909-164-3	-09-909-1	-09-909-164-4	06-60-
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16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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RESULT 1

Sequence 8, Application US/09909164

Sequence 8, Application US/09909164

Sequence 8, Application US/09909164

Sequence 8, Application No. 2820020068702A1

Sequence 9, Application No. 2820020068702A1

SEPHICANT COVERENT INCOME.

APPLICANT LIEWY, Oddie 8

APPLICANT LIEWY, Oddie 8

APPLICANT SETUN NOVEL PETINES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

CURRENT PETING DATE: 2000-07-21

PRIOR PELING DATE: 2000-07-21

PRIOR PELING DATE: 2000-07-21

PRIOR PELING DATE: 2000-07-21

PROTEST PERIOR NOVEL SEQUENCE

FROM APPLICANT NOVEL SEQUENCE

FROM SECUL IN VERSION 3.1

FRAUTE: NORMATION: 11-mer synthesized according to example 1

FRAUTE: NORMATION: 11-mer synthesized according to example 1

FRAUTE: NORMATION: 11-(1)

OTHER INFORMATION: ACETYLATION

FRAUTE: NORMATION: 05-(2)

OTHER INFORMATION: 05-(2)

OTHER I
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Sequence 22, Application US/09909164
Sequence 22, Application US/09909164
Sequence 22, Application US/09909164
Sequence 22, Application No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corves International, Inc.
APPLICANT: Lin-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terce K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFREENCE: IN01192-US
CURRENT FILING DATE: 2003-03-25
PRIOR PLILING DATE: 2003-07-21
PRIOR PLILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                   OTHER INFORMATION: 11-mer synthesized according to example 1
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  CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 5000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC_FEATURE
LOCATION: (8)..(9)
CTHER INFORMATION: D-amino acids
US-09-909-164-13
                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1) (1)
OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
FRATURE:
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ORGANISM: artificial sequence
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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OTHER INFORMATION: AMIDATION
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US-09-909-164-22
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LENGTH: 11
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Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile B

APPLICANT: Levy, Odile B

APPLICANT: Lovy, Odile B

APPLICANT: Lovy, Odile B

CURRENT BETTOR : 100192-105

CURRENT APPLICATION NUMBER: US/09/90,164

CURRENT PILING DATE: 2003-03-25

PRIOR APPLICANTON NUMBER: 60/220,101

PRIOR APPLICANTON NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 12

LENGTH: 11
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Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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                                                                        Query Match
96.3%; Score 52, DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 11; Conservative 0; Mismatches 0; Indels
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NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE LOCATION: (8). 7(8) OTHER INFORMATION: D-amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: AMIDATION
; OTHER INFORMATION: AMIDATION US-09-909-164-8
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Best Local Similarity 100.
Matches 11; Conservative
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NAME/KEY: MOD_RES
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US-09-909-164-13
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TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE 100192-08
CURRENT APPLICATION NUMBER: 60/20,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PARENT APPLICATION NUMBER: 3.1
SOFTWARE: PETING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PETING DATE: D
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Pred. No. 0.0097;
0; Mismatches 1
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OTHER INFORMATION: norvaline-(CO)
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LOCATION: (8)..(9)

OTHER INFORMATION: D-amino acids
US-09-909-164-27
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LOCATION: (1)...(1)
CTHER INFORMATION: ACETYLATION
FRATURE:
NAME, KEY: MOD_RES
LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: artificial sequence
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Best Local Similarity 90.9
Matches 10; Conservative
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NAME/KEY: MISC_FEATURE
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Sequence 26, Application US/09909164
Sequence 26, Application US/09909164
Sequence 26, Application US/09909164
Sequence 26, Application No. US20020068702A1
SEQUENCE NO. US20020068702A1
SEPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRESENCE: 1001192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
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Pred. No. 0.0097;
0; Mismatches 1; Indels
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Pred. No. 0.0097;
0; Mismatches 1; Indels
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OTHER INFORMATION: 11-mer synthesized according to example
FEATURE:
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Publication No. US20020068702A1
GENERAL INFORMATION
APPLICANT: Corves International, Inc.
APPLICANT: Lim-Wilby, Marguerita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (6).7(6)
OTHER INFORMATION: norvaline-(CO)
OTHER INFORMATION: norvaline-(CO)
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COTHER INFORMATION: D-amino acid
US-09-909-164-26
                                                        NAME/KEY: MISC_FEATURE
J. COCATION: (9)...(9)
CTHER INFORMATION: D-amino acid
US-09-909-164-22
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SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 11
TYPE: PRT
ORGANISM: artificial sequence
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative (
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC_FEATURE
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Best Local Similarity
Matches 10; Conserv
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Sequence 10, Application US/09909164
; Sequence 10, Application US/09909164
; Publication No. US20020068702A1
; GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-whiby, Marguerita
APPLICANT: Lim-whiby, Marguerita
APPLICANT: Lim-whiby, Marguerita
APPLICANT: Lim-whilby, Marguerita
APPLICANT: Brunck Free R8
FILE REFERENCE: IN01192-US
CURRENT FILING DATE: 2000-07-25
FRIOR PRIOR PLING DATE: 2000-07-21
FRIOR PLING DATE: 2000-07-21
FRIOR PLING DATE: 2000-07-21
FRIOR PLING DATE: DATE: Lim-whilby Marguerita
SEQ ID NO 10
LENGTH: Lim-whilby Marguerita
LENGTH: LIM-whilby 
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE Brunck, Terence K
TITLE LOUISENING NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: IN01192-08
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILLING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 11
TYPE: PRI
CREMINE: TENTE TENT
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OTHER INFORMATION: norvaline-(CO)
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LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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OTHER INFORMATION: AMIDATION
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NAME/KEY: MOD RES
LOCATION: (11)...(11)
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NAME/KEY: MOD_RES
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APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Levy, Odie E
APPLICANT: Levy, Odie E
APPLICANT: Levy, Odie E
APPLICANT: Levy, Odie E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INDI192-US
FILE REFERENCE: INDI192-US
FILE REFERENCE: LONDISCE: 0503-03-25
PRIOR APPLICATION NUMBER: US/09/20,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                   Query Match 85.2%; Score 46; DB 12; Length 11; Best Local Similarity 90.9%; Pred. No. 0.015; Matches 10; Conservative 0; Mismatches 1; Indels
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Publication No. USZ0020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
     OTHER INFORMATION: norvaline-(CO)
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: D-amino acid
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OTHER INFORMATION: ACETYLATION
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US-09-909-164-6
                                        FEATURE:

NAME/KEY: MOD RES

LOCATION: (11)

OTHER INPORMATION: AMIDATION
US-09-909-164-5
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NAME/KEY: MOD RES
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US-UY-104-35
; Sequence 35. Application US/09909164
; Publication No. US20020068702A1
; Publication No. US20020068702A1
; GENERAL INFORMATION:
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Brunck, Terence K
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; TITLE OF INVENTION: NUMBER: US/09/909,164
; CURRENT APPLICATION NUMBER: 60/220,101
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 35
; LENGTH: L1

APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS (
FILE REFERENCE: INO1192-05
CURRENT APPLICATION WIMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN version 3.1
SEQ ID NO 32
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) LOCATION: (9)...(9)
; CTHER INFORMATION: D-amino acid
US-09-909-164-32
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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US-09-909-164-35
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Sequence 31, Application US/0909164
Sequence 31, Application US/0909164
Sequence 31, Application US/0909164
Sequence 31, Application No. US20020068702A1
SERERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: INO3192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
SURING APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
SOFTWARE: Patentin version 3.1
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US-09-909-164-32
US-09-909-164-32
; Publication No. US20020068702A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (6). (6)
COTHER INFORMATION: norvaline-(CO)
US-09-909-164-31
                           OTHER INFORMATION: AMIDATION FEATURE:
NAME/KEY: MISC FEATURE
OCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
PEATURE:
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NAME/KEX: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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90.9%;
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ORGANISM: artificial sequence
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserva
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Publication No. US20020068702A1
GENERAL INFORMATION:
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| Sequence 40, Application US/0909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Lim-Wilby, Marguerita
| CURRENT FILING DATE: 2003-03-25
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SEQ ID NO 40
| Lim-Wilby, Marguerita
| Lim-Wilby, Marg
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Pred. No. 0.015;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 12; Length 11; Pred. No. 0.015; 0; Mismatches 1; Indels
                                                          FEATURE:

NAMEX KEY: MISC_FEATURE

LOCATION: (6)...(6)

OTHER INFORMATION: norvaline-(CO)

FEATURE:

NAMEX KEY: MISC_FEATURE

LOCATION: (9)...(9)

CTHER INFORMATION: D-amino acid
US-09-909-164-35
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OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: artificial sequence
                    OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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RESULT 15 US-09-909-164-41 ; Sequence 41, Application US/09909164

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APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Lovy, Odile B
APPLICANT: Lovid B
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Pred. No. 0.015;
0; Mismatches 1; Indels
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (8). (9)
; OTHER INFORMATION: D-amino acids
US-09-909-164-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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90.9%;
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ORGANISM: artificial sequence
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LOCATION: (11\overline{1})...(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw OM protein - protein search,

June 3, 2004, 11:35:47; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec Run on:

US-09-909-164-8 54 Perfect score:

1 EEVVPXGMDYS 11 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

disease resistance RND multidrug effl hypothetical prote hypothetical 367K partial transposas hypothetical prote fibroblast.growth hypothetical prote conserved hypothet unknown protect	transposase ISC105 hypothetical prote pantoate-beta-alan transposase ISC105
148899 F83335 T310330 A99427 A99427 A99427 A906335 B57021 A966001 A966001	C90307 C64417 G83055 B90487
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908 10662 34722 1128 1128 1128 1228 7225 7225	2267 283 293
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4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	
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## ALIGNMENTS

hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
Nylternate names: hypothetical protein 02612; hypothetical protein YOL303.3
C,Species: Saccharomyces cerevisiae
C,Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C,Accession: S54619; S66879
R,de Haan, M.; Maarse, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54617
A;Reference number: S54617
A;Residues: 1-156 < DEH>
A;Residues: 1-156 < DEH>
A;Cross-references: EMBL: X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
submitted to the Protein Sequence Database, July 1996

A;Accession: S66879
A;Molecule type: DNA
A;Roledudes: 1-156.
A;Coss-references: EMBL:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR0
A;Experimental source: strain S288C

C, Genetics:

A,Cross-references: SGD:S0005539 A,Map position: 15R C,Superfamily: hypothetical protein YOR013w

Length 156; 5

Gaps ö Indels ore 40; DB 2 ed. No. 1; Mismatches 14.1%; Score 40; ilarity 77.8%; Pred. No. Conservative 1; Mismatc Query Match Best Local Similarity Best Loc Matches

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2 EVVPXGMDY 10 ઠે

EVMPLGMDY 58 20 셤

conserved hypothetical protein AF2411 - Archaeoglobus fulgidus

Species: Archaeoglobus fulgidus Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

hypothetical prote probable hexosyltr

i-lactate dehydrog phenylalanine-tRNA succinate dehydrog

ABC transporter AT disease resistance

A70164 F81138 T48898

06-methylguanine-D

**D98182** G69290

CiAccession: D6551
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodso R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodso Glodek, A.; Zhou, L.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae A;Tele: The Complete genome sequence of the hyperthermophilic, sulfate-reducing archae A;Telesension: D69551
A;Accession: D69551
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative

A;Molecule type: DNA A;Residues: 1-363 <KLE>

d

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sucrose-phosphate synthase (EC 2.4.1.14) isoform 3 - Citrus unshiu (fragment)
C,Species: Citrus unshiu
C,Species: Citrus unshiu
C,Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C,Accession: 875650
R,Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
A,Title: Cloning and molecular analysis of CDNAs encoding three sucrose phosphate synt A,Reference number: 872648; MUDD:96439842; PMID:8842155
A,Accession: 872650
A,Returs number: Gaquence not shown
A,Residues: 1-348 «KOM»
A,Residues: 1-348 «KOM»
A,Residues: 1-348 «KOM»
A,Residues: BMBL;AB006666; NID:92351059; PIDN:BAA22071.1; PID:92351060
A,Residues: BMBL;AB006666; NID:92351069; A,Residues: BMBL;AB006666; NID:92351060
A,Residues: SPS
C,Genetics:
A,Genetics:
A,Genetic
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unknown protein P25P22.17 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: 0896764
C;Accession: 0896764
C;Accession: 0896764
C;Aribeologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
Chin, C.W.; Huphes, B.; Hurzar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jun, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial
C;A.; M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
A;Authors: A;Mitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Pathway: sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology
C;Kpywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
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C; Genetics:
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66.7%; Score 36; DB 2; Length 348;

Best Local Similarity 66.7%; Pred. No. 17;

Matches 6; Conservative 2; Mismatches 1; Indels
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Pred. No. 2
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70.0%;
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234 VIPPGMDFS 242
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hes 7; Conserv
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VI procein - tobacco yellow dwarf virus (strain Australia)
C'Species: tobacco yellow dwarf virus
C'Species: tobacco yellow dwarf virus
C'Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C'SAccession: A42452
R'Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
Virology 187, 633-642, 1992
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yellogate and the component of the component of tobacco yellogate and the component of tobacco yellogate and tobacco yellogate and tobacco yellogate and tobacc
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Mol. Gene. Zez, 346-351, 1996
A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate synths
A;Reference number: S72648; MUID:9643942; PMID:8842155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructose A; Description: sucrose biosynthesis (); Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology (); Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis (); Reywords: sucrose/sucrose-phosphate synthase homology (fragment) <8SPS>
                                                                                                        A;Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265068
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A;Experimental source: fruit, cv. Miyagawa-Wase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Accession: S72649
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A, Molacule type: DNA
A; Residues: 1-102 «MOR»
A; Cross-references: GB: M31103; NID: G335283; PIDN: AAA47947.1; PID: G335284
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                                                                                                                                                                                                                Score 38; DB 2; Length 363;
Pred. No. 6.8;
3; Mismatches 2; Indels
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Score 36; DB 2 Pred. No. 4.3; 3; Mismatches

66.7%;

Query Match
Best Local Similarity 60.0
Matches 6; Conservative

2 EVVPXGMDYS 11

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A, Accession: S72649 A, Status: nucleic acid sequence not shown

A;Residues: 1-341 <KOM>

A; Molecule type: mRNA

Conservative

Query Match Best Local Similarity Matches 6; Conserv

228 VIPPGMDFS 236

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RESULT 5

3 VVPXGMDYS 11

and D-fruc

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sucrose-phosphate synthase homolog F28M11.40 - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispate: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
Cispate: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.)
Bibmitted to the Protein Sequence Database, March 1999
A;Reference number: 215184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 4
A;Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3; 5
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lant Sci. 112, 207-217, 1995
'Title: Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS) gene that
       A;Title: Analysis of cDNA clones encoding sucrose-phosphate synthase in relation to sug: A;Reference number: 216874; MUID:97451773; PMID:9306694
A;Accession: T09837
                                                                                                                                                                                                                                                                                                                                                                                                            A)Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fr. A;Pathway: sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology C;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
P;176-674/Domain: sucrose/sucrose-phosphate synthase homology <8SS>
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                                                                                                           A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1081 <ING>
A;Cross-references: EMBL:Y11795; NID:g2190349; PIDN:CAA72491.1; PID:g2190350
A;Experimental source: ABA-treated callus
C;Genetics:
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
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C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate
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Pred. No. 60;
2; Mismatches 1; Indels
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A;Residues: 1-1083 <BEV>
A;Cross-references: BMBL:AL049487
A;Experimental source: cultivar Columbia; BAC clone F28M11
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A;Cross-references: EMBL:D45890; PIDN:BAA08304.1
A;Experimental source: subsp. Japonica
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Best Local Similarity 66.7%;
Matches 6; Conservative
Plant Physiol. 115, 113-121, 1997
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483 VIPPGMDFS 491
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                                                                                                                                                                                                                                                  A/Molecule type: mRNA
A/Residues: 1-1049 <7NL>
A/Cross-references: GB:U33175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
A/Cross-references: GB:U33175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
A/Note: UDPG1ucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDPg1ucosylt
C/Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: JQ1329; PQ0260
R;Morrell, A.C.; Bruneau, J.M.; Summerfelt, K.; Boersig, M.; Voelker, T.A.
R;Morrell, A.C.; Bruneau, J.M.; Summerfelt, K.; Boersig, M.; Voelker, T.A.
Plant Cell 3, 1121-1130, 1991
A;Title: Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohyd A;Reference number: JQ1329; MUID:92338837; PMID:1840396
A;Accession: JQ1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: protein
Residues: 71-74;206-212,471-481,872-892 <WOR1>
Residues: 71-74;206-212,471-481,872-892 Group from UDBglucose to fructose-6-phosph
Moment: This enzyme transfers the glucosyl group from UDBglucose to fructose-6-phosph
(Comment: This enzyme is involved in the regulation of carbon partitioning in the leave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
                                                                     B.; Herrera-Estrella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
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Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JINTIONS: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;Pathway: sucrose biosynthesis
J;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
2;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;180-663/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Craterostigma plantagineum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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                                  'Accession: JC4783

'Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herre
lene 170, 217-222, 1996

'Trile: Characterization of a rice sucrose-phosphate synthase-encoding gene.
'Reference number: JC4783; MUID:96235138; PMID:8666248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cispecies: Craterostigma plantagineum
Cispate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
   :/Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Zea mays (maize)
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Residues: 1-1068 <WOR>
Cross-references: GB:M97550; NID:g168625; PIDN:AAA33513.1; PID:g168626
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F;178-666/Domain: sucrose/sucrose-phosphate synthase homology <8SPS>
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C.ACCESSION: 109837
R.Ingram, J.; Chandler, J.W.; Gallagher, L.; Salamini, F.; Bartels,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 2; Length 1049;
Pred. No. 58;
2; Mismatches 1; Indels
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Best Local Similarity 60.,
-hea 6; Conservative
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436 VIPPGMDFS 444
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A; Map position: 1

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Accession: T24111

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C; Species: Aeropyrum pernix
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C; Accession: H72784
R; Kawarabayasi, Y; Hino, Y; Horikawa, H; Yamazaki, S; Haikawa, Y; Jin-no, K; Taka
awa, H; Takamiya, M; Masuda, S; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J;
DNA Res. 6, 83-101, 1999
A; Tille: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A; Reference number: A72450; MUID:99310339; PMID:10382966
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A;Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               A)Residues: 1-440 <KAW>
A)Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA79178.1; PID:g5103657
A)Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Rosaidues: 1-1150 - SMBL; Z81486, PIDN:CAB03994.1, GSPDB:GN00023, CESP:C53A5.2
A,Experimental source: clone C53A5
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A;Experimental source: clone R02D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C53A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20173; T23857
R;Mortimore, B.
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                                             probable alkaline proteinase APE0263 - Aeropyrum permix (strain K1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.8%; Score 35; DB 2; Length 440; 66.7%; Pred. No. 35; 1; Indels trive 2; Mismatches 1; Indels
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A;Molecule type: DNA
A;Residues: 1-1150 <MI2>
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A;Reference number: Z19808
A;Accession: T23857
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Matches 6; Conservative
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A; Accession: T20173
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Risen, J.; Heidelberg, J.
B.; Laub, M.T.; Desoy, R.T.; Doson, R.J.; Burkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
h, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complere Genome Sequence of Caulobacter crescentus.
A;Title: Complere Genome Sequence of Caulobacter crescentus.
A;Accession: H87660
A;Introns: 120/3; 200/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2 C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology C;Reywords: 91ycosyltransferase, hexosyltransferase F;196-680/Domain: sucrose/sucrose-phosphate synthase homology <8SPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R/PETCY, C.
submitted to the EMBL Data Library, October 1996
A/Reference number: Z19842
A/Reference number: Z19842
A/Accession: T24111
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Residues: 1-425
A/Residues: 1-425
A/Experimental source: clone R10D12
A/Experimental source: clone R10D12
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A;Molecule type: DND
A;Residues: 1-433 <STO>
A;Cross.references: GB:AE005673; NID:q13425020; PIDN:AAK25284.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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64.8%; Score 35; DB 2; Length 425;
Best Local Similarity 50.0%; Pred, No. 34;
Matches 5; Conservative 3; Mismatches 2; Indels
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A;Map position: 5 A;Introns: 23/3; 56/3; 113/3; 257/2

Gene: CESP:R10D12.10

Genetics:

RESULT 13

Query Match
Best Local Similarity 54.5°
Conservative

A, Gene: CC3322

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117.693 Million cell updates/sec
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ECB1 HALEL
ECB2 HUMAN
ECR2 CHICK
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ENV SFV3L
ERPOC VIBCH
ZEP1 HUMAN
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Maximum Match 100%
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NEW (III)

P08203 escherichia P06190 salmonella Q9wzr1 thermotoga Q04827 ratuus norv P30279 homo sapien P30280 mus musculu Q90459 brachydanio P50755 xenopus lae P49706 gallus gall P53169 gallus gall P53169 gallus gall
ARAD ECOLI ARAD SALTY HIS9 THEMA CGD2 HWAN CGD2 HWAN CGD1 BRAKE CGD1 BRAKE CGD2 CHICK CGD2 CHICK CGD2 CHICK CGD2 CHICK CGD2 THICK CGD2 THICK CGD3 HWAN
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 25586;

MEDINE2=21886394; PubMed=11889109;

Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Rapatral V., Anderson I., Ivanova N., Grechkin G., Zhu L.,

Rapatral V., Chaga N., Walumas T., Chaga O., Goltsman E., Bernal A.,

N. D'Souza M., Walumas T., Pusch G., Haselkorn R.,

Larsen N., D'Souza M., Overbeek R.;

Ronstein M., Kyrpides N., Overbeek R.;

Ronstein M., Kyrpides N., Overbeek R.;

T. GARALYTT ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +

C. CATALYTT ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +

Dhosphare + L-glutamare + carbamoyl phosphare.

C. CATALYTA Arginine biosynthesis.

C. PATHWAY: Arginine biosynthesis.

C. PATHWAY: Pyrimidine biosynthesis, the small (or glutamine) chain

promotes the hydrolysis of glutamine to ammonia, which is used by

the large (or ammonia) chain to synthesize carbamoyl phosphate (By

similarity).

C. SIMILARITY: Belongs to the carB family.
                               Z8-FEB--2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
                                                                                                                                                                Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
PRT; 1058 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE010554; AAL94625.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAWAP; MF 01210; -; 1.
InterPro; IPR006275; CarA Lglu.
InterPro; IPR006343; CPase L.
InterPro; IPR005493; CPase L. D2.
InterPro; IPR005496; CPase L. D3.
InterPro; IPR005491; CPase L. N.
InterPro; IPR004961; CPase L. N.
InterPro; IPR004362; MGS IIKe.
Pfam; PF00208; CPSSASe L. Chain; 2.
Pfam; PF027087; CPSASe L. D2; 2.
Pfam; PF027087; CPSASe L. D2; 2.
STANDARD;
                                                                                                                                                                                                                                   NCBI_TaxID=76856;
                                                                                                                                                                                                                 Fusobacterium.
  FUSNN
                      QBRGBG
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7 QVVPSGINYS 16

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92188538; PubMed=1546458; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonus plants."; Virology 187:633-642(1992).
                                                                                                                                                  153 210 ATP (POTENTIAL).
302 352 ATP (POTENTIAL).
302 352 ATP (POTENTIAL).
294 294 MANGANESE 1 (BY SIMILARITY).
298 298 MANGANESE 2 (BY SIMILARITY).
300 MANGANESE 2 (BY SIMILARITY).
820 MANGANESE 3 (BY SIMILARITY).
831 MANGANESE 3 (BY SIMILARITY).
832 MANGANESE 3 (BY SIMILARITY).
1058 AA; 117451 MW; ED7037AF77CLE39F CRC64;
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                      70.4%; Score 38; DB 1; Length 1058; 60.0%; Pred. No. 9.4; ive 3; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

66.7%; Score 36; DB 1; Length 102;
Best Local Similarity 60.0%; Pred. No. 2.2;
Matches 6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l protein."
102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002661; Gemini mov. Pfam; PP01708; Gemini mov; I. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                  60.08;
                                                                                                                                                                                                                                                                 Local Similarity 60.0
es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                       190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                 2 EVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          Y11K TYDVA
P31619;
                                                                                                                                                                                                                     METAL
SEQUENCE
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NP BIND
METAL
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                                                                                                                                                                                                                                                                                                                                                      RESULT 2
Y11K_TYDVA
                                                                                                                                                                                      METAL
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Matches
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The gene. The control of the control of carbon partitioning in the control of plants. May regulate the synthesis of sucrose and leaves of plants. May regulate the synthesis of sucrose and therefore play a major role as a limiting factor in the export of control of photosasimilates out of the leaf.

CC TALALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP + sucrose 6-phosphate.

CC -I CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP + sucrose 6-phosphate.

CC -I ENZYMB REGULATION: Activity regulated by phosphorylation and moderated by concentration of metabolites and light.

CC -I PATHWAY: Sucrose synthesis.

CC -I PATHWAY: Sucrose synthesis.

CC -I PATHWAY: Homodimer or homoterramer (By similarity).

CC -I PATHWAY: Belongs to the glycosyltransferase family 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                          Oryza sativa (Rice).
Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of a rice sucrose-phosphate synthase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               695 698 POLY-GLU.
775 779 POLY-ARG.
1049 AA; 116455 MW; ED862E2819AA4B04 CRC64;
                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase (RC 2.4.1.14)
(UDF-glucose-fructose-phosphate glucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,
Herrera-Betrella L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; JC4785; C. Granene; Q43802; -. Gramene; Q43802; -. InterPro; 1PR001296; Glyco_trans_I. Pfam; PF00534; Glycos_transferase; Phosphorylation. Transferase; Glycosyltransferase; Phosphorylation. 22 29 POLY-GLY. C. C98 POLY-GLY.
                                  PRT; 1049 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1068 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Indica-IR36; TISSUE=Leaf; MRDLINE=96235138; PubMed=8666248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPS MAIZE STANDARD;
P31<u>9</u>27;
01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U33175; AAC49379.1; -.
                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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SPS_MAIZE
SPS_ORYSA
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2 EVVPXGMDYS 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craterostigma plantagineum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots; asterids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                              marya marya (Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last anotation update)
Sucrose-phosphate synthase 2 (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase 2).
                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
01-JUL-1993 (Rel. 26, Last sequence update)
01-ZUN-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (BC 2.4.1.14) (UDP-glucose-fructose-
phosphate glucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the glycosyltransferase family 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%; Score 36; DB 1; Length 1068; 66.7%; Pred. No. 25; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 1068 AA; 118575 MW; 074679B5E9A1D282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MaizeDB; 22534; - ...
InterPro; IPR001296; Glyco_trans_1.
Pfam; PF00554; Glycos_transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
nomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1081 AA.
                                                                                                                                                                                   STRAIN-CV. PIONEER 3184; TISSUE-Leaf;
MEDLINE-92338837; PubMed=1840396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M97550; AAA33513.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 66.7 les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JQ1329; JQ1329.
                                                                                                                             NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MaizeDB; 25294;
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ID SPS2_CRA
AC 004933;
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Ingram J., Chandler J.W., Gallagher L., Salamini F., Bartels D.;
Ingram J., Chandler J.W., Gallagher L., Salamini F., Bartels D.;
Ingram J., Chandler J.W., Gallagher E., Salamini F., Bartels D.;
Inalysis of cDNA clones encoding sucrose-phosphate synthase in
relation to sugar interconversions associated with dehydration in the
relation to sugar interconstains associated with dehydration in the
Plant Physiol. 115:113-121(1997).
I. FONGTION: Involved in the regulation of carbon partitioning in the
leaves of plants. May regulate the synthesis of sucrose and
therefore play a major role as a limiting factor in the export of
photoassimilates out of the leaf.
I. PATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
sucrose 6-phosphate.
I. PAZYME REGULATION: Activity regulated by phosphorylation and
moderated by concentration of metabolites and light.
I. PATHWAY: Sucrose synthesis.
I. PATHWAY: Sucrose synthesis.
I. PATHWAY: Homodimer or homocetramer (By similarity).
II PTM: Phosphorylated. However, phosphorylation is not essential for
enzyme function (By similarity).
II PTM: Phosphorylated. However, phosphorylation is not essential for
enzyme function (By similarity).
II SIMILARITY: Belongs to the glycosyltransferase family 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PESER4; GOVGZ7;
20-1NOV-1997; (Rel. 35, Created)
21-NOV-1997 (Rel. 35, Created)
21-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 43, Last annotation update)
17-MAR-2004 (Rel. 43, Last annotation update)
18-MAR-2004 (Rel. 43) Last annotation update)
18-
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Pfam; PP00534; Glyco_trang 1.
Pfam; PP00534; Glycos_trangf_1; 1.
Transferase; Glycosyltrangferase; Phosphorylation; Multigene family.
DOWAIN 256 264 POLY-SER.
DOMAIN 256 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 1; Length 1081;
Pred. No. 25;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
lamiids; Lamiales; Lamiales incertae sedis; Lindernieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fischer-Vize J.A., Rubin G.M., Lehmann R.;
                                                                                                                                                                                                                                        MEDLINE=97451773; PubMed=9306694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Eye imaginal disk,
MEDLINE=93202020; PubMed=1295747,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y11795; CAA72491.1; -. PIR; T09837; T09837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%;
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445 VIPPGMDFS 453
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Best Local Similarity
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                                                                                            NCBI_TaxID=4153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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The fat facete gene is required for Drosophila eye and embryon the logic penetric 116:985-1000(1992).

The SQUENCE FROM the No. 1  
STALINGERCALLY.

THE SQUENCE FROM THE SET SOURCE TO THE STALINGE CAN. Gotcayne J.D.;

The GOTCOG R. A. Contamn J.R.; Yandel 1071132;

The GOTCOG R. A. Contamn J.R.; Yandel M. D.; Zhang Q., Chen L.K.

The GOTCOG R. A. Contamn J.R.; Yandel M. D.; Zhang Q., Chen L.K.

The GOTCOG R. A. Contamn J.R.; Yandel M. D.; Zhang Q., Chen L.K.

The GOTCOG R. A. Contamn J.R.; Yandel M. D.; Zhang Q., Chen L.K.

The GOTCOG R. A. Contamn J.R.; Yandel M. D.; Zhang Q., Chen L.K.

The GOTCOG R. A. Contamn J.R.; Yandel M. D.; Zhang Q., Chen L.K.

The GOTCOG R. A.; Dout D. S.; Dout J. P. Contamn J. Contamn J. S.; Dout J. D.; Dout J. C.; Dout J. C
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DR EMBL; 104955; AAF01146.1; --
DR EMBL; 104955; AAF01146.1; --
DR EMBL; 104956; AAF01146.1; --
DR EMBL; 104960; AAF01146.1; --
DR EMBL; 104960; AAF01148.1; --
DR EMBL; AC005779; AAF57198.1; --
DR EMBL; AE007779; AAF57198.1; --
DR EMBL; AE007779; AAB5521.1; --
DR EMBL; AE007779; AAB5521.1; --
DR EMBL; AE007779; AAB75108.1; --
DR GO; GO:007749; P:Cellularization; IMP.
GO; GO:007749; P:Cellularization; IMP.
DR GO; GO:007749; P:mortery cell fate differentiation (sensu Dr. .; IMP.
DR GO; GO:000789; P:mortery cell fate differentiation; IMP.
DR GO; GO:0005511; P:ubiquitin-dependent protein catabolism; IGI.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IGI.
DR FROSITE; PS00973; UCH 2.1; 1.
DR PROSITE; PS00973; UCH 2.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isoid=P55824-3; Sequence=VSP_005269;
-1- TISSUB SPECIPTCITY: Eye disks and ovaries.
-1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-1- SIMILARITY: Belongs to peptidase family C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
function.
-!-CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0
ubiquitin + a thiol.
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase, Thiol protease,
                                                                                                                                                                                                                                                                                                                IsoId=P55824-2; Sequence=VSP_005270;
                                                                                                                                                                                                                                                      lsoId=P55824-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 54.5
les 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ubl conjugation pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Developmental I
ACT_SITE 1677
ACT_SITE 1976
ACT_SITE 1986
VARSPLIC 2705
                                                                                                                                                                                                                           Name=1;
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CONFLICT
SEQUENCE
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Matches
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Qy 1 EEVVPXGMDYS 11 | : | | : | Db 1394 EVIVPDGQDFS 1404

RESULT 7

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15577 MW;
Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                     135
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154
139
142
                                    ដ
                                                127 EEVVP-GMDF
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147
154 AA;
                                    1 EEVVPXGMDY
                                                                                                                                                            Oryza sativa (Rice)
                                                                                                                                                                                                                                                                           SEQUENCE OF 58-154
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transit peptide.
TRANSIT 1
CHAIN 58
                                                                                                                                                                                              NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gramene; P20423;
                                                                                                PLAS_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
SEQUENCE
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                                                                                       PLAS_ORYSA
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                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed, Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                  SEQUENCE FROM N.A.

TISSUB=brain;

MEDLINE=20277482; PubMed=10819331;

Nagase T., Xikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;

"Prediction of the coding sequences of unidentified human genes. XVII.

The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606;
                                                                                                       MEDLINE=20347694; PubMed=10888605; Kobb M.D., Nemes J.P., Benzow K.A., March M.D., Nemes J.P., Benzow K.A., M.D., Nemes J.P., Encoperation of transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHL1)."; Hum. Mol. Genet. 9:1543-1551 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
KELCH 5.
                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- TISSUB SPECIFICITY: Highly expressed in brain.
-i- SIMILARITY: Contains 1 BTB/PCZ domain.
-i- SIMILARITY: Contains 6 Relch repeats.
KHL1 HUMAN STANDARD; PRT; 748 AA. CONTEG4; OPPG38; COPFC-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Kelch-like procein 1. KELCH. OK KIAA1490. HOMO sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF252283; AAF81719.1; -.
EMBL; AF55279; AAF81716.1; -.
EMBL; AB040923; BAA96014.1; ALT_INIT.
EMBL; AL533738; CAC16128.1; -.
Genew; HGNC:6352; KLHL1.
                                                                                                                                                                                                                        for large proteins in vitro.";
DNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460
507
555
601
649
701
748 AA;
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REPEAT
REPEAT
REPEAT
REPEAT
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SEQUENCE
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                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular cloning and characterization of plastocyanin precursor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000923; BlueCu 1.
InterPro; IPR001235; Copper_blue.
InterPro; IPR001235; Copper_blue.
InterPro; IPR001235; Copper_blue.
Pram; PR00127; Copper-blud; 1.
PRINTS; PR00125; Copper_blue.
PROGUTS; PR001285; Copper_blue.
PROGUTS; PR001285; Copper_blue; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
Score 34.5; DB 1; Length 748; Pred. No. 35;
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASTOCYANIN.
PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                            P20423; Q9SBB8; 01-FRB-1991 (Rel. 17, Created) 28-FRB-2003 (Rel. 41, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) Plastocyanin, chloroplast precursor.
                                                                                                                                                                                                                                                                          154 AA
                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-cv. Ilpoom; TISSUE-Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF093636; AAC78108.1; -.
HSSP; P00289; 2PCF.
     63.9%;
                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. NK 1558;
MEDLINE=94039081; PubMed=8223592;
Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter region.";

Bur. J. Biochem. 217:97-104(1993).

-!-FUNCTION: Participates in electron transfer between P700 and the cytochrome bef complex in photosystem I.

-!-SUBCELLULAR LOCATION: Loosely bound to the inner thylakoid membrane surface in chloroplasts.

-!-SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae,
Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Bomi;
Nielsen O.S., Gausing K.;
Nielsen O.S., Gausing K.;
Nielsen O.S., Gausing K.;
Sithe precursor of barley plastocyanin: sequence of cDNA clones and gene expression in different tissues.";
PEBS Lett. 225:159-162(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R PIR) S38255; S38255.
R HSES; PO0289; 22PCF.
R InterPro; IRRO00923; BlueCu.1.
R InterPro; IRRO00923; BlueCu.1.
R InterPro; IRRO01235; Copper_blue.
R PRINTS; PRO01275; Copper_blue.
R PRINTS; PRO01256; COPPERBLUE.
R PRODOM; PD001256; COPPER BLUE; 1.
R PROSITE; PS00196; COPPER_BLUE; 1.
R CALOCOPLAST; Copper blue; 1.
R Transit peptide.
TRANSIT
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0
Query Match 63.0%; Score 34; DB 1; Length 154; Best Local Similarity 54.5%; Pred. No. 8.7; Matches 6; Conservative 2; Mismatches 3; Indels
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PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
02-FEB-2003 (Rel. 41, Last amnotation update)
Plastocyanin, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y00704; CAA68696.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hordeum vulgare (Barley).
                                                                                                                                                                                                100 EDAVPSGVDVS 110
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                     1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                              PLAS HORVU
                                                                                                                                                                                                                                                                                                                                                                                              P0824B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                        PLAS HORVU
ACTORNA BARRAN
ACTORNA BA
                                                                                                                                                                                                                                                                                                   RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Populus nigra (Lombardy poplar).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.

NCBL_TaxID=1691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, Z50186; CAA90565.1; -.

PIR; S80210; S00210.

PIR; S82208; S82208.

PIR; S82208; S82208.

PIR; S82208; S82208.

ROS29; PRO0299; IPIC.

InterPro; IPR000923; Cupred oxin.

Pfam; PF00127; Copper bine.

ProDom; PR00125; Copper bine.

ProDom; PR00125; Copper bine; I.

ProDom; PR00126; COPPER Bine; I.

PR017F; PR00126; COPPER Bine; I.

PR017F; PR017F; PR017F; Copper bine; I.

PR017F; PR017F; PR017F; Copper bine; I.

PR017F; PR017F; PR017F; Copper bine; I.

PR017F; PR
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                                                                          63.0%; Score 34; DB 1; Length 155; 54.5%; Pred. No. 8.7; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Italica; TISSUE=Leaf;
Reichert J., Jenzelewski V., Haehel W.;/DBJ databases.
Submitted (AdG-1995) to the BMEL/GenBank/DDBJ databases.
120 120 T -> N (IN CV. NK 1558).
155 AA; 15709 MW; DAA7EABESF6F4F91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASTOCYANIN B.
PLASTOCYANIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         PRT; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plastocyanin B, chloroplast precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COPPER.
                                                                                                    Local Similarity 54.5
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                   101 EDAVPSGVDVS 111
                                                                                                                                                                                    1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     PLAT POPNI
P11970;
VARIANT
SEQUENCE
                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                Matches
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S

RESULT SYFB_BO

à g

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PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
DOMAIN 10 45 LEUCINE-ZIPPER.
566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homologs;
WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro, IPR000767, Disease resist.
Interpro, IPR001611; LRR.
Interpro, IPR002182; NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK117163; BAC41841.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00560; LRR; 2.
Pfam; PF00931; NB-ARC; 1.
                                                                                                                                                                                                                               STANDARD;
                                                                                                                                         169 VPFGMDY 175
                                                                                                       4 VPXGMDY 10
                                                  Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                               R8L4 ARATH
SEQUENCE
                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tabata S.
                                                                                                                                                                                                                                            Q9FJKB;
                                                                       Matches
                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 35210 / B31;

MEDLINE=98065943; PubMed=9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,

Lathigra R., White O., Ketchum K.A., Dodson R., Hickey B.K., Gwinn M.,

Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,

van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,

Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B.,

Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain family. Subfamily 2.
                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF03484; B5; 1.
TIGREMBs, TIGRO0471; pheT_arch; 1.
Aminoacy-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Complete proteome.
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=AFCC 35210 / B31;
Barbour A.G., Hinnebusch J.;
"Phenylalanyl-tRNA synthetase genes (alpha and beta subunits) and thioredoxin reductase gene of Borrelia burgdorferi.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                        tRNA ligase beta chain) (PheRS).
PHET OR BBOS14.
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                     Length 168;
                                                                         3; Indels
   16981 MW; F20DA6EA2038AEEA CRC64;
                                     63.0%; Score 34; DB 1;
54.5%; Pred. No. 9.5;
                                                                                                                                                                                                                                   566 AA
                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IIGR: BB0514; -, 1.
HAWAP; ME 00284; -, 1.
INCEPPRO; IPR005147; B5.
INCEPPRO; IPR004531; PheT_arch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U82978; AAB41019.1; -.
EMBL; AE001153; AAC66870.1; -.
PIR; A70164; A70164.
TIGR; BB0514; -.
HAMAP; MF_00284; -; 1.
                                                                         6; Conservative
                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                         112 EDAVPSGVDVS 122
                                                                                                          1 EEVVPXGMDYS 11
     168 AA;
                                                    Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=139;
                                                                                                                                                                                                                                    BORBU
     SECUENCE
                                   Query Match
                                                                                                                                                                                                                                 SYFB B(
P94283;
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                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPPB14 OR ATSG48620 OR KISN18.9.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots; rossids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C. Columba,
MEDLINE-99087489; PubMed=9872454;
MEXEMUTA Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned P1 and TAC clones.";
DNA Res. 5:297-308(1998).
                                                              ;
0
63.0%; Score 34; DB 1; Length 566; llarity 85.7%; Pred. No. 33; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable disease resistance RPP8-like protein
                                                                                                                                                                                                                                                                                                                             908 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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MEDLINE=99030193; PubMed=9811794;
MCDOWell J.M., Dhandsydham M., Long T.A., Aarts M.G.M., Goff S.,
HOlub E.B., Dangl J.L.;
"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPPB locus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cooley M.B., Pathirana S., Wu H.-J., Kachroo P., Klessig D.F.;
"Members of the Arabidopsis HRT/RPPB family of resistance genes confer
resistance to both viral and comycete pathogens.";
Plant Cell 12:663-676(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPPB ARATH STANDARD; PRI; 908 AA.
QWM4J9; Q8GWG5; Q9MA1; Q9ZSY3; Q9ZSY4;
10-OCT-2003 [Rel. 42, Created]
10-OCT-2003 [Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Disease resistance protein RPPB (Resistance to Peronospora parasitica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIATE-2595480; Pubmed-14593172; MEDIATRE-22595480; Pubmed-14593172; MEDIATRE-22595480; Pubmed-14593172; MEDIATRE-22595480; Pubmed-14593172; Mediatre-2595480; Pubmed-14593172; Mediatre-2595480; Pubmed-14509772; Mediatre-2595480; Pubmed-1509548, Mediatre-2595480; 
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDOCEIN BY OR AT5G43470 OR WWF20.19.

Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliplantae; Streptophyres; Embryophyta; Tracheophyta;

Spermatophyta; Magmoliophyta; endicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2 AND RPP8-3, AND VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN>cv. Columbia;
MEDLINE-20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                             Score 34; DB 1; Length 908;
Pred. No. 54;
                                                                                                                                                                                                                                                       2; Indels
   146 459 NB-ARC.
575 599 LRR 1.
600 623 LRR 3.
842 867 LRR 3.
192 199 ATP (POTENTIAL).
908 AA; 104448 MW; 3111991B17239693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS.
                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Di-17;
MEDLINE=20271766; Pubmed=10810142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis.";
Plant Cell 10:1861-1874(1998)
                                                                                                                                                                                          63.0%;
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                        |::|| | ||
883 EKLVPGGEDY 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clones.";
DNA Res. 7:31-63(2000).
                                                                                                                                                                                                                                                                                                       1 EEVVPXGMDY 10
                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein 8)
DOMAIN
REPEAT
REPEAT
REPEAT
NP BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   labata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
SPETER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specifically recognizes the Emcos avirulence protein from Perconospora parasitica, while it is not the case in cv. Di-17, where it confers resistance to Turnip Crinkle Virus uppon recognition of the viral capsid protein.

-!- SIMILARITY: Belongs to the disease resistance NB-LRR family.
-!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
-!- SIMILARITY: Contains 1 NB-ARC domain.
-!- DATABASE: NAME-NIB-LRRS,
-!- DATABASE: NAME-NIB-LRRS,
-!- NOTE-Functional and comparative genomics of disease resistance gene
                                                                                                                                                                                                                                                                                                                                                                       MEDINE-20496823; PubMed=11041886;
Ren T., Qu F., Morris T.J.;
Ren T. Gapsid protein to confer resistance to turnip crinkle virus.";
Plant Cell 12:1917-1926(2000).
I- FUNCTION: Disease resistance protein. Resistance proteins guard
the plant against pathogens that contain an appropriate avirulence
protein via an indirect interaction with this avirulence protein.
That triggers a defense system including the hypersensitive
response, which restricts the pathogen growth. The interaction
with TIP (TCV-interacting protein) may be essential for the
recognition of the avirulence proteins, and the triggering of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isode_08044J9-2; Sequence=VSP_007171, VSP_007172;
Note=Has been shown to exist only in cv. Columbia so far;
Note=Has been shown to exist only in cv. Columbia so far;
DOMAIN: The LRR repeats probably act as specificity determinant of
pathogen recognition.
POLYMORPHISM: The strong polymorphisms present in cv. Di-17 and
cv. Columbia are probably due to an unequal crossing-over between
the highly related RPPs and RPH8A genes present in cv. Landaberg
erecta. Such variations probably modify the specificity of
Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Satou M., Tamafe R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y., Yuan S., Shinozaki K., Davis R.M., Theologis A., Ecker J.R., "Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                     STRAIN=cv. Columbia;
Seki M., Iida K., Satcu M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogen recognition.
MISCELLANEOUS: In cv. Columbia and cv. Landsberg erecta, RPP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Interacts with the NAC protein TIP. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q8W4J9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000767; Disease resist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF089710; AAC83165.1; -.
EMBL; AF089711; AAC78631.1; -.
EMBL; AF234174; AAF36987.1; -.
EMBL; AB025638; BAA97426.1; -.
EMBL; AY062514; AAL32592.1; -.
EMBL; AX18862; BAC43449.1; -.
                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                Science 302:842-846(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  defense response.
                                                                                                                                                                                                                                                                                                                                                               INTERACTION WITH TIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
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Sundaberg erecta).

GKGV -> EKGI (in cv. Landsberg erecta).

GKGV -> EKGI (in cv. Landsberg erecta).

C -> R (in cv. Landsberg erecta).

E -> L (in cv. Landsberg erecta).

Q -> QQ (in cv. Di-17).

Q -> QQ (in cv. Di-17).

G -> V (in cv. Di-17).

G -> V (in cv. Di-17).

G -> C (in cv. Di-17).

G -> C (in cv. Di-17).

G -> C (in cv. Di-17).

A -> T (in cv. Di-17).

R -> F (in cv. Di-17).

A -> T (in cv. Di-17).

A -> Y (in cv. Di-17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N -F Fi.
N -F Fi.
N -F Fi.
N -F Fi.
DESIGNING.

DESIGNING F.
DESIGNING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erecta).

C -> S (in cv. Di-17 and cv. Landsberg erecta).

T -> I (in cv. Di-17).

S -> R (in cv. Di-17).

S -> R (in cv. Di-17).

H -> Q (in cv. Di-17).

I -> L (in cv. Landsberg erecta).

KNXT -> RNAM (in cv. Di-17).

K -> N (in cv. Landsberg erecta).

K -> N (in cv. Landsberg erecta).
                                                                                                                                                                                                                / FridavSP 007171.
Missing (In isoform 2).
FridavSP 007172.
FridavSP 007172.
IDGOL -> VDEQI (in cv. Landsberg erecta)
G -> E (in cv. Di-17).
SGK -> RGE (in cv. Di-17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erecta)

P -> S (in cv. Di-17 and cv. Landsberg erecta).

W -> C (in cv. Di-17 and cv. Landsberg erecta).

C -> R (in cv. Di-17 and cv. Landsberg crecta).
                                                                                                                                          LRR 1.
LRR 2.
ATP (POTENTIAL).
WKMLLTSRNEGVGIH -> ELLWYIHEALFLLINS (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRF -> SRFK (in cv. Di-17).
Y -> F (in cv. Di-17).
S -> Y (in cv. landsberg erecta).
C -> S (in cv. landsberg to cv. landsberg).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> R (in cv. Di-17 and cv. Landsberg
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
Pfam; PF00500; LRR; 2.
Pfam; PF00501; NB-ARC; 1.
PRINTS; PR00364; DISBASERSIST.
PRINTS; PR00364; AFP-binding; Repeat; Leucine-rich repeat; Alternative splicing; Polymorphism.
                                                                                                              LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erecta).
N -> F (i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erecta).
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DOMAIN
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That briggers a defense system including the hypersensitive protein guard the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein.

That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. In contrast to RPB, it does not specifically recognize the Bmco5 avirulence protein from Peronospora parasitica.

"NESCELLANEOUS: In ov. Columbia and cv. Di-17, this protein is not present due to an unequal crossing over between the RPPB and RPBHA present due to an unequal crossing over between the RPPB and RPBHA consent that creates a unique RPBB gene.

"SIMILARITY: Belongs to the disease resistance NB-LRR family.

RPBB/HRT subfamily.

"SIMILARITY: Contains 2 leucine-rich (LRR) repeats.

"SIMILARITY: Contains 2 leucine-rich (LRR) repeats.

"SIMILARITY: Contains 1 NB-ARC domain.

"OVER-Punctional and comparative genomics of disease resistance gene
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"Intragenic recombination and diversifying selection contribute to the
evolution of downy mildew resistance at the RPP8 locus of
Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                        Gaps
                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicacese; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGUENCE FROM N.A., AND FUNCTION.
STRAINE-OV. Landsberg erecta;
MEDLINE-99030193; Pubmed-9811794;
MCDowell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
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InterPro; IPR00167; Disease_resist.

InterPro; IPR00151; LRR.

InterPro; IPR00182; NB-ARC.

Pfam; PF00560; LRR; 2.

Pfam; PF00560; LRR; 2.

PRIMI; PF0031; NB-ARC; 1.

PRIMI; AFP-binding; Repeat; Leucine-rich repeat.

DOWAIN 146 459 NB-ARC.

REPEAT 602 625 LRR 1.
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Pred. No. 55;
2; Mismatches 2; Indels
63.0%; Score 34; DB 1; Length 908; 60.0%; Pred. No. 54; ive 2; Mismatches 2; Indels
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192 199 ATP (POTENTIAL).
910 AA; 105263 MW; 5B1E9F65A19A12EE CRC64;
                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Disease resistance protein RPHSA (RPPS homolog A).
                                                                                                                                                                                                            910 AA
                                                                                                                                                                                                            PRT;
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885 EKLVPGGEDY 894
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883 EKLVPGGEDY 892
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                                                                              1 EEVVPXGMDY 10
                      Best Local Similarity
Matches 6; Conserv
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P59584;
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This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

MEDLINE=96337999; PubMed=8688087;

Built C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams N.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,

Utterback R., K., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; MJ0939; ...
InterPro; IPR01163; snRNP Sm.
InterPro; IPR005358; UPF0153.
Pfam, PF03692; UPF0153; ...
Pfam, PF03692; UPF0153; ...
Rypothetical protein; Complete proteome.
SEQUENCE 276 AA; 33454 MW; 97BD69D392BC8FDF CRC64;
                                                                                                                                                                                             Archaea, Euryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus.
                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0939.
                                        276 AA
                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U67537; AAB98946.1; -.
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                                        STANDARD;
                                                                                                                                                                                Methanococcus jannaschii
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Best Local Similarity
Matches 5; Conservi
                                                                                                                                                                                                                                        NCBI_TaxID=2190;
                                        Y939_METUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jannaschii.
RESULT 15
Y939_METJA
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Search completed: June 3, 2004, 11:49:52 Job time: 5.86667 secs

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1 EEVVPXGMDYS 11

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us-09-909-164-8.rspt

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STRAIN=FY1679;
MEDLINE=94169519; PubMed=7764548;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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030260 archaeoglob
08dih0 synechococc
Q822b4 enterococcu
022081 citrus unsh
022096 citrus unsh
08w568 arabidopsis
Q9c9t7 arabidopsis
Q9c9t7 arabidopsis
Q9sn30 arabidopsis
Q9sn30 arabidopsis
Q8m30 oryza sativ
Q8g004 entocheir s
Q8xpa8 clostridium
O5c2367 rhizobium t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q12479 saccharomyc
                                                                                                                   3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                           1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                    1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
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1: sp_archea:*
2: sp_bacteria:*
4: sp_hungi:*
5: sp_hungi:*
5: sp_hunan:*
5: sp_hunan:*
5: sp_nhor:*
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6: sp_phage:*
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Q8XPA8
O52367
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030260
Q8DIH0
Q82ZB4
022081
022096
Q8W568
Q9C9T7
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Gapop 10.0 , Gapext 0.5
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sp_bacteriap:*
sp_archeap:*
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54
I EEVVPXGMDYS 11
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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No.
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		O	Q9a382 caulobacter	Q9yfi3 aeropyrum p			Q8xz15 ralstonia s	^			O17704 caenorhabdi		O52666 escherichia	027146 methanobact	Q98k29 rhizobium l	ဌ				Q7v6q4 prochloroco	Q855k6 mycobacteri	-	Q8u7j0 agrobacteri	m	Q7uf95 rhodopirell	7	9920	O29451 archaeoglob
08800	Q8KL43	Q9XVK4	Q9A382	Q9YFI3	0831.92	052680	OBXZL5	0946J7	Q95P46	Q9U6A3	017704	052673	052666	027146	Q98K29	Q8TBJ7	QBR9L5	QBESL9	QBDZW9	Q7V6Q4	Q855K6	Q8GP33	080730	O9YET8	Q7UF95	Q815A7	029920	029451
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308	368	425	433	440	474	511	517	595	745	1031	1150	1410	1420	1474	1828	748	215	222	222	245	251	284	290	296	337	344	357	366
64.8	64.8	4	64.8	64.8	64.8	4.	64.8	4.	64.8	64.8	64.8	4.	64.8	64.8	64.8	63.9	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0		63.0	63.0
35			35											35	35	34.5	m		34	34	34	34	34	34	34	34	34	34
17	18	13	20	21	22	23	24	25	36	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

SEQUENCE FROM N.A.
STRAIN=FYL679;
STRAINS-94019318; PubMed=8413243;
Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G., CYC2 encodes a factor involved in mitochondrial import of yeast Saccharomyces cerevisiae (Baker's yeast). Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. De haan M., Maarse A.C., Grivell L.A.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases De haan M., Grivell L.A., Maarse A.C.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases 012479; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-UND-2003 (TrEMBLrel. 24, Last annotation update) ORF YOR013W. 156 AA cytochrome c."; Mol. Cell. Biol. 13:6442-6451(1993) PRT; PRELIMINARY;

15

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Query Match
Best Local Similarity 54...
6, Conservative
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SEQUENCE 1044 A
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                                                                                                                                                                                                                                                                              Venter J.C.;
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Matches
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Q8DIH0
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STRAIN=HIEB31 / DSM 14371 / JCM 11309;
MEDLINE=222220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
Nucleic Acids Res. 30:3927-3935(2002).
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHS1, which complements a drug-hypersensitive mutation of the yeast Saccharcomyces cerevisiae.";
Biosei. Biotechnol. Biochem. 58:391-395 (1994).

EMBL, Z74920; CAA692201.1; -.

EMBL, X87331; CAA60762.1; -.

EMBL, S84619, S84619.

SGD, S000539; YORQ13W.

SGD, S000539; YORQ13W.
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes, Bacillales, Bacillaceae, Oceanobacillus
NCBI_TaxID=182710;
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                                                                                                                                                                                                                                                                                               Query Match

14.1%; Score 40; DB 3; Length 156;
Best Local Similarity 77.8%; Pred. No. 3;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP004594; BAC12465.1; -.
InterPro; IPR01279; Blactmase-like.
Pfam; PF00753; Jactamase-B; I.
Hypothetical protasse-B; Complete protecme.
SEQUENCE 319 AA; 35617 MW; 3BDAE4BF13E79E37 CRC64;
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Archaeoglobaceae, Archaeoglobus.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein AF2411.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical conserved protein.
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Best Local Similarity 60.0
Matches 6; Conservative
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Q8ESV7
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Thermospinechococus elongatus BP-1.";

DNA Res. 9:123-130(2002).

R EMBL; AP005374; BAC09170.1; -.

R GO; GO:0005015; F:transporter activity; IEA.

R GO; GO:0005015; F:transporter activity; IEA.

InterPro; IPR001036; Acrilvin_res.

R InterPro; IPR004764; HARI.

Pram; PP00973; ACR ! HARI.
Ketchum K.A., Dodson R.J., Gwinn M., Hickey B.K., Peterson J.D.,
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Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Badow P.W., D'Andraa K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364.370(1997).
EMBL, AEO01109; AAB91255.1; -.
PIR; D69551; D69551.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.4%; Score 38; DB 17; Length 363; 54.5%; Pred. No. 20; tive 3; Mismatches 2; Indels
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR002103; Bac_luciferase.
Pfam; PF00296; bac_luciferase; 1.
Hypothetical protein; Complete protecome.
BEQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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MEDLINE=22225144; PubMed=12240834;
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PRINTS; PR00702; ACRIFLAVINRP.
TIGRFAMS; TIGR00915; 2A0602; 1.
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TLL1618.
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RESULT 082ZB4

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66.7%; Score 36; DB 66.7%; Pred. No. 51; tive 2; Mismatches
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01-JAN-1998 (TrEMBLrel. 05, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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01-MAR-2002 (TrEMBLrel, 20, Cr

01-MAR-2003 (TrEMBLrel, 20, La
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                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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Best Local Similarity
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Q8W568
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SEQUENCE FROM N.A.

STRAIR=V583 / 87CC 700802;

MEDLINE=225.0857; PubMed=12663927;

Paulsen I.T., Banerjei L., Myere G.S.A., Nelson K.E., Seshadri R.,

Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,

Tettelin H., Dodson R.T., Umayam L., Brinkac L., Beanan M.,

Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,

Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,

Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;

"Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                     Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 20;
0; Mismatches 3; Indels
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                                                                           Q82ZB4 PRBLIMINARY; PRT; 149 AA.
Q82ZB4;
Q1-JUN-2003 (TrEMBLrel. 24, Created)
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Large conductance mechanosensitive channel protein.
MSCL OR EF3152.
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Last annotation update)
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GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0006910; P:transport; IEA.
InterPro; IPR001185; MS. Channel.
PFUNTS; PR01241; MscL; 1.
PRINTS; PR01264; MECHCHANNEL.
PRODOW; PD007253; MS. Channel; 1.
TIGRFAMS; TIGR00220; mscL; 1.
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Sucrose-phosphate synthase (Fragment)
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01-37A-1998 (TrEMBLrel. 05, Created)
01-37A-1998 (TrEMBLrel. 05, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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EMBL; AE016956; AA082828.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
70.0%;
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SEQUENCE 149 AA;
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SEQUENCE FROM N.A.
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STRAIN=cv. Miyagawa-Wase; TISSUE=Juice sacs and segment epidermis; Komateu A.; Takanokura Y.; Moriguchi T.; Omura M.; Akihama T.; Indiferential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.)."; Plant Sci. 140:169-178 (1999).

EMBL; AB006319; BAA23215.1; -.

PIR; S72649; S72649.

NOW TER 1 1

SEQÜENCE 341 AA; 38136 MW; 61417A69C4560777 CRC64;
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Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;

Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;

"Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.).";

EMBL, AB006660; BAA22071.1; -.

PIR, S72650; 872650.

NON TER 1 1

NON TER 348 348

SEQÜENCE 348 AA; 38556 MW; EBIC21BBA6FF5C5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Citrus unshiu (Satsuma orange).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Sapindales; Rutaceae; Citrus.
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MEDLINE-96439842; PubMed=8842155;
Komatsu A., Takanokura Y., Omura M., Akihama T.;
"Cloning and molecular analysis of CDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                          66.7%; Score 36; DB 10; Length 341; 66.7%; Pred. No. 50;
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Last sequence update)
Last annotation update)
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Last annotation update)
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414 VIPPGMDFS 422
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Matches 6; Conserv
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                                                                                                                                                                                                                                   thaliana.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subjuance From M., Cheuk R., Shinn P., Banh J., Bowser L.,

A Kim C.J., Chen H., Cheuk R., Shinn P., Banh J., Bowser L.,

A Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

Bishida J., Jones T., Karlin-Neumann G., Kawai J., Lam B.,

Lee J.M., Lin J., Miranda M., Narusaka M., Suyen M., Onodera C.S.,

A Tang C.C., Toriudi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,

Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Arabidopsis ORF clones.";

I. Submitted (MAY-2502) to the EMBL/GenBank/DDBJ databases.

EMBL; AY113044; AAM47352.1; ...

BRBL; AY113044; AAM47352.1; ...

GO; GO:0004281; F:caralytic activity; IEA.

GO; GO:0004281; F:caralytic activity; IEA.

GO; GO:0004281; F:proteolysis and peptidolysis; IEA.

RO; GO:0004281; P:proteolysis and peptidolysis; IEA.

RO; GO:0005379; Sez_estrs.

InterPro; IPR000379; Sez_estrs.

R ROSEQUENCE 452 AA; 49682 MW; A159955B21742C4A CRC64;
                                                                                                                                                                                 Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carnincil P., Dale J.M., GoldBmith A.D., Hayashitzaki Y.,
Bowser L., Carnincil P., Dale J.M., GoldBmith A.D., Hayashitzaki Y.,
Kawai J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Phan P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southmick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
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Pred. No. 69;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                    "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.78;
70.08;
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                           SEQUENCE FROM N.A.
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Q9C9T7
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Sugilarities, Sakakibara H., Sugiyama T.;

"Differential Expression of Two Genes for Sucrose-Phosphate Synthase in Sugarcane: Molecular Cloning of the cDNAs and Comparative Analysis of Gene Expression.";

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, AB001337; BAA19241.1;

EMBL, AB001337; BAA19241.1;

GO, GO:00046524; F:sucrose-phosphate synthase activity; IEA.

GO, GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.

GO; GO:0009058; P:biosynthesis; IEA.

InterPro; IPR001296; Glycoc trans 1.

Pfam; PF00534; Glycoc trans 1.

Glycosyltransferase; Transferase.

NON TER.
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Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Malti R., Mazziali A., Maltiecher J., Miranda M., Nighraman W.C., Osborne B.I., Pai G., Peterson J., Pham P. K., Rizzo M., Rooney T., Rowley B.I., Sakano, H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
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10.1-MXY-1997 (TrEMBLrel. 03, Created by 19782.)

10.1-MXY-1997 (TrEMBLrel. 03, Last sequence update)

10.1-MXY-1997 (TrEMBLrel. 24, Last annotation update)

10.1-GNN-2003 (TrEMBLrel. 24, Last annotation update)

Socrose-phosphate synthase (BC 2.4.1.14) (Fragment).

Socharum officinarum (Sugarcane).

Saccharum officinarum (Sugarcane).

Saccharum officinarum (Sugarcane).

Saccharum officinarum (Sugarcane).

PACCAD officinarum (Sugarcane).

PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
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66 7%; Score 36; DB 10; Length 460;
Best Local Similarity 70.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SROUTENCE 460 AA; 50564 MW; B94B27B5C4B249EC CRC64;
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Conservative
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                                                                                                                                                                                                                                                                                                                       Nature 408:816-820(2000)
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Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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469 VIPPGMDFS 477
                                                                                                                                                                                                                                                                                                                          453 VIPPGMDFS 461
                                                                                                                                                                                                                                                                        3 VVPXGMDYS 11
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SEQUENCE FROM N.A.
TISSUE=G111;
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Q9G204
Q9G204
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Q8S064;
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Matches
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BU Arabidopsis sequencing project;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL164164 (ARAP0135.1; -

EMBL; AL164164; CAB70135.1; -

EMBL; AL164164; CAB70135.1; -

EMBL; AL164164; CAB70135.1; -

ENRI, 704065; T04065.

GO; GO:0016757; F:transferase activity; IEA.

GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.

GO; GO:001675; F:transferase activity, transferring glycosyl. .; IEA.

InterPro; IPR01296; Glyco_trans 1.

Fram; PF00354; Glyco trans 1.

GO; GO:001676; Glyco trans 2.

GO; GO:001676; Glyco trans 2.

GO; GO:001676; Glyco trans 2.

GO; GO:001676; Glyco trans 3.

GO; GO:001676; Glyco Transferase 3.

GO; GO:001676; Glyco Transferase 3.

GO; GO:001676; Glyco Transferase 3.
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                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 24, Last sequence update)
8ucrose-phosphate synthase-like protein (EC 2.4.1.14).
F28M11.40 OR AT4G10120.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thalianae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Spermatophyta; I. Brassicales, Brassicaceae; Arabidopsis.
NCBL_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
Mayor K.F.X., Lemcke K., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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SEQUENCE FROM N.A.
SEU Arabidopsis sequencing project;
SUD Arabidopsis sequencing project;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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  PRT; 1083 AA
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Best Local Similarity 66.7
Matches 6; Conservative
  PRELIMINARY;
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483 VIPPGMDFS 491
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Q9SN30
Q9SN30,
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P0678F11.14.
P0678F11.14.
P0678F11.14.
P0678F11.14.
Subaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Ehrhartophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Sasaki T., Mateumoto T., Yamamoto K.;
Susaki T., Mateumoto T., Yamamoto K.;
Susaki Sasaki T., Mateumoto T., Yamamoto K.;
Submitted (MAR.-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; ABO03437; BAB86107.1; -
R GO; GO:000458; F:L-lactate dehydrogenase activity; IEA.
R GO; GO:0005058; P:biosynthesis; IEA.
R GO; GO:0006056; P:glycolysis; IEA.
R InterPro; IPR001296; Glyco Lrann=1.
R InterPro; IPR001295; L.DH.
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01-MAR-2001 (TrEMBirel. 16, Created)
01-MAR-2001 (TrEMBirel. 16, Last sequence update)
01-MAR-2001 (TrEMBirel. 16, Last sequence update)
01-MAR-2001 (TrEMBirel. 16, Last annotation update)
Na+/K+/2Cl-cotransporter (Fragment).
Exicohelir sinensis (Chinese mitten crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Bucarida; Decapoda; Plecoyemata; Brachyura;
Eubrachyura; Grapsoidea; Varunidae; Eriocheir.
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR001296; Glyco_trans_1.
InterPro; IPR001557; L.LDH.
Pfam; PF00534; Glycos_transf_1; 1.
PROSITE; PR00064; L.LDH; 1.
SEQUENCE 1084 AA; 119417 MW; 4D0D79AFEDD2F92B CRC64;
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66.7%; Pred. No. 1.9e+02;
tive 2; Mismatches 1
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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MEDLINE=21664373; PubMed=11792842;
Shimizu T., Ohtenina K., Hirakawa H., Ohehima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
Weihrauch D., Towle D.W.; Mak/K+/2Cl- -cotransporter are expressed in Mak/H+-exchanger and Nak/K+/2Cl- -cotransporter are expressed in gills of the euryhaline Chinese crab Eriocheir sinensis."; Comp. Biochem. Physiol. 126:S158-S158 (2000). While the Expression of AG39938.1; -... NON TER.
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1502;
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64.8%; Score 35; DB 5; Length 219;

Best Local Similarity 75.0%; Pred. No. 49;

Matches 6; Conservative 1; Mismatches 1; Indels
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Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).
BEMBL, PAB19763.1. -
GO, GO:0003824; F:catalytic activity; IEA.
InterPro: IPR0005036; MoeB.
InterPro: IPR000594; ThiF Gomain.
Pram. PRO0899; ThiF Gomain.
Prochetical protein; Complete proteome.
SEQUENCE 253 AA; 27714 MW; 814DF79D3E0D7486 CRC64;
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219 AA; 24159 MW; 599442DA26P0D3F1 CRC64;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein CPE0057.
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Q8XPA8
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Search completed: June 3, 2004, 11:57:32 Job time: 30.8667 secs

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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Abg03621 N
Abg08173 N
Abg05826 N
Abb80546 F
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       (CORV-) CORVAS INT INC
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     Abb80521 Hepatitis
Abb80522 Hepatitis
Abb80563 Hepatitis
Abb80563 Hepatitis
Abb80569 Hepatitis
Abb80559 Hepatitis
Abb80569 Hepatitis
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Abb80560 Hepatitis
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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protesse. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a peptide compound of the invention having the hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                          ABB80521 standard; peptide; 11 AA.
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                                                                                                                                              Local Similarity 100. es 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                               Hepatitis C virus, HCV; serine protease, inhibitor; alpha-ketoamide;
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                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
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100.0%; Pred. No. 0.002;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                 'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
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                                                                                                ABB80522 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                        residue 7
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1 EEVVPXGMSYS 11
                          1 EEVVPXGMSYS 11
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                   /note= "Valyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                               'note= "N-terminal acetyl"
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                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46
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ID ABB80566 standard; peptide; 11 AA.
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Brunck TK;

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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/note= "C-terminal amide"
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                             Novel peptide compound having hepatitis C virus protesse inhibitory activity useful for treating disorders associated with hepatitis C ^{\circ}
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100.0%; Pred. No. 0.002;
ive 0; Mismatches (
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                                Brunck TK;
                                                                                                                               Claim 17; Page 65; 69pp; English.
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Best Local Similarity 100...
Thes 11; Conservative
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        (CORV-) CORVAS INT INC.
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                                Levy OE,
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                                                        WPI; 2002-361643/39
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                                                                                                                                                                                                                                                            Sequence 11 AA;
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                                Lim-Wilby M,
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                                                                                                        protease.
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ABB80559
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DB 5; Lenso, 0.002;

Mismatches

96.2%; Score 50; 100.0%; Pred. No. :ive 0; Mismatch

English.

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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus, HCV; serine protease, inhibitor, alpha-ketoamide, virucide.
                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
                                                                                                                                                                                                                                                                                                      ABB80526 standard; peptide; 11 AA.
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Best Local Similarity 100.0
Matches 11, Conservative
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                                                   Claim 17; Page 65; 69pp;
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         Novel peptide
activity usefu
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                              protease
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'note= "N-terminal acetyl"

Location/Qualifiers

/note= "C-terminal amide"

Brunck TK;

Levy OE,

notes "D-form residue" note= "D-form residue"

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.
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                                                                                                                                                                           96.2%; Score 50; DB 5; Length 11;
100.0%; Pred. No. 0.002;
.ive 0; Mismatches 0; Indel8
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                                                                                                                                                                                             Local Similarity
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                                                                                                                                             Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                              virus
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                ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
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ABB80561 standard; peptide; 11 AA.
                                            08-OCT-2002
                                                                                                               Synthetic.
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                           ABB80561;
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                                                                                                                                                                                                                                                                     'note= "Alpha-propynyl-glycinyl-carbonyl residue forming keto-amide linkage with residue 7"
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                   Gaps
                                                                                                                                                                                   Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48
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 Score 50; DB 5; Length 11;
Pred. No. 0.002;
0; Mismatches 0; Indels
  Length 11;
                                                                                                                                                                                                                                                      'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                   note= "C-terminal amide"
                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                        ABB80568 standard, peptide, 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 65; 69pp; English.
) Similarity 100.0%; Post Conservative 0;
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                                                                                                                                              (first entry)
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ses 11; Conservative
                                      1 EEVVPXGMSYS 11
                                                          EEVVPXGMSYS 11
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  Query Match
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Matches 11;
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                                                                                                                                                                                                                 Synthetic.
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Matches
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                                                                                                                                                                                                                                                           'note= "Norvalyl carbonyl forming keto-amide linkage with
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                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
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Pred. No. 0.013;
); Mismatches 1
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                                                                                                                                                                                                                                                                                                                                         note= "Oxymethionine"
                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                         residue 7"
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Matches 10; Conservative
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                                                                                                                                         /note= "Norvalyl carbonyl forming keto-amide linkage with-residue 7"
                                                                                                                                                                                                                                                                                                                                                                           ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
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                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
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Pred. No. 0.013;
); Mismatches 1
                                                                                                                     note= "N-terminal acetyl"
                                                                                                                                                                                                  /note= "C-terminal amide"
                                                                                                                                                                            note= "D-form residue"
                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                    Brunck TK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80529 standard; peptide; 11
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90.9%;
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                                                                                                                                                                                                                                                                    19-JUL-2001; 2001WO-US023169
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Best Local Similarity 90.97
10; Conservative
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                                                                                                                                                                                                                                                                                                               (CORV-) CORVAS INT
                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                              Novel peptide
activity usefu
                                                                                                Key
Modified-site
                                                                                                                                Modified-site
                                                                                                                                                                                       Modified-site
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                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                       protease.
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                                              /note= "Norvalyl carbonyl forming keto-amide linkage with residue ?"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of invention are alpha-keroamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture as medicament to trat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredist useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C ^\circ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8
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Pred. No. 0.013;
0; Mismatches 1; Indels
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                                     'note= "N-terminal acetyl"
                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                note= "D-form residue"
                                                                                                      note= "D-form residue"
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        Location/Qualifiers
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90.9%;
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Best Local Similarity 90.>
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                                                                                                                    Misc-difference
                                                                                          Misc-difference
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                                                                                                                                                                                        WO200208251-A2
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 88.5%; Score 46; DB 5; Length 11; Best Local Similarity 90.9%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 1; Indels
                                                           /note= "C-terminal amide"
                               'note= "D-form residue"
                                                                                                                                                                                                                                                              Lim-Wilby M, Levy OE, Brunck TK;
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                                                                                                                                                              19-JUL-2001; 2001WO-US023169.
                                                                                                                                                                                             21-JUL-2000; 2000US-0220101P.
residue 7"
                                                                                                                                                                                                                             (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                           WPI; 2002-361643/39.
                 Misc-difference 8
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                                                                                            WO200208251-A2.
                                             Modified-site
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Search completed: June 3, 2004, 11:48:23 Job time: 45.9333 secs

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Sequence 3738, Application US/09134000C

Sequence 3738, Application US/09134000C

Patent No. 6617156

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DATE: 1998-08-13

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 3738

LENGTH: 382
                                                                                                                                                                                                                                                                                          US-09-408-020-4

US-09-408-020-4

§ Sequence 4, Application US/09408020

§ Sequence 4, Application US/09408020

§ Patent No. 6622937

§ GENERAL INFORMATION:

§ APPLICANT: Swanson, Robert A.

§ APPLICANT: Schleper, Christa

§ TITLE OF INVERTION: UNCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM

FILE REFERENCE: DOORP. 002A

§ CURRENT APPLICATION NUMBER: US/09/408,020

§ CURRENT FILING DATE: 1998-09-29

§ PRIOR FILING DATE: 1998-09-29

§ NUMBER OF SEQ ID NOS: 123

§ SEQ ID NO 4

§ SEQ ID NO 4

**LENGTH: 3472
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Pred. No. 1.1e+02;
4; Mismatches 1; Indels
                              US-08-463-717-6
US-08-246-361A-4
PCT-US93-05000-4
PCT-US93-05000-6
US-08-464-517-23
US-08-246-361A-6
US-08-246-361A-23
US-08-246-361A-23
US-08-246-361A-23
US-08-463-172-23
US-08-461-172-8
US-08-461-617-19
US-08-464-517-20
US-08-464-517-20
US-08-464-517-20
                                                                                                                                                                                                                                                      ALIGNMENTS
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ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-09-408-020-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 73.1%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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RESULT 2
US-09-134-000C-3738
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Sequence 73, Appl
Sequence 73, Appl
Sequence 2902, Ap
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 236, App
Sequence 236, App
Patent No. 5177197
Patent No. 5177197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 66, Appl
Sequence 66, Appl
Sequence 23, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 21, Appl
Sequence 22, Appl
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                                                                                       June 3, 2004, 11:36:47 ; Search time 11.7333 Seconds
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-134-000C-3738

US-09-540-236-2902

US-09-540-236-2902

US-09-360-946-3

US-09-760-946-3

US-09-760-946-3

US-08-671-7598-236

US-08-871-7598-236

US-08-871-7598-236

US-08-86-888-66

US-09-521-656-66

US-09-521-66-66

US-09-168-888-66

US-09-168-888-66

US-09-168-888-66

US-09-168-888-66

US-08-460-694-4

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US-08-460-744-4

US-08-460-744-2

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Maximum Match 100%
Listing first 45 summaries
                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Result

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Gaps

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Sequence 7885, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRESENTE GF09-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7885
LENGTH: 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us-us-ve-ve-lobblication US/09760946

sequence 2, Application US/09760946

patent No. 6608027

GENERAL INFORMATION:

APPLICANT: Cameron, Dale R.

APPLICANT: Cameron, Dale R.

APPLICANT: Guideau, Nathalie

APPLICANT: Halmos, Teddy

APPLICANT: Alines Pruck, Montse

APPLICANT: Blancs 2000-08-23

PRIOR EFFENCE: 13/076-1-C1

CURRENT APPLICATION NUMBER: US 09/542,675

PRIOR PILING DATE: 2000-08-23

PRIOR PILING DATE: 1999-04-06

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 2

LEASTHAND AND 3.1

SEQ ID NO 2

LEASTHAND AND 3.1

LEASTHAND AND 3.1
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Pred. No. 2.5e+02;
2; Mismatches 1; Indels
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Patent No. 6608027
GENERAL INFORMATION:
APPLICANT: Teantrizes, Youla S.
                                                                                                                                                                                                                                                                                                                            , ORGANISM: Acinetobacter baumannii
US-09-328-352-7885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 45.5
Matches 5; Conservative
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US-09-760-946-3
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APPLICANT: GATY L. BRECON et al.
APPLICANT: GATY L. BRECON et al.
TITLE DE INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE DE INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2902
LENGTH: 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cell8
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION UNMERR: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FASISEQ for Windows Version 3.0
SEQ ID NO 73
LENGTH: 947
                                                   NAME/KEY: MISC_FEATURE

1 LOCATION: (327)...(328)

2 OTHER INFORMATION: Amino acids 327 & 328 are Xaa wherein Xaa = any amino acid.

US-09-134-0006-3738
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Pred. No. 2e+02;
3; Mismatches 1; Indel8
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Pred. No. 1.6e+02;
2; Mismatches 1; Indels
                                                                                                                                                               69.2%; Score 36; DB 4; Length 382; 66.7%; Pred. No. 22; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-540-236-2902; Sequence 2902, Application US/09540236; Patent No. 6673910
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 73, Application US/09228986 Patent No. 6359198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.4%;
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Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                Query Match
Best Local Similarity 66.77
These 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |::| ||:|
783 EILPVGMAY 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT;
ORGANISM: Pinus radiata
US-09-228-986-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  686 VMPSGISYS 694
                                                                                                                                                                                                                                                                                          332 LIPEGMSYS 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VVPXGMSYS 11
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US-09-328-352-7885
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                                                                                                                                                                                                      63.5%; Score 33; DB 2; Length 45; 60.0%; Pred. No. 7.8; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                           US-08-871-355A-236

US-08-871-355A-236

Sequence 236, Application US/08871355A

Patent No. 6015669

Patent No. 6015669

TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:
ADDRESSER: Patrea L. Paber

STREET: 1201 West Peachtree Street

CITY: Atlanta

COUNTRY: USA

ZIP: 3009-348

ZIP: 3009-348

COUNTRY: USA

ZIP: Flopy disk

COMPUTER READALE FORM:
MEDIUM TYPE: Flopy disk

COMPUTER PEALABLE FORM:
MEDIUM TYPE: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A

FILING DATE: 09-JUN 1997

CLASSIFICATION: 435

PRIOR APPLICATION 1435

CLASSIFICATION: 435

ATTORNEY/AGET INFORMATION:
NAME: PADET, PATENE AL.
REGISTRATION: NUMBER: 31,284

REGISTRATION THORMATION:
NAME: PADET NUMBER: 31,284

REGISTRATION NUMBER: 31,284

REGISTRATION NUMBER: 31,284

REGISTRATION NUMBER: 31,284

REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
               i ENGTH: 45 amino acids

i TYPE: amino acid

i TYPE: amino acid

i STRANDEDNESS: single

i TOPOLICY: linear

i MOLECULE TYPE: protein

i HYPOTHETICAL: NO

US-08-637-7599-236
                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0
Matches 6; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                   1 EEVVPXGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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; MOLECULE TYPE:
; HYPOTHETICAL:
US-08-871-355A-236
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                 APPLICANT: Halmos, Teddy
APPLICANT: Halmos, Teddy
APPLICANT: Linas-Brunet, Montse
TITLE OF LINAS-Brunet, Montse
FILE REPERENCE: 13/076-1-C1
CURRENT APPLICATION NUMBER: US/09/760,946
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/542,675
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PARENT NOS: 5
SOFTWARE: PARENT NOS: 5
LENGTH: 12
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NAME/KEY: MOD_RES
LOCATION: (1)
COTHER INFORMATION: Asp at position 1 is biotinylated
NAME/KEY: MOD_RES
LOCATION: (10)
COTHER INFORMATION: Tyr at position 10 is iodinated with I-125
US-09-760-946.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 4; Length 12;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
CONTRY: USA
ZIP: 30309-3450
COMPUTER READMBLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
FILING DATE: 11-DEC-1995
TLING DATE: 11-DEC-1995
FILING DATE: 11-DEC-1995
TLING DATE: 11-DEC-1995
FILING DATE: 11-DEC-1995
TELEFRATION NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEFRATION FOR SEQ 1D NO: 236:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 236, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%;
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
Goudreau, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 45.5
Matches 5; Conservative
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Gaps

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Sequence 66, Application US/09357952

Patent No. 6248904

GENERAL INFORMATION:

APPLICANT: Zhang, Han-Zhong

APPLICANT: Cai, Sui Xiong

APPLICANT: Drewe, John A.

TITLE OF INVENTION: No. 6248904e1 Fluorescence Dyes and Their Applications for Whole

TITLE OF INVENTION: Pluorescence Screening Assays for Caspases, Peptidases, TITLE OF INVENTION: Other Enzymes and the Use Thereof

FILE REFERENCE: 1735.0030001

CURRENT APPLICATION NUMBER: US/09/357,952

CURRENT FILING DATE: 1999-07-21

EARLIER APPLICATION NUMBER: US 60/093,642
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                                                                                                                                                                                                                                          APPLICANT: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;
;WERNSTEDT, CHRISTER;HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH,
;LENA;HELDIN, CARL-HENRIK
;TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
;HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
;NUMBER OF SEQUENCES: 53
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/487,343
;FILING DATE: 27-FEE-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; ; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH, ; LENA; HELLDIN, CARL-HENRIN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH, ; LENA; HELLDIN, CARL-HENRIN, ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING; HUMAN TRANSFORMING GROWTH PACTOR-BETA1-BINDING PROTEIN CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

PILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%; Score 33; DB 6; Length 1394; 45.5%; Pred. No. 3.9e+02; Anismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.5%; Score 33; DB 6; Length 410; 45.5%; Pred. No. 97;
       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
          5; Conservative
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hes 5; Conservative
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Best Local Similarity 45.5
Matches 5; Conservative
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                                                        1 EEVVPXGMSYS 11
                                                                                     52 KEICPGGMGYT 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:1:
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;Patent No.
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          Matches
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;WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
;LENA, FELDIN, CARL-HENREN,
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.5%; Score 33; DB 4; Length 45; Best Local Similarity 60.0%; Pred. No. 7.8; Matches 6; Conservative 1; Mismatches 3; Indels
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
                                         Sequence 236, Application US/09201945
Fatent No. 63422L5
GENEMAL INFORMATION:
APPLICANT: David William Holden
FITEE OF INVENTION:
NUMBER OF SECUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
ADRESSEE: Patrea L. Pabst
STREET: 1200 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (404) 873-8794
TELEPAX: (404) 873-8794
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%;
45.5%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                      CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Patent No. 5177197
RESULT 10
US-09-201-945-236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:51:
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5177197-51
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Sequence 66, Application US/09521650

Sequence 66, Application Sex Manager 100 Ma
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                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-357-952-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 61.5%; Score 32; DB 3; Length 10; Best Local Similarity 50.0%; Pred. No. 2.3; Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.5%; Score 32; DB 4; Length 10; 50.0%; Pred. No. 2.3;
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 66
LENGTH: 10
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Matches 5; Conservative
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Search completed: June 3, 2004, 12:03:07 Job time: 11.8 secs

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TYPE: PRT
ORGANISM: artificial sequence
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NAME/KEY: MOD RES
LOCATION: (11). (11)
COTHER INFORMATION: AMIDATION
US-09-909-164-5
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LENGTH: 11
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                                                                                                              June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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Sequence 10,
Sequence 47,
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Sequence 50,
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Sequence 5
Sequence 8
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/ cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.ppp:*

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/ cgn2_6/prodata/1/pubpaa/USO9_PUBCOMB.ppp:*

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/ cgn2_6/prodata/1/pubpaa/USO06_PUBCOMB.ppp:*

/ cgn2_6/prodata/1/pubpaa/USOO6_PUBCOMB.ppp:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-6
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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16 45 86.5 11 12 US-09-909-164-19 Sequence 19, Appl 19 45 86.5 11 12 US-09-909-164-21 Sequence 20, Appl 20 44 84.6 11 12 US-09-909-164-29 Sequence 21, Appl 20 44 84.6 11 12 US-09-909-164-29 Sequence 29, Appl 22 44 84.6 11 12 US-09-909-164-29 Sequence 29, Appl 22 44 84.6 11 12 US-09-909-164-39 Sequence 29, Appl 24 84.6 11 12 US-09-909-164-31 Sequence 29, Appl 25 44 84.6 11 12 US-09-909-164-31 Sequence 31, Appl 26 41 12 US-09-909-164-31 Sequence 31, Appl 26 41 12 US-09-909-164-31 Sequence 31, Appl 30 41 78.8 11 12 US-09-909-164-22 Sequence 41, Appl 31 12 US-09-909-164-22 Sequence 26, Appl 31 41 78.8 11 12 US-09-909-164-22 Sequence 26, Appl 31 41 78.8 11 12 US-09-909-164-22 Sequence 27, Appl 31 41 78.8 11 12 US-09-909-164-21 Sequence 27, Appl 31 40 76.9 11 12 US-09-909-164-21 Sequence 21, Appl 31 40 76.9 11 12 US-09-909-164-21 Sequence 21, Appl 32 40 76.9 11 12 US-09-909-164-21 Sequence 31, Appl 34 40 76.9 11 12 US-09-909-164-21 Sequence 31, Appl 34 40 76.9 11 12 US-09-909-164-31 Sequence 31, Appl 34 40 76.9 11 12 US-09-909-164-31 Sequence 41, Appl 39 75.0 11 12 US-09-909-164-31 Sequence 46, Appl 41 39 75.0 11 12 US-09-909-164-31 Sequence 31, Appl 42 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 44 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 44 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 44 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 44 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 44 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 44 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 44 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 44 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 44 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 44 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 44 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 44 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 45 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 45 39 75.0 11 12 US-09-909-164-31 Sequence 34, Appl 46 30 US-09-909-164-30 Sequence 34, Appl 46 30 US-09-909-164-30 Sequence 34, Appl 46 30 US-09-909-164-3
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## ALIGNMENTS

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RESULT 1

UB-09-164-5

Sequence 5, Application US/09909164

Publication No. US2020068702A1

GENERAL INFORMATION 1

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby Marguerita

FRIGHT FILING DATE: 2000-07-21

FRIGHT PROMATION: UNSER 60/220,101

FRAUPE: PROPER FILING DATE: 2000-07-21

SOFTWARE: PATCHICATION NOTES: Limer synthesized according to example 1

FRAUTE: MARGINE: MODERS

LOCATION: (6).-(6)

OTHER INFORMATION: norvaline-(CO)

FRAUFE: NAME/KEY: MISC. FEATURE

NAME/KEY: MODERS

LOCATION: (11).-(11)

OTHER INFORMATION: ANIDATION

WIS-09-909-164-5

NAME/KEY: MODERS

LOCATION: (11).-(14)

OTHER INFORMATION: ANIDATION

WIS-09-909-164-5
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OTHER INFORMATION: 11-mer synthesized according to example 1
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
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100.0%; Pred. No. 0.0014;
tive 0; Mismatches 0;
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OTHER INFORMATION: norvaline-(CO)
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NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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; OTHER INFORMATION: D-amino acid
US-09-909-164-9
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NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
PEATURE:
                                SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 11
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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LOCATION: (11\overline{1})...(11)
OTHER INFORMATION: AMIDATION
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OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
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Publication No. US20200068702A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION NUMBER: 2003-03-25
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
SOFTWARE OF SEQ ID NOS: 62
SOFTWARE PATEURING DATE: PRIOR PR
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Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Lim.Wilby, Marguerita
APPLICANT: NOVIE PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
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OTHER INFORMATION: 11-mer synthesized according to example 1
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100.0%; Pred. No. 0.0014;
tive 0; Mismatches 0; Indels
100.0%; Pred. No. 0.0014; ive 0; Mismatches 0; Indels
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NAME/KRY
(9)...(9)
COCATION: (9)...(7)
OTHER INFORMATION: D-amino acid
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
US-09-909-164-6
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Best Local Similarity 100.
Matches 11; Conservative
    Best Local Similarity 100.
Matches 11; Conservative
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
DECATION: (1)..(1)
OTHER INFORMATION: ACTIVATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: ACTIVATION
FEATURE:
RAME/KEY: MOD_RES
LOCATION: (11)..(11)
FEATURE:
FEATURE:
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COTHER INFORMATION: leucine-(CO)
US-09-909-164-48
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NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 11
                                                                                                                                                          TYPE: PRT
ORGANISM: artificial sequence
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Sequence 47, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Corves International, Inc.

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEBATITIS C

FILE REFERENCE: IN01192-US

CURRENT APPLICATION NUMBER: 60/200,101

PRIOR APPLICATION NUMBER: 60/200,101

PRIOR PLING DATE: 2003-03-25

PRIOR PLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 47
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Odile E
APPLICANT: Brunck, Odile E
APPLICANT: Brunck F
PILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
PILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
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                                                                                                                      Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
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            ; OTHER INFORMATION: D-amino acids US-09-909-164-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MOD_RES
LOCATION: (1)..(1)
LOCATION: (1)..(1)
PEATURE: INFORMATION: ACETYLATION
PEATURE: LOCATION: RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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LOCATION: (6)..(6)
OTHER INFORMATION: valine-(CO)
US-09-909-164-47
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ORGANISM: artificial sequence
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RESULT 11
US-009-109-164-8
Sequence 8, Application US/09909164
; Publication No. US20020068702A1
                        NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
                                                                                  FEATURE:
NAME/KEY:
MOD RES
LOCATION: (11)...(11)
OTHER INFORWATION: AMIDATION
FEATURE:
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OTHER INFORMATION: AMIDATION
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FEATURE:
NAME/KEY: MOD RES
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US-09-909-164-52
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| Sequence 50, Application US/09909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc.
| APPLICANT: Lim-Wilby, Marguerita
| MUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 50
| LENGTH: 11
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LOCATION: (6). (6)
OTHER INFORMATION: 2-amino-butyric acid-(CO)
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LOCATION: (1):..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
MAME/KEY: MOD_RES
LOCATION: (11):.(11)
OTHER INFORMATION: AMIDATION
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ORGANISM: artificial sequence
1 EEVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
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NAME/KEY: MISC_FEATURE

LOCATION: (6)...(6)

OTHER INFORMATION: (8,8)-allothreonine-(CO)
US-09-909-164-51
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NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: propynyl glycine-(CO)
US-09-909-164-52
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Sequence 13, Application US/09009164

| Sequence 13, Application World US/09009164
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| APPLICANT: Lim-Wilby, Marguerita
| TILE OF INVENTION: NOVER: US/09/909,164
| CURRENT FILING DATE: 2000-07-21
| VINDER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 13
| Lim-Grafia 11
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Pred. No. 0.0091;
0; Mismatches 1; Indels
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Pred. No. 0.0091;
0; Mismatches 1; Indels
DOCATION: (11)
COLATION: (11)
COLATION: (11)
COLATURE INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
COTHER INFORMATION: norvaline-(CO)
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)...(8)
COTHER INFORMATION: D-amino acid
US-09-909-164-12
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OTHER INFORMATION: norvaline-(CO)
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i OTHER INFORMATION: D-amino acids
US-09-909-164-13
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE: NESS: MOD_RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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ORGANISM: artificial sequence
FEATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Best Local Similarity 90.9%;
Matches 10; Conservative
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  APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Lovy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
UTRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 11
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US-09-909-164-12

Sequence 12, Application US/09909164

Sequence 12, Application US/09909164

Sequence 12, Application O. US20020068702A1

Sequence 12, Application O. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Lim-Wilbly, Marguerita
APPLICANT: Lim-Wilbly, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Lim-Wilbly DEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21
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11-mer synthesized according to example 1
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
NO RES
COCHION: (1)..(1)
OCHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC.FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MISC FEATURE LOCATION: (9). . . (9) OTHER INFORMATION: D-amino acid
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 11
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ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (11)...(11)
; OTHER INFORMATION: AMIDATION
US-09-909-164-8
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                                                                                                                                              FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER_INFORMATION: norvaline-(CO)
       LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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NAME/KRY: MISC FEATURE
COCATION: (8). (8)
CTHER INFORMATION: D-amino acid
US-09-909-164-11
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Sequence 7, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, ddile E

APPLICANT: Levy, ddile E

APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin Version 3.1

SEQ ID NO 7

LENGTH: 11
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEFATITIS C
FILE REPERENCE: INOI132-US
CURRENT APPLICATION NUMBER: US/09/909,164
PRIOR FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PERCENCE NOS: 62
SOFTWARE: PERCENCE NOS: 62
SOFTWARE: PERCENCE NOS: 62
LENGTH: 11
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ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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Pred. No. 0.015;
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Sequence 11, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
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NAME/KEY: MISC_FEATURE
LOCATION: (9)..(9)
OTHER INFORMATION: D-amino acid
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DOCATION: (11)...(11)

OTHER INFORMATION: AMIDATION

US-09-909-164-7
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sulfate permease -
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DNA-binding protei
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DNA-directed RNA p
                                                      3, 2004, 11:35:47 ; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                            283366 seqs, 96191526 residues
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                                     - protein search, using sw model
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A34203
S54619
H69491
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T39116
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A42452
B97355
S57810
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D82352
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AF3286
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A35626
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 su
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1 EEVVPXGMSYS 11
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Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Maximum DB
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hypothetical prote	masking protein pr	hypothetical prote	transport protein	rho protein GDP-di	hypothetical prote	cyclin D2 - rat	cyclin D2 - rat	cyclin D2 - mouse	cyclin D2 - human	cyclin D1 - Africa	cyclin D2 - Africa	cyclin D2 - chicke	cyclin D1 - zebra	cyclin D3 - human	cyclin D1 - human
T04456	A38261	E97333	PQ0616	T01457	B72481	JC4011	158372	A41984	A42822	S57922	S57925	JC4579	S62730	B42822	A38977
N	α	N	N	N	N	N	N	N	N	N	N	N	N	N	N
1548	1712	84	175	223	279	288	288	289	289	291	291	291	291	292	295
63.5	63.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5
33	33	32	32	35	32	32	32	32	32	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	33	40	41	42	4.3	44	45

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Cypecies: Cenarchaeum symbiosum Control of the cont
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #text_change O3-Dec-1999
C;Accession: T39116
R;Hunt, C;, Aves, S; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
R;Hunt, C;, Aves, S; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
A;Reference number: Z21829
A;Recession: T39116
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: DNA
A;Residues: 1-840 <HUN>
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Pred. No. 60;
4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                   hypothetical 367K protein - Cenarchaeum symbiosum
ALIGNMENTS
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Best Local Similarity 54.5%;
Matches 6; Conservative 4
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Best Local Similarity 77.8
Matches 7; Conservative
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Gene: SPDB:SPAC869.05c
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A;Reference number: Z19842
A;Recession: T24111
A;Accession: T24111
A;Accession: T24111
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-425 <WIL.>
A;Cross-references: EMBL:Z81109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
A;Experimental source: clone R10D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accessins: T24111
R;Percy, C.
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C;Species: Rattus norvegicus (Norway rat)
C;Species: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: 225233; I78623; I78623; I78623; I7863;
R;Mitchelmore, C.; Traboni, C.; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Lycopersicon esculentum (tomato)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Accession: 557810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Finiligan, S.B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
Ajritle: Mature and regulation of pistil-expressed genes in tomato.
Ajritle: Mature and regulation of pistil-expressed genes in tomato.
Ajrecesion: SS7810
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    DB 2; Length 1498;
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Pred. No. 13;
3; Mismatches 2
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Pred. No. 26;
3; Mismatches
Score 36;
Pred. No. 6
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A; Introns: 23/3; 56/3; 113/3; 257/2
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Best Local Similarity 54.5%;
Matches 6; Conservative 3
        69.2%;
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Best Local Similarity 50.0.
        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                           1276 EQKIPMGMSY 1285
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32 DEVVPNGKTYA 42
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CiSpecies: tobacco yellow dwarf virus
CiSpacession: A44452
Rimorris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.B.
Rimorris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.B.
A;Title: tubectide sequence of the infectious cloned DNA component of tobacco yellow A;Reference number: A44452
A;Reference number: A44452
A;Accession: A44452
A;Accession: A44452
A;Accession: A44452
A;Cross-references: GB:MB1103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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J. Bacteriol. 183, 4823-4838, 2001
A. Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A, Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA segregation Arpase, FtsK/SpoiliB family, YUKA B. subtilis ortholog [imported] - Clos C.Species: Clostridium acetobutylicum C.Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
                                                                                                          sulfate permease - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40413
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
Submitted to the EMBL Data Library, August 1998
A;Reference number: Z21926
A;Accession: T40413
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Resdidues: 1-877 cLYN.
A;Resdidues: 1-877 cLYN.
A;Resdidues: BMBL;AL031261; PIDN:CAA20298.1; GSPDB:GN00067; SPDB:SPBC3H7.02
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A;Molecule type: DNA
A;Molecule type: DNA
A;Reaidues: 1-1498 <KUR>
A;Reaidues: 1-1498 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK81629.1; PID:g15026814; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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69.2%; Score 36; DB 2; Length 102;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 6; Conservative 3; Mismatches 1; Indels
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7 QVVPSGINYS 16
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\,Gene: SPDB:SPBC3H7.02
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Matches
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Rixlenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson Stleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 801-1072, NY,1074-1168, KY,1170-1225, VY,1227-1434, NY,1436-1607, IY,1609-14
A;Croser references: GB:M32019
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Keywords: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                           A,Molecule type: mRNA
A;Readdudes: L-2717 <FRNA
A;Cross-references: EMBL:X51435; NID:g38017; PIDN:CAA35798.1; PID:g38018
A;Cross-references: EMBL:X51435; NID:g38017; PIDN:CAA35798.1; PID:g38018
R;Baldwin Jr., A.S.; Leclair, K.P.; Singh, H.; Sharp, P.A.
Mol. Cell. Biol. 10; 1466-1444, 1990
Mol. Cell. Biol. 10; 1466-1444, 1990
A;Reference number: A34779; MUID:90205817; PMID:2108316
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A;Residues: 1-156 <DEW>
A;Cross-references: EMB1:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YORO
A;Experimental source: strain S288C
                                            ,Title: A DNA-binding protein containing two widely separated zinc finger motifs that J.Reference number: A34203; MUID:90169514; PMID:2106471; A34203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ny Alternate names: hypothetical protein VOR013w - yeast (Saccharomyces cerevisiae)

Ny Alternate names: hypothetical protein 02612; hypothetical protein VOL303.3

C, Species: Saccharomyces cerevisiae

C; Date: 08-Unl-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002

C; Accession: S54619; S66879

R, Accession: S54619

A, Accession: S54619

A, Accession: S54619

A, Molecule type: DNA

A, Reference number: S54617

A, Accession: S54619

A, Residues: 1-156 cDEH>

A, Residues: 1-156 cDEH>

A, Residues: 1-156 cDEH>

A, Residues: 1-156 cDEH>

A, Reference number: S68877

A, Reference number: S66877

A, Reference number: S66877

A, Accession: S66877

A, Molecule type: DNA

A, Reference number: S66877
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
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Pred. No. 1.9e+02;
2; Mismatches 1; Indels
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Pred. No. 14;
1; Mismatches 2; Indels
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C;Superfamily: hypothetical protein YOR013w
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Best Local Similarity 66.7%;
Matches 6; Conservative 5
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Best Local Similarity 66.7
Matches 6; Conservative
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2405 VVPAGLTYS 2413
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Cypersonance: Xylella fastidiosa
Cypersonance: Navier assistation of the Xylella fastidiosa
Cybersonic H82691
Ryanonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
AyTitle: The genome sequence of the plant pathogen Xylella fastidiosa.
AyTitle: The genome sequence of the plant pathogen Xylella fastidiosa.
AyAccession: H82691
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R. Simpson, A. G. G. Reinach, F. C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H Sabmitted to GenBank, June 2000

A,Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, B.E.; Laigr Gado, M.M., Madeira, A.M.B.N.; Madeira, H.M.F.; Menck, C.F.M.; Marques, M.V.; Martins, E.A.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Ayuthors: da Silva, A.C.R.; da Silva, A.M.; Salwasak A,Authors: A.G.R.; da Silva, A.M.; Silva, Jr.; N.A.; da Silva, A.M.; Silva, Jr.; N.A.; da Silva, A.M.; Silva, Jr.; N.A.; da Silva, A.L.; S.A.; A.R.; A.R.; A.R.; A.R.; M.A.; A.R.; A.R.; M.A.; A.R.; A.R.; M.A.; A.R.; 
A;Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-A;Reference number: IS8280; MUID:91187610; PMID:1901405
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C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 topoisomerase IV subunit XF1353 [imported] - Xylella fastidiosa (strain 9a5c)
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MAN-binding protein PRDII-BF1 - human
NyAlternate names: major histocompatibility complex enhancer-binding protein
CiSpecies: Homo sapiens (man)
CiSpecies: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
CyAccession: A342703; A34779
RiFan, C.M.; Maniatis, T.
Genes Dev. 4, 29-42, 1990
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                                                                                                                                                                              A; Status: mucleic acid sequence not shown
A; Molecule type: mRMT
A; Molecule type: mRMT
A; Residues: 1.670 «MIT»
A; Cross-references: EMBL: X54250; NID: 957519; PIDN: CAA38151.1; PID: 957520
A; Note: the authors did not translate the codon for residue 1
C; Superfamily: HIV-EP2 enhancer-binding protein
C; Keywords: DNA binding; transcription regulation; zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 749;
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Pred. No. 48;
0; Mismatches 2
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77.8%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C;Accession: 140758; 847317
E;Hani, B.K.; Chan, V.L.
J. Bacteriol. 177, 2396-2402, 1995
A;Title: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyć
A;Reference number: 140758; MUID:95247673; PMID:7730270
Ajauthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.K.; Venter, J.C.

Smith, H.O.; Woese, C.K.; Venter, J.C.

Trile: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Reference number: A69280; MUID:98049343; PMID:9389475

A; Reference number: A69280; MUID:98049343; PMID:9389475

A; Returs: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA

A; Returs: preliminary; nucleic acid sequence not shown; translation not shown A; Returs: PAS & REASONO CB: AEONO CB: AEON
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A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-544 <CLAA
A;Cross-references: GB:AE002133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable ABC substrate-binding protein, iron UU359 [imported] - Ureaplasma urealyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Ureaplasma urealyticum

);Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000

);Accession: CB2900

);Glass, J.I.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.

submitted to Genbank, February 2000

);Description: The Complete sequence of Ureaplasma urealyticum: Alternate views of a 1

4,Reference number: A82870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 544;
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Pred. No. 14;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 2;
Pred. No. 55;
1; Mismatches
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A;Molecule type: DNA
A;Residues: 1-94 <RES>
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Best Local Similarity 55.6%;
Matches 5; Conservative
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Best Local Similarity 70.0%;
Matches 7; Conservative
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26 DIFPSGMSY 34
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81 EVIPAGMS 88
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A;Genetic code: SGC3
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505 ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Species: Aday-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: E90544
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul
A;Reference number: A99512; MUID:21267165; PMID:11353084
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                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL445566; PID:g14089674; PIDN:CAC1343.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.5%; Score 33; DB 2; Length 116; 77.8%; Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: MYPU 2610
A;Genetic code: SGC3
C;Superfamily: Escherichia coli ribosomal protein L20
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Best Local Similarity
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Q8rg86 fusobacteri
074377 schizosacch
024351 clostridium
024352 homo sapien
P15822 homo sapien
0260312 homo sapien
028qv0 mycoplasma
024xb0 vibrio chol
034xb0 vibrio chol
036qs clostridium
028cgl mus musculu
028cgl mus masculu
028cgl mus musculu
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clostridium
homo sapien
neurospora
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archaeoglob
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xenopus lae
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                                                                       3, 2004, 11:32:06 ; Search time 4.86667 Seconds (without alignments) 117:693 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                          141681 seqs, 52070155 residues
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MOUSE
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Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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52
1 EEVVPXGMSYS 11
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Match Length DB
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P44677 haemophilus O75355 homo sapien Q99016 homo sapien P90218 crithidia f P52284 human herpe P52284 human herpe P52843 human herpe P52841 human herpe P52841 human herpe P52841 retus norv P28931 tomato aspe P16916 escherichia P16916 escherichia
TOLB HAEIN ENP3_HUMAN S216_HUMAN S216_HUMAN S2P_CRIFA PRTP_HSV6U SCT1_YEAST SCT1_YEAST END_RAT RASA_ECOLI RHSG_ECOLI RHSB_ECOLI
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427 529 7191 726 726 759 920 1337 1411
6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5 6.1.5
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Q9y616 homo sapien P90518 crithidia f P52344 human herpe P32744 acadharomyc Q62671 rattus norv P28931 tomato aspe P16916 escherichia P16917 escherichia	The Carba FUSNN STANDARD; FRT; 1058 AA. The Carba FUSNN STANDARD; FRT; 1058 AA. OF GRAGE; OF GRA
1 S216_FUMAN 1 GSP_GRIFA 1 PRTP_HSV6U 1 PRTP_HSV6U 1 SCT1 YEAST 1 BDD FAT 1 VIA_TAV 1 VIA_TAV 1 RHSG_ECOLI 1 RHSG_ECOLI 1 RHSB_ECOLI 1 RHSB_ECOLI 1 RHSB_ECOLI	reated) ast sequence update) ast sequence update) thase large chain (EC monia chain). (subsp. nucleatum). (subsp
61.5 61.5 61.5 719 61.5 726 61.5 726 61.5 920 61.5 1377 61.5 1377	STANDARD; (Rel. 41, Car (Rel. 44), Las hosphate 41, Las hosphate 41, Las (Rel. 44), Las hosphate 41, Las (Rel. 44), Las Anchetase anmucleatum uschacteria; Jan 76856; M. N. Anderson I. 76856; M. Anderson I. 7834; Pubmed ana, L. Kogan Chu
44444000000000000000000000000000000000	TLT 1 CARB FUSNN STANDARD; PROGREGE, 28-FEB-2003 (Rel. 41, Last seque Pusobacterium nucleatum (subsp. Pusobacterium. NCBI_TAXID=76856; SEQUENCE FROM N.A. STRAIN=ATCC 25586; MEDLINES-1886391; PubMed=118891(Kapatral V., Anderson I., Ivano Bhattacharyya A., Bartman A., Ga Vasieva O., Chu L., Kogan X., Clarson N., Souza M., Walumas Fonstein M., Kyrpides N., Overb "Genome sequence and analysis of nucleatum strain ATCC 25586.", J. Bacteriol. 184:2005-2018(200; -!- CATALTIC CATIVATY: 2 ATP + -!- CATALTIC Camposed of two ch phosphate + L-dutamate + ic!- CATALTIC Composed of two ch promotes the hydrolysis of promotes the hydrolysis of the large (or ammonia) chail similarity)!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- PATHWAY: Parintidine biosynthe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyribe -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyrib -!- SIMILARITY: Belongs to the swinss-PROT entry 1s copyrib -!- SIMILARITY: Belongs to t
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MEDLINE=21848401; PubMed=11859360;

MEDLINE S., Gavilliam B., Robind D., Bowman S.,

MEDLINE S., Goble A., Hayles J., Harris D., Hidalgo J., Hodgson G.,

MEDLINE S., Goble A., Howarth S., Huckle E.J., Hunt S., Jagels K.,

MEDLINE S., Goble A., Howarth S., Huckle E.J., Hunt S., Jagels K.,

MEDLINE S., Goble B., Murghy L., Nibbett D., Odell C.,

MEDLINE S., Moule S., Murghy L., Nibbett D., Odell C.,

MEDLINE S., Sunders D., Seeger K., Sharp S.,

MILLE S., Sunders D., Seeger K., Sharp S.,

MELTINE S., Vaniture S., Sunders D., Seeger K., Sharp S.,

MELTINE S., Vaniture S., Sunders D., Seeger K., Murleller-Auer S.,

Meltipen I., Vanitures C., Holzer E., Moestl D., Hilbert H.,

Meltipen I., Vaniture S., Hurt C., Moore K., Purnelle B.,

Goffeau A., Cadieu E., Diemano S., Gloux S., Lelaure V., Mottier S.,

Meltos M., Rochet M., Gaillardin C., Fallada V.A., Gazzon A., Thode G.,

Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

Moninguez A., Revuelta J.L., Moreno S., Amustrong J., Forsburg S.L.,

And Mille S., McCombie W.R., Reulsen I., Potashkin J.,

Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
                                                                                                                                                                                                                                                                                                                   ö
R PRINTS; PRO0098; CPSASE.

R RINTS; PRO0098; CPSASE.

R TIGREAMS; TIGRED1369; CPSASE.1.2.

DR PROSITE; PSO0866; CPSASE.1; 2.

DR Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KW Arginine biosynthesis; Omplete proteome.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

FT DOMAIN 402 546 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

FT TOMAIN A10 547 1058 ALLOSTERIC DOMAIN.
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                                                                                                                                                                        10 ATP (POTENTIAL).
52 ATP (POTENTIAL).
64 MANGANESE 1 (BY SIMILARITY).
68 MANGANESE 2 (BY SIMILARITY).
60 MANGANESE 2 (BY SIMILARITY).
60 MANGANESE 3 (BY SIMILARITY).
61 MANGANESE 3 (BY SIMILARITY).
62 MANGANESE 3 (BY SIMILARITY).
63 MANGANESE 3 (BY SIMILARITY).
64 MANGANESE 3 (BY SIMILARITY).
65 MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                         73.1%; Score 38; DB 1; Length 1058; 60.0%; Pred. No. 7; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
PORTOBATION OF THE PERMEASE C3H7.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                 877 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                             547 105
153 21
302 35
284 28
298 29
300 30
820 88
832 83
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NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                       Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
SULH SCHPO
ID SULH SCHPO
AC 074377;
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SEQUENCE
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DOMAIN
REPEAT
REPEAT
NP BIND
NP BIND
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METAL
METAL
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                                                                                                     -i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
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MEDINE-92188538, PubMed-1546458;

MCTIS B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

MCTIS B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

"The nucleotide sequence of the infectious cloned DNA component tobacoo yellow dwarf virus reveals features of geminiviruses infecting monococtyledonous plants.";

Virology 187:633-642(1992).
                     -i- FUNCTION: HIGH AFPINITY UPTAKE OF SULFATE INTO THE CELL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.2%; Score 37; DB 1; Length 877; 77.8%; Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56995A8493371E43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
genome sequence of Schizosaccharomyces pombe."; e 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-011.
01-011.1993 (Rel. 26, Last sequence update)
01-011.1993 (Rel. 27, Last annotation update)
11-0CT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GeneDB SPombe; SPBG3H7.02; -.
InterPro; IPR002645; STAS.
InterPro; IPR01902; Sulph_transpt.
Pfam; PP00140; STAS; 1.
Pfam; PP00916; Sulfate_transp; 1.
TCGRAMS; TIGR00815; Sulfate_transp; 1.
PROSITE; PS01130; SLC264; 1.
PROSITE; PS00801; STAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL031261; CAA20298.1; -. PIR; T40413; T40413.
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TRANSMEM 133 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SIMILARITY: Contains 2 FtsK domains.
-!- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts in positions 76 and 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 824 (DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin B.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.2%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 1.6; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ll protein. -
102 AA; 11178 MW; A40ECFIE0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 28, Created)
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-108 FROM N.A.
STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-93273706; Pubmed-8501044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, X65276; CAA46379.1; -.
PIR, B97355; B97355.
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                                                                                                                                                                                                                                                                                                                                                PIR; A42452; A42452.
InterPro; IPR002621; Gemini mov.
Jemi, PF01708; Gemini mov; I.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2003 (Rel. 42, Last ar
Hypothetical protein CAC3709.
CAC3709.
                                                                                                                                                                                                                                                                                                              EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLOAB
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PIR; B97355; B97355. InterPro; IPR002543; Ft8K SpoIIIE.

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                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-
binding protein 1) (HIV-BP) (Major histocompatibility complex binding
protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1."; Blochemistry 31:3907-3917(1992).

1- FUNCTION: THIS PROTEIN SEBCIFICALLY BINDS TO THE DNA SEQUENCE 5'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMBEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HILL IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MC. INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACTIVATION.

1- SUBSCELLULAR LOCATION: Nuclear.
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NWR OF 2113-2142.
MEDLINE=91064333; PubMed=2248949;
Omichinsesti 0.G., Clore G.M., Appella E., Sakaguchi K.,
Gronenborn A.M.;
"High-resolution three-dimensional structure of a single zinc finger
"High-resolution three-dimensional protein in solution.";
Efrom a human enhancer binding protein in solution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: MOLECULAR STREET.
-1- INDUCTION: By mitogens and phorbol ester.
-1- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fan C.M., Maniatis T., "A DNA-binding is protein containing two widely separated zinc finger motifs that recognize the same DNA sequence."; Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92232684; PubMed=1567844; Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E., Gronenborn A.M.;
                                                                                                                                                                           ..
0
                                  Complete proteome; Repeat
                                                                                                                                   Score 36; DB 1; Length 1498; Pred. No. 27;
                                                                                                                                                                           Indels
                                                                                   675 682 ATP (POTENTIAL).
1498 AA, 168968 MW; FF42037A335A9649
                                                                                                                                                                                                                                                                                                                                      2717 AA.
                                                                                                                                                                           2; Mismatches
 Pfam; PFULSOU; FLEX, 2.
PROSITE; PSS091; PTSK; 2.
Hypothetical protein; ATP-binding; Cc
DOMAIN 655 857
FTSK 1.
                                                                                                                                                                                                                                                                                                                                        PRT;
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-!- SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=90169514; PubMed=2106471;
Pfam; PF01580; FtsK_SpoIIIE; 2.
                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 2087-2142
                                                                                                                                           69.2%;
                                                                                                                            Query Match
Best Local Similarity 60.0.
                                                                                                                                                                                                                                                  1276 EQKIPMGMSY 1285
                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                  1188
                                                                                                                                                                                                                1 EEVVPXGMSY 10
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                                                                    DOMAIN
NP BIND
SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94188926; PubMed=8140616;
Sandal N.N., Marcker K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91129256; Pubmed=1825178;
MEDLINE=91129256; Pubmed=1825178;
Metter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recognition elements of cys-14, the structural gene for sulfate permease II in Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                     ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurospora crassa.
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                               67.3%; Score 35; DB 1; Length 2717;
66.7%; Pred. No. 80;
live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                  2127 2135
2717 AA; 297217 MW; D45D3CA951FEA561 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 30:1780-1787(1991).
                                              EMBL; X51415; CAA35798.1; -. PIR; A34203; A34203. PDB; 3ZNF; 15-JAN-92. PDB; 4ZNF; 15-JAN-92. PDB; 1BBO; 31-0CT-93. TRANSFAC; T00497; -. Genew; HGNC:4920; HIVEP1.
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Best Local Similarity 66...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2405 VVPAGLTYS 2413
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SEQUENCE
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CY14_NEUCR
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permease II and a putative human tumour suppressor.";
Trends Biochem. Sci. 19:191994).
Trends Biochem. Sci. 19:191994).
-- FUNCTION: UPTAKE OF SULFATE INTO THE CELL.
-- SUBCELLULAR LOCATION: Integral membrane protein.
-- INDUCTION: Highly expressed, but only in cells subject to sulfur limitation, and it is turned on by the positive-acting Cys.3 sulfur regulatory protein.
-- SUBCELLANEOUS: SULFATE PERMEASE II IS MAINLY FOUND IN MYCELLÀ.
-- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
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BEDLINE-21225279; PubMed=11326269;
Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S., Oshimura M.;
Shimura M.;
A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome.";
Nat. Genet. 28:19-20(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A10A HUMAN STANDARD; PRT; 1499 AA.

060312; 096914;
30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
(Potential phospholipid-transporting ATPase VA (EC 3.6.3.1) (ATFVA)
ATP10A OR ATP10C OR ATPVC OR KIAA0566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhíni; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
4FC604B6079BCB77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%; Score 34; DB 1; Length 788; 66.7%; Pred. No. 36; 1; Indels ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M59167; AAA33615.1; ALT_SEQ.
PIR; A37956; A37956.
InterPoor, IPR001902; Sulph_transpt.
Pfam; PR00916; Sulface transp; 1.
TIGRFAMS; TIGR00815; Sulface transp; 1.
TRANSMEM; TANSMEM TANSM
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POTENTIAL.
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les 6; Conservative
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SEQUENCE FROM N.A.
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Aloa HUMAN
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SEQUENCE FROM N.A.
  rissum=skin
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EMEL; AY029494; AAK3310011; JOINED.
EMEL; AY029495; AAK3310011; JOINED.
EMEL; AY029495; AAK3310011; JOINED.
EMEL; AY029499; AAK331001; JOINED.
EMEL; AY029499; AAK331001; JOINED.
EMEL; AY029499; AAK331001; JOINED.
EMEL; AY029500; AAK331001; JOINED.
EMEL; AY029501; AAK331001; JOINED.
EMEL; AY029502; AAK331001; JOINED.
EMEL; AY029503; AAK331001; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:13542; ATP10A.
MIM; 605855; -.
MIM; 105830; -.
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Best Local Similarity
Matches 8; Conserv
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DOMAIN 1
TRANSMEM 87
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12233
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       SOTION STATES ST
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**The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."

**DNA Res: 5:31-39(1998)

**C. - CATALIVITCA ACTIVITY: ATP + H(2)0 = ADP + phosphate.

**INDERLUMAR LOCATION: Integral membrane protein (By similarity).

**INDERLUMAR LOCATION: Integral membrane syndrome (AS)

**INDERLUMAR LOCATION: Integral membrane syndrome (AS)

**INDERLUMAR LOCATION: Integral membrane intellectual retardation, microcephaly, ataxia, frequent jerky limb movements and flapping of the arms and hands, hypotomia, hypotom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@leb-sib.ch).
                                                                                                                                                                                                                                                                                      MEDLINE=22388257; PubMed=12477932;
Atlastore R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlastore R.D., Collins P.S., Wagner L., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Butcow K.H., Schemer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marushima K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchenko L., Marushima K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Raha S.S., Longuellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Dosak S.A., McDwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Willalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
A Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butceffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length
Human and mouse cDNA sequences",
"Independence of M.S. Schoule S. (2002).
MEDLINE=21313119; PubMed=11353404;
Herzing L.B.K., Kim S.-J., Cook B.H. Jr., Ledbetter D.H.;
"The human aminophospholipid-transporting ATPase gene ATP10C maps
adjacent to UBE3A and exhibits similar imprinted expression.";
Am. J. Hum. Genet. 68:1501-1505(2001).
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0
                                                     Gaps
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                        Score 34; DB 1; Length 1499;
Pred. No. 70;
3; Mismatches 3; Indels
AA; 167687 MW; D4996A4D0635A68D CRC64;
                                                                                                                                                                                                        (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                       o,
                              65.4%;
                                                                                                                                                                               STANDARD;
                                                                                                                                                  RESULT 8
RIZO MYCPU
ID RIZO MYCPU
AC 0980V0;
DT 28-FEB-2003 (
DT 28-FEB-2003 (
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EWBL; AY029504; AAK33100.1; EWBL; AY029487; AAK33100.1; JOINED.
EWBL; AY029489; AAK33100.1; JOINED.
EWBL; AY029499; AAK33100.1; JOINED.
EWBL; AY029490; AAK33100.1; JOINED.
EWBL; AY029491; AAK33100.1; JOINED.
EWBL; AY029492; AAK33100.1; JOINED.

PHOSPHORYLATION (BY SIMILARITY). MAGNESIUM (BY SIMILARITY). MAGNESIUM (BY SIMILARITY).

-> R (IN REF. 4)

EXTRACELLULAR (POTENTIAL).
POTENTIAL.

CYTOPLASMIC (POTENTIAL).

POTENTIAL

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

POTENTIAL. EXTRACELLULAR (POTENTIAL) POTENTIAL.

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

CYTOPLASMIC (POTENTIAL)

POTENTIAL

CYTOPLASMIC (POTENTIAL).

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'1990 CAMJE STANDARD; PRT; 253 AA. P4599 CAMJE STANDARD; PRT; 253 AA. P4569; QSPNVO; 16-0CT-2001 [Rel. 40, Last sequence update) 16-0CT-2001 [Rel. 40, Last annotation update) Hypothetical protein Cj0990c.
                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 177:2396-2402(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 160-253 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                   60 EESIPDGASY 69
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=197;
                                                                             Venter J.C.;
                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                             STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
MEDLINE=21267165; PubMed=11353084;
Membaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                            of that subunit (By similarity).
-!- SIMILARITY: Belongs to the L20P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINE-VC-16, DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
50S ribosomal protein L20.
RPLT OR MYPU 2610.
Mycoplasma pulmonis.
Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2107;
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Hardrap, MP 00382; -; 1.

Hardrap, MP 00382; -; 1.

Hardrap, MP 00382; -; 1.

InterPro; IPR005812; Ribosomal_L20.

Refan, PR00453; Ribosomal_L20; 1.

PRINTS; PR00062; RIBOSOMÄLL20.

PRODOM; PR00937; RIBOSOMÄLL20.

TIGRFAMM; TIGR01032; rplT bact; 1.

PROSITE; PS00937; RIBOSOMÄL L20; 1.

Ribosomal protein; rRNA-binding; Complete proteome.

SEQUENCE 116 AA; 13565 MW; CS9C748901B18F14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.5%; Score 33; DB 1; Length 116; 77.8%; Pred. No. 8.1;
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Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL445563; CAC13434.1; -. PIR; E90544; E90544.
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                        SEQUENCE FROM N.A.
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ID YJ49_ARCFU
AC O28330;
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Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., MoNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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MEDLINE=20150912; PubMed=10688204;
Parkhil J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervarials sequences.";
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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MEDLINE=95247673; PubMed=7730270;
Hani E.K., Chan V.L.;
"Expression and characterization of Campylobacter jejuni benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000968; AAB89307.1; -.
PIR, D5943; D69433.
HYPOthetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 161 POTENTIAL.
165 AA; 17588 MW; BBC17054810ADBF8 CRC64;
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Matches
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RE SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

REAL STRAIN-657BL/6J; TISSUE-Embryonic head;

REAL STRAIN-657BL/6J; TISSUE-Embryonic head;

REAL STRAIN-8105660; PubMed=1117851;

REAL STRAIN-8105660; PubMed=1117851;

REAL STRAIN-810560; PubMed=1117851;

REAL STRAIN-810560; PubMed=1117851;

REAL STRAIN-810560; PubMed=1117851;

REAL STRAIN-810560; REAL STRAIN-810560; Rearward T.,

REAR STRAIN-810560; 
the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                Similarity 55.6%; Pred. No. 18; S. Conservative 2; Mismatches 2; Indels
                                                                                                                                                                           EMBL; AL139076; CAB73246.1; -.
EMBL; Z36940; CAA85392.1; -.
PIR; C81374; C81374.
PIR; 1,40758; L40758.
PYPothetical protein; Complete proteome.
SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTX3 MOUSE STANDARD; PRT; 280 AA. Q9D387; Q9CXQ4; 28-FEB-2003 [Rel. 41, Last sequence update) 10-OCT-2003 [Rel. 42, Last annotation update) Procein C20orf103 homolog precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 DIFPSGMSY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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CTX3 MOUSE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=09D387-2; Sequence=VSP 003820;
CAUTION: Ref.1 sequence differs from that shown due to frameshifts
in positions 174 and 239.
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E., Jones S.J.M., Marra M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-I. SUBCELLULAR LOCATION: Type I membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (BC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSP Synthase)
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53 N-LINKED (GLCKAC. . . ) (POTENTIAL).
102 N-LINKED (GLCKAC. . . ) (POTENTIAL).
113 M-MISSING (IN 180 FORM 2).
114 M-MISSING (IN 180 FORM 2).
125 E -> V (IN REF. 1; BAB31124).
126 P -> A (IN REF. 1; BAB31124).
127 N-LINKED (GRCKAC. . ) (POTENTIAL).
128 P -> A (IN REF. 1; BAB31124).
139 P -> A (IN REF. 1; BAB31124).
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Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 1; Length 280;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AK014127, BAB29169.1, -.
EMBL, AK018222, BAB31124.1, ALT_FRAME.
EMBL, BC004791, AAH04791.1, -.
MGI, MGI:1920368, 3110005N03Rik.
MGD, MGI:1923411, 6330527006Rik.
Transmembrane, Signal, Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9D387-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 2
238 2
280 AA;
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Q9KRB0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=1;
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AROA, VIBCH
ID AROA, VIBCH
ID 28-FEB
DT 28-FEB
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[2]
SEQUENCE FROM N.A.
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REQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-EI TO'N KIGSON (1)

RA MEDLINE-204068313; PubMed=10952301;

RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

RA Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

RA Gill S.R., Nelson K.B., Relian H., Richardson D.,

RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,

RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

RA Fraser C.M.;

Raser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions at long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                             Nature 406:477-483(2000).
-1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.
-1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
110-CT-2003 (Rel. 42, Last annotation update)
Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
CDC37 OR SPBC9B6.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGERAMS; TIGRO1356, arch, 1.
PROSITE; PSO0104; EPSP_SYNTHABE 1; 1.
PROSITE; PSO0164; EPSP_SYNTHABE 2; 1.
Aromatic amino acid biosynthesis; Transferase; Complete proteome.
SEQUENCE 426 AA; 46101 MW; 38852D6483BPEIC3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBUNIT: Monomer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-1- SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 31;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR, VC.732; -...
HAMAP, ME_00210; -; 1.
InterPro; IPR001986; EPSP Synth.
InterPro; IPR001986; EPSP Synth.
Pfam; PF00275; EPSP Synthäse; 1.
ProDon; PD001867; EPSP Synthäse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004251; AAF94882.1; -.
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NCBI_TaxID=4896;
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094740;
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CC37 SCHPO
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DT 28-FEB
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DE HSPDO
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WEDLINE=21848401; PubMed=11859360;
WEDLINE=21848401; PubMed=11859360;
WEDLINE=21848401; PubMed=11859360;
WEDLINE=21848401; PubMed=11859360;
WEDLINE=21848401; PubMed=11859360;
WEDLINE=21848401; PubMed=11859560;
WEDLINE S., Garilliam D., Elayis P., Feltwell T., Fraser A., Brooks K., Connon R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Gobbe A., Hamin N., Harris D., Hidalgo J., Hodgeon G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Monosy P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Ablor K., Rutter S., Saunders R., Starps K., Sharp S., Sketton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor K. G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Heltjans I., Vanstreels B., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Furchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Shamermann W., Wedler H., Wambutt R., Purnelle B., Caffmermann W., Wedler H., Wambutt R., Purnelle B., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Roreno S., Allows S., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shaperveki G.V., Usesry D., Barrell B.G., Nurse P., Nature 415:871-880(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
MEDLINE=2274545; PubMed=12861001;
Tatebe H., Shiozaki K.,
Tatebe H., Shiozaki K.,
Idencification of cdc37 as a novel regulator of the stress-responsive mitogen-activated protein kinase.";
Mol Cell. Biol. 23:513-5142(2008)
Mol Cell. Biol. 23:513-5142(2008)
Interaction of the Happo complex, resulting in stabilization and promotion of their activity.
-: SUBCELLULAR LOCATION: Nuclear, and cytoplasmic. When in the nucleus associated with chromatin.
-: SIMILARITY: Belongs to the CDC37 family.
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GeneDB SPombe; SPBC9B6.10; -.

InterPro; IPR04918; Cdc37.

Pfam; PF03234; Cdc37; Cclaperone; Cell dision; Cell cycle; Nuclear protein.

SRQUENCE 466 AA; 52554 MW; 647238B34CABB3C5 CRC64;
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Nuclear protein; Polymorphism.
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146
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01-JAN-1988 ()
01-OCT-1994 ()
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P08696;
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Matches
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  REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932;
A Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
A Stapleron M.S., Soarea M.B., Danaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Rosak S.A., McEwan P.J., McZernan R.J., Malek J.A., Gunarane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Nadan A., Rodrigues S., Sanchez A.,
A Miting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,
B Bakesley R.W. Touchman J.W. Green E.D., Dickson M.C.,
B Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
B Generation and initial analysis of more than 15,000 full-length
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MEDI-INE-99214318; PubMed=10196275;
Baruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins ICP22 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after infection.";
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE-20175430; PubMed=10708517;
MEDLINE-20175430; PubMed=10708517;
Sirit J.G., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Verk K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                                                                                          Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
GSR2 HUMAN STANDARD; PRT; 478 AA.
Q9NZM5; Q9BTC6; Q9HAX6; QNPP1; Q9NPR4; Q9UFI2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2003 (Rel. 40, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 12-478 FROM N.A.
Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virol. 73:3810-3817(1999).
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                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                          MEDLINE-89939249; PubMed=2460717;

MEDLINE-89939249; PubMed=2460717;

Garnier T. Cole S.T.;

"Studies of Uniducible promoters from Clostridium perfringens in vivo and in vitro.";

vivo and in vitro.";

-1- FUNCTION: MAY FUNCTION AS AN IONOPHORE.

-1- INDUCTION: By UV irradiation.
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890 AA; 96699 MW; F4E5E8971C31C6C6 CRC64;
perfringens and molecular genetic analysis of the bacteriocin-encoding gene."; J. Bacteriol. 168:1189-1196(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M14481; AAA98248.1; -.
EMBL; M32882; AAA98249.1; -.
PIR, A30481; A30481.
InterPro; IRR00034; Peptidase_M14.
InterPro; IRR00346; SH3 bac.
Fram; PR00246; Zn carbOpept; 1.
SMART; SMO0297; SH3b; 3.
AARIBIOLIC; Bacteriocin; Plasmid.
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Search completed: June 3, 2004, 11:49:53 Job time : 5.86667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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52
1 EEVVPXGMSYS 11
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Q7Z6R0 Q9BH83 Q9BHA5 Q8I5S7 Q01487	Q8PMI6 Q8PAT2 Q9PDM6 Q14122 Q12479	Q971S2 Q28342 Q96MU1 Q92MD6 Q8IYM3	098BPS 09PQD2 07UWU7 09URR4 08G4IS 08XT05 08XT05	Q8TX62 Q8PPPS Q8VUA8 Q8KTQ4 Q8KES6 Q7SY67
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) F-	01-MAR-2003	(TrEMBLrel.		Created)	≘		
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г	01-JUN-2003	(Tremelr	el. 24,	Last ar	motatio	Last annotation update)	
D23	Multidrug efflux transporter.	flux tran	nsporter				
z	TLL1618.						
က	Synechococcu	ıs elonga	tus (The	гтовупе	schococc	Synechococcus elongatus (Thermosynechococcus elongatus).	
ຍ	Bacteria; Cy	anobacte	ria; Chz	2000000	les; Sy	mechococcus.	
×	NCBI TaxID=3	12046;				NCBI TaxID=32046;	
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ρı	SEQUENCE FROM N.A.	M N.A.					
Ų	STRAIN-BP-1;						
×	MEDLINE=22225144; PubMed=12240834;	5144; Pul	bMed=122	40834;			
4	Nakamura Y.,	Kaneko	T., Sato	S., I	euchi M	0	S.,
4	Watanabe A.,	Iriguch	1 M., Ka	washime	1 K., Ki	imura T., Kishida Y.,	
4	Kiyokawa C.,	Kohara	M., Mate	umoto N	1., Mats	suno A., Nakazaki N.,	
4	Shimpo S., S	ugimoto 1	M., Take	uchi c.	, Yamad	la M., Tabata S.;	
H	"Complete ge	genome structure of	ucture c	if the t	hermoph	the thermophilic cyanobacterium	
H	Thermosynechococcus	occcus (elongatus BP-1.";				
ij	DNA Res. 9:123-130(2002).	.23-130 (2)	002).				
굕	EMBL; AP005374; BAC09170.1;	174; BACO	9170.1;	÷			
æ	GO; GO: 00160	21; C:in	C:integral to membrane;	o membr		IEA.	
ŭ	GO; GO: 00052	15; F:tr	ansporte	ir activ		IEA.	
œ	GO; GO: 0006810; P:transport; IEA.	110; P:tra	ansport;	IEA.			
껉	InterPro; IP	IPR001036; Acrflvin_res.	Acrflvi	n rea.			
œ	InterPro; IP	IPR004764; HAEL.	HAE1.	ı			
œ	Pfam; PF0087	13; ACR t:	ran; 1.				
œ	PRINTS; PR00702; ACRIFLAVINRP	702; ACR	IFLAVINE	<u>ب</u> ب <u>ہ</u>			
œ	TIGREAMS; TIGR00915;	GR00915;	2A0602;	1,			
×	Complete pro	proteome.					
Q	٠.	1044 AA;	113205 MW;		E9C13F0	00E9C13F0F636D2F CRC64;	
ğ	Query Match		75.08;	Score 39;		DB 16; Length 1044;	
Be	Best Local Simi	larity	63.68;	Pred. No.	No. 28;		
Σ	Matches 7;	7; Conservative	tive	2; Mie	Mismatches	2; Indels 0;	Gaps

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Pfam; PF01546; Peptidase M20; 1.
Hydrolase; Complete proteome.
SEQUENCE 387 AA; 41180 MW; 131BPF8E64306829 CRC64;
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NCBI_TaxID=4896;
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STRAIN=MAPP303099;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; Makanora Y., Sato S., Asamizu E., Kato T., Sasamoto S., Kaneko T., Nakanua Y., Sato S., Asamizu E., Kimura T., Kindida Y., Kilyokawa C., Kohara M., Matsumoto M., Matsumo A., Kishida Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Dinnes S., Sugimoto M., Tomoplate genome structure of the nitrogen-fixing symbiotic bacterium Mesophizobium loti: ", Makanora M. Makanora
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22608415; PubMed=12721630; Ivanova N., Candelon B., Rapatva N., Sorokin A., Anderson I., Galleron N., Candelon B., Rapatval V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N.; Grechkin S. D., Grechkin S. D., Bacillus anthracis."; Bacillus anthracis."; Mature 423:87-91(2003).
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                                                                                                                                            Q815A7 PRELIMINARY, PRT, 344 AA.
Q815A7,
Q815A7,
Q1-JUN-2003 (TrEMBLrel. 24, Created)
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter substrate-binding protein.
BEC5252
Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacilluse.
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GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR002933; Peptidase M20.
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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InterPro; IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROXAR LIPOPROTEIN; 1.
Complete proteome 344 AA; 38539 MW; C5526BACB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium loti (Mesorhizobium loti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                            |||:| |: ||
843 EEVLPNGIGYS 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||: | |:||
152 EEIAPLGLSY 161
      1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hippurate hydrolase.
MLR3583.
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q98FX1
Q98FX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
                                                                                                         RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical proclain.
Cenarchaeum symbiosum.
Archaea, Crenarchaeota, Thermoprotei; Cenarchaeales, Cenarchaeaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
STRAIN=972h-;
Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
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Schleper C., DeLong B.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
Score 38; DB 16; Length 387;
Pred. No. 15;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. _ _ _ A7780707030F9355 CRC64; SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Probable sulfate permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; I
Pred. No. 1.7e+02;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
Interpro; IPR000515; BPD_transp.
Interpro; IPR001680; WD40.
SMART; SM00320; WD40; 2.
                                                                                                                                                                                                                                                                                     PRT; 3472 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.1%;
54.5%;
        73.1%;
60.0%;
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Best Local Similarity 54....
Best Local 6; Conservative
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Gaps

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MEDLINE=22354683; PubMed=12466851;
MEDLINE=22354683; PubMed=12466851;
The FANTON Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 11; Length 484;
Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 11; Length 471;
Pred. No. 51;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OL-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
1-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to glidma tumor suppressor candidate region gene 2.
GLTSCR2 OR AW536411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UMR-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene 2
                                                                                                                                 Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025810; AA4125810.1; -.
MGD; MGI:2124441; Gltscr2.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUES-Salivary gland;
Strausberg N.A.
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC01/637; AAH17637.1; -.
MGD; MGI:2154441; Gliecr2.
SEQUENCE 484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
                                                                                                                                                                                                                                                                                                      NON TER 1 1 SEQUENCE 471 AA, 54506 MW, E0DA685C374A9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 EVIPAGASYN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 EVIPAGASYN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                             SEQUENCE FROM N.A.
              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8BTX4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAR REPRESENTATION OF THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
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"The complete ganomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
EMBL; APO0417; BAC44062.1;
InterPro; IPR009985; ConA.like.
InterPro; IPR007326; Lipoprotein.
Pfam; PF04200; Lipoprotein.17; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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ORST126

ORST126.

OL-JUN-2002 (TEMBLrel. 21, Created)

OL-JUN-2002 (TEMBLrel. 21, Last sequence update)

OL-OCT-2003 (TEMBLrel. 25, Last annotation update)

Hypothetical protein (Fragment).

GLISCR2.

Hymothetical (Mouse).

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; ALI32779; CABG0015.1; -.

R GeneDB SPOWDe; 39166.05c; -.

GO; GO: 0016020; C: membrane; IEA.

GO; GO: 0008271; F: sulfate porter activity; IEA.

R GO; GO: 0008271; F: sulfate transport; IEA.

R GO; GO: 0008275; P: sulfate transport; IEA.

R InterPro; IPR001902; Sulph_transpt.

R Pfam; PF01740; STAS; 1.

R Pfam; PF01740; STAS; 1.

R Pfam; PF01740; STAS; 1.

R Pfam; PF01718; SULP; 1.

R Pfam; PF01718; Sulfate_transp; 1.

R PROSITE; PS50801; STAS; 1.

R PROSITE; PS50801; STAS; 1.

R PROSITE; PS50801; STAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 3; Length 840;
Pred. No. 59;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1123 AA; 123636 MW; A4D707330E3DB4AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MYPE 2560 paralog, 57%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22354719; PubMed=12466555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.2%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            658 EYVPMGLSYS 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 VVPQGMSYA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=HF-2;
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SEQUENCE 1123 A
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QBEWD4; Q8EWD4

RESULT 6 QBEWD4

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Gaps

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Q889X7
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Q889X7
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C2534603; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration of search consortium,
The FANTOM Consortium,
The RIKEN Genome Exploration of the mouse transcriptome based on functional annotation of 60,770 full.length cDNAs.";
Nature 420.563-573 (2002).
BMBL: AK077341; BAC36760.1;
SEMEL; AK077341; Glescr2.
SEQUENCE 484 AA; 55792 MW; EB67949BCBE92D44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=V683 / ATCC 700802;
MEDLINE=22550857; PubMed=12663927;
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettedin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamarthevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Bacteria, Firmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
NCBL_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
GITSCR2.
Mus musculus (Mouse).
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus.
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                                                                                                                                                                                                                                                     69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 53; 2; Indels tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBEX35;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene 2
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL, AKO89461; BAC40367.1; -.
MGD; MGI:2154441; Gltscr2.
SEQUENCE 484 AA; 55806 MW; B3056425B5ECAD8 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 559 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pheromone binding protein, putative EF0063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       2 EVVPXGMSYS 11
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288K3
AC Q88K3
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DE Simil.
DE Simil.
DE Simil.
DE SIMIL
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RA NAMM
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0839T9
0839T4
AC 0839T
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JC
DE Phero
GN BRICH
OC BRCTE
OC BRCTE
OC BRCTE
OC RATE
RR SEQUE
RR SERUE
RR SERU
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PREQUENCE FROW. W.T.

BY SEQUENCE FROW. W.T.

BY STRAIN=DG3000;

BY BY JOACRAT V. Khouri H., Fedorova N., Tran B., Russell D., R. Buell R., Joacrat V., Van Aken S., Feldblyum T., Gwinn M. Dodson R., DeBoy R., Durkin A., Kolomay J., Madupu R., Daugherty S., Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T., R. Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T., R. Mite O., Fraser C., Collmer A., Selengut J., Nelson W., Davidsen T., R. Davidsen C., Collmer A., Selengut J., Nelson W., Davidsen T., R. Davidsen C., Collmer A., Selengut J., Nelson W., Davidsen T., R. Davidsen C., Collmer M. D., Selengut J., Nelson W., Davidsen T., R. D., Colosofoso, Percangal C. R. D., Colosofoso, Percangal C. R. D., Colosofoso, Percangal C. R. D., Colosofoso, Percangarian, IEA.

DR GJ, GO:0003899; F:DNA-directed RNA polymerase activity; IEA.

DR GJ, GO:0003899; F:DNA-directed RNA polymerase activity; IEA.

DR HIGFPO: IPR007089; RNA pol Rpbl J.

DR InterPro: IPR007089; RNA pol Rpbl J.

DR Ffam; PF04999; RNA pol Rpbl J.; I.

RM DNA-directed RNA pol Rpbl J.; I.

RM DNA-directed RNA pol Rpbl J.; I.

BR Pfam; PF04999; RNA pol Rpbl J.; I.

RM DNA-directed RNA polymerase; Complete proteome.
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TROLE of mobile DNA in the evolution of vancomycin-resistant
Thereoccus facealis.";
Science 299-2071-2074[2003].
Thereoccus Frontal AAO79943.1;
This Frontal F
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DNA-directed RNA polymerase, beta' subunit.
RPOC OR PSPTO0620.
PSeudomonas syringae (pv. tomato).
Bacteria; Proteobacteria, Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI TaxID=323;
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Best Local Similarity 66.79,
Best Local Similarity 66.79,
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581 QVVPAGLSY 589
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RESULT 15
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                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
11-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypochetical procesin precursor.
Lycopersicon esculentum (Tomato).
Eukaryora, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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Ancap G., Lariner F.W., Lamerdin D., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
                                                                                                                                                                                                                                                                                                                                                                                        (1)

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=VF36, TISSUE=Pistil;

XX MEDLINE=95375233, PubMed=7647301,

RA Miligan S.B., Gasser C.S.;

RI Mature and regulation of pistil-expressed genes in tomato.";

RI Plant Mol. Biol. 28 691-711 (1995).

BRHS, U20592; AA880497.1; -.

DR EMBL; U20592; AA880497.1; -.

DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.

DR GO; MOIO 1 PRO0216; Kunitz_legume.

PROMO952; Kunitz_legume.

DR PRINTS, PRO0291; Kunitz_legume.

DR SMART; SMO0492; STI, 1.

DR SMART; SMO0492; STI, 1.

DR PROSTTE; PSGO283; SOTSEAN KUNITZ; 1.

RHYDOTHETICAL DETOLEIN; SIGNAI.

ATGNAL.

TRAIL 10000991; CUNINOWN.

TRAIL 10000991; CUNINOWN.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipid and glycerol acyltransferase (From 'motifs_6.msf').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 67.3%; Score 35; DB 10; Length 225; Best Local Similarity 54.5%; Pred. No. 37; Matches 6; Conservative 3; Mismatches 2; Indels
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Nature 424:1042-1047(2003).
EMBL: BXS72099 CAEZISG7.1; -.
ACYLransferase; Transferase; Complete proteome.
SEQUENCE 245 AA; 26907 MW; 106F7C4CBE2C6427 CRC64;
                                                                      225 AA.
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                                                                      PRT;
                                                                PRELIMINARY;
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                                                             Q40129
Q40129;
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Q7V6Q4;
RESULT 13
Q40129
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67.3%; Score 35; DB 16; Length 245;

Query Match

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                          Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
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                          Indels
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Submitted (OCT-1996) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Transferase.
SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RIOD12.10 protein.
                                                                                                                                                                                                                                 425 AA.
  Pred. No. 41;
2; Mismatches
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Job time: 29.8667 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology.";
Science 282:2012-2018(1998).
EMBL; 281109; CAB03241.1; --
PIK; T241111; T241111.
60.08;
  Best Local Similarity 60.0
Matches 6; Conservative
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les 5, Conservative
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                                                                                                  179 QVVPVGLGYS 188
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                                                                         2 EVVPXGMSYS 11
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SEQUENCE FROM N.A.
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Run on:

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Abb80554 Hepatitis
Abb80552 Hepatitis
Abb80552 Hepatitis
Abb80545 Hepatitis
Abb80540 Hepatitis
Abb80543 Hepatitis
Abb80543 Hepatitis
Abb80547 Hepatitis
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Abg03621 Novel hum
Abg08546 Hepatitis
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    Misc-difference
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                                                                          3, 2004, 11:31:01 ; Search time 45.9333 Seconds (without alignments) 67.664 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                             1586107 segs, 282547505 residues
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1 EEVVPXGMSYS 11
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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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Best Local Similarity
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ive 0; Mismatches
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1 EEVVPXGMSYS 11
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EEVVPXGMSYS 11

RESULT

DB 5; 0.002;

Score 50; Pred. No.

96.2%; S

Query Match Best Local Similarity

1BB80566 ID ABB80566 ABB80566;

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                 standard, peptide, 11 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2001; 2001WO-US023169
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Best Local Similarity 100.
                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
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Modified-site
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                                                                                                                                                                                             Synthetic
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Sequence 11 AA;
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                                                               Novel peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "(8,8)allothreonyl carbonyl residue forming a keto -amide linkage with residue 7"
                                                                                                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47.
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 11
/note= "C-terminal amide"
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                                                                                                                   Lim-Wilby M, Levy OE, Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                          ABB80567 standard; peptide; 11 AA.
                                                                                                                                                                                           Claim 17; Page 65; 69pp; English.
                                                                               21-JUL-2000; 2000US-0220101P.
                                                              19-JUL-2001; 2001WO-US023169
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Matches 11; Conservative
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                                                                                                  (CORV-) CORVAS INT INC
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Modified-site
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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with RTO processe. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treat disorders associated with hepatitis C virus
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                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels
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                                                             Lim-Wilby M, Levy OE, Brunck TK;
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Best Local Similarity 100.
Matches 11; Conservative
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(CORV-) CORVAS INT INC.
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
           ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
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                                                              65; 69pp; English.
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Best Local Similarity 100.
Matches 11; Conservative
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                                                              Claim 17; Page
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ABB80526
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Claim 17; Page 64; 69pp; English.

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     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.
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                                                                                                                                                            Local Similarity 100.
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DB 5; Length 11; 0.002; indels

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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
                  ABB80561 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                         note= "Alpha-propynyl-glycinyl-carbonyl residue forming a keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                            Gaps
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                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48.
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'^. 0.002;
0; Indels
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       96.2%; Score 50; DB 100.0%; Pred. No. 0.0 ive 0; Mismatches
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/note= "C-terminal amide"
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                                                                                                                     ABB80568 standard; peptide; 11 AA.
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                              11; Conservative
                                                1 EEVVPXGMSYS 11
                                                                 EEVVPXGMSYS 11
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        Query Match
Best Local Similarity
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Modified-site
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Best Local Si
Matches 11
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                                                                                                                                                                                                           /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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88.5%; Score 46; DB 5;
Best Local Similarity 90.9%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 1
                                                                                                                                                                                    'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                      note= "Oxymethionine"
                                                                                                                               Location/Qualifiers
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EEVVPXGMSYS 11

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note= "Norvalyl carbonyl forming keto-amide linkage with

residue 7"

/note= "C-terminal amide" note= "D-form residue"

note= "N-terminal acetyl"

Location/Qualifiers

(first entry)

08-OCT-2002

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
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                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
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                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 64; 69pp; English.
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nes 10; Conservative
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Levy OE,

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                                                      'note= "Norvalyl carbonyl forming keto-amide linkage with esidue 7"
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Pred. No. 0.013;
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                                'note= "N-terminal acetyl"
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Best Local Similarity 90.9%;
Matches 10; Conservative
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                                                                                                         Misc-difference
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Score 46; DB 5; Length 11; Pred. No. 0.013; 0; Mismatches 1; Indels

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(first entry)

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoandle peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                      /note= "C-terminal amide"
                                          /note= "D-form residue"
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residue 7"
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Brunck TK;

Gaps ö Query Match 88.5%; Score 46; DB 5; Length 11; Best Local Similarity 90.9%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 1; Indels

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Search completed: June 3, 2004, 11:48:23 Job time: 45.9333 secs

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Sequence 4, Application US/09408020 Patent No. 6632937 GENERAL INFORMATION:
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54.5%;
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1. /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

3. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/2/iaa/6E_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

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5. /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-134-000C-3738
US-09-228-986-73
US-09-340-236-2902
US-09-360-352-7885
US-09-760-946-2
US-09-670-946-2
US-08-637-759B-236
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Sequence 7885, Application US/09328352
Patent No. 656296
GENERAL INFORMATION.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE REPERENCE: GET099-0394
FILE REPERENCE: GET099-0394
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
ENGINE SEQ ID NOS: 8252
ENGINE 1407
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Sequence 2, Application US/09760946

Patent No. 6608027

GENERAL INFORMATION:

APPLICANT: Tantrinos, Youla S.

APPLICANT: Gameron, Dale R.

APPLICANT: Galto, Else

APPLICANT: Halmos Teddy

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APPLICANT: Application NUMBER: US 09/542,675

PRIOR FILING DATE: 2001-08-23

PRIOR FILING DATE: 1999-04-06

NUMBER OF SEQ ID NOS: 5

SSOFTARE: PatentIn version 3.1

SSOFTARE: PatentIn version 3.1

LENGTH: 12
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Best Local Similarity 45.5%; Pred. No. 1.7;
Matches 5; Conservative 4; Mismatches 2; Indels
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Pred. No. 2.5e+02;
2; Mismatches 1
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                                                                                                                                                                                                                                                                                                              ) ORGANISM: Acinetobacter baumannii
US-09-328-352-7885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EEVVPXGMSYS 11
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596 EVVPEGLSF 604
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Patent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/540,236
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2902
LENGTH: 1191
                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-09-228-986-73
US-09-228-986-73
Sequence 73, Application US/09228986
Farent No. 6359198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION NUMBER: US/09/228,986
CURRENT PILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 73
TENGTH: 947
                 ; FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (327)..(328)
COTHER INFORMATION: Amino acids 327 & 328 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-3738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 947;
                                                                                                                                                   Query Match 69.2%; Score 36; DB 4; Length 382; Best Local Similarity 66.7%; Pred. No. 22; Manatches 1; Indels Matches 1; Indels
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: M.catarrhalis
US-09-540-236-2902
                                                                                                                                                                                                                                                                              332 LIPEGMSYS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     686 VMPSGISYS 694
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783 EILPVGMAY 791
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US-09-540-236-2902
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US-09-328-352-7885
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CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBW C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: BPLICATION NUMBER: US/08/371,355A
FILING DATE: 10-DUN-1997
CLASSIFICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORVATION:
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REGISTRATION NUMBER: 31,284
RESTERENCE/DOCKET NUMBER: 31,284
REJERENCE/DOCKET NUMBER: 31,284
REJERENCE/DOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 236, Application US/08871355A

Patent No. 6015669
GENERAL INFORMATION:
TITLE OF INVENTION: I dentification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabet
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 3
Pred. No. 7.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                Score 33; DB Pred. No. 7.8;
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Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 60.0%;
Matches 6; Conservative
                                                   LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: sind:
COPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO.
US-08-637-759B-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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US-08-871-355A-236
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APPLICANT: Goudreau, Nathalie
APPLICANT: Halmos, Teddy
APPLICANT: Halmos, Teddy
APPLICANT: Lilias-Brunet, Montse
APPLICANT: Lilias-Brunet, Montse
TILE OF INVENTION: Macrocyclic Peptides Active Against the Hepatitis C Virus
FILE REFERENCE: 13/076-1-C1
CURRENT APPLICATION NUMBER: US/09/760,946
PRIOR APPLICATION NUMBER: US 09/542,675
PRIOR APPLICATION NUMBER: US 09/542,675
PRIOR PILING DATE: 2000-04-03
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 12
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OTHER INFORMATION: Tracer for NS3 protease assay

NAME/ENT (1)

OTHER INFORMATION: Asp at position 1 is biotinylated

NAME/ENT: MOD RES

LOCATION: (10)

OTHER INFORMATION: Tyr at position 10 is iodinated with I-125

US-09-760-946-3
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Pred. No. 1.7;
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Sequence 236 Application US/08637759B
Sequence 236 Application US/08637759B
Sequence 236 Application US/08637759B
SEQUENCE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE BATEAL
STREET: 2800 One Atlantic Center
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COMPTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 11-DEC-1995
CLASSIFICATION AT3:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 4335
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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NAME: Pader, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
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RESULT 14
US-09-357-952-66

US-09-357-952-66

Sequence 66, Application US/09357952

Patent No. 624804

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cal, Sul Xiong
APPLICANT: Cal, Ohn A.
TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole
TITLE OF INVENTION: Pluorescence Screening Assays for Caspases, Peptidases,
TITLE OF INVENTION: Cher Enzymes and the Use Thereof
FILE REFERENCE: 1735.0030001

FILE REFERENCE: 1039-07-21

CURRENT APPLICATION NUMBER: US/09/357,952

CURRENT FILING DATE: 1999-07-21

SARLIER APPLICATION NUMBER: US 60/093,642
                                                                                                                                                                                                                                    FACTOR NO. 5177197

PATENT NO. 5177197

PAPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;

PAPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;

PAPLICANT: CHRISTER, HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,

IENN; HELDIN, CARL-HENRIK

TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING

HUMAN TRANSFORMING GROWIT RACTOR-BETAL-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA;

PRILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
5177197.
FALCEL NO. 5177197
FACTOR NOTE: HELLMAN, ULF, MIYAZONO, KOHEL; CLAESSON-WELSH, TINA, HELDIN, CARL-HENRIN, ULF, MIYAZONO, KOHEL; CLAESSON-WELSH, TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING HUMAN TRANSPORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
FULLING APPLICATION DATA:
APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
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Pred. No. 3.9e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.5%; Score 33; DB 6; Length 410; 45.5%; Pred. No. 97; tive 3; Mismatches 3; Indels
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   <u>ب</u>
   3; Mismatches
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Best Local Similarity 45.5
Matches 5; Conservative
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Best Local Similarity 45.5
Matches 5; Conservative
5; Conservative
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52 KEICPGGMGYT 62
                                                                1 EEVVPXGMSYS 11
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      Matches
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5177197-51
; PATENT SANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
APPLICANT: CHRISTER, HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
; LENA; HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWITH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
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Pred. No. 7.8;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                  STKERI: 1401 MCCOUNTRY: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
FILING DATE:
CLASSIFICATION:
PRICASSIFICATION:
PRICASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION
   RESULT 10
US-09-201-945-236
Sequence 236, Application US/09201945
Sequence 236, Application US/09201945
Sequence 236, Application US/09201945
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
WUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
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Matches 6; Conservative
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or Fluorescent Reporter Molecules and
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APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Standy John F.W.
APPLICANT: Standy John A.
APPLICANT: Standy Han-Zhong
TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescence
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Therefore 1735.0290002
TITLE OF INVENTION: Use Therefore 123000.03-08
EARLIER FILING DATE: 1998-1-0-10
EARLIER FILING DATE: 1998-10-00
EARLIER FILING DATE: 1998-10-00
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SEQ ID NO 66
IBRACHER PLEATH NOT VET. 2.0
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                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
JS-09-357-952-66
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                                                                                                                                                                                                                                                                                                                                       Query Match 61.5%; Score 32; DB 3; Length 10; Best Local Similarity 50.0%; Pred. No. 2.3; Matches 5; Conservative 3; Mismatches 2; Indels
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50.0%; Pred. No. 2.3;
tive 3; Mismatches 2; Indels
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EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Search completed: June 3, 2004, 12:03:07 Job time: 11.8 secs 1 DDIVPCSMSY 10 q

1 EEVVPXGMSY 10

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Gaps ö

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-51
US-09-909-164-51
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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52
1 EEVVPXGMSYS 11
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Match Length
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Sequence:
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	16	17	18	19	20	21	23	23	24	52	56	27	28	53	30	31	32	33	34	35	36	37	38	99	40	41	42	4.3	44	4.5

ALIGNMENTS

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USEGUTT 18 SEQUENCE 5, Application US/09909164

SEQUENCE 5, Application US/09909164

SEQUENCE 5, Application US/09909164

SEQUENCE 5, Application No.

APPLICANT: COTATE INTERTACTIONAL

APPLICANT: Lim-wilby, Marguerita

APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TURENT FILING DATE: 2003-03-25

FILE REFERENCE: 100.12-5

FURENT APPLICATION NUMBER: 60/220, 101

PRIOR FILING DATE: 2000-07-21

SEQ ID NOS: 62

SOFTWARE: PARTICALION NUMBER: 60/220, 101

PRIOR FILING DATE: 2000-07-21

SEQ ID NOS: 62

SOFTWARE: PARTICALION NUMBER: 60/220, 101

PRIOR FILING DATE: 2000-07-21

SEQ ID NO S

SEQ ID NOS: 62

SOFTWARE: NETWING ALITICAL SEQUENCE

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (1) ... (1)

OTHER INFORMATION: ADETYLATION

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (1) ... (1)

OTHER INFORMATION: AMIDATION

OTHER INFORMATION: AMIDATION

OTHER INFORMATION: AMIDATION
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Length 11;

DB 12;

96.2%; Score 50;

Query Match

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US-09-909-164-10

US-09-909-164-10

US-09-909-164-10

Sequence 10, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN01190-US

FURENT FILING DATE: 2003-03-25

PRIOR FILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQUENCE: NOVEL PRIOR PR
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96.2%; Score 50; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                               TYPE: PRT
ORGANISM: artificial sequence
PEATURE:
OTHER INFORMATION: 11-mer synthesized according to example
PEATURE:
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LOCATION: (6)._(6)
OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: norvaline-(CO)
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (11)...(11)
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NAME/KEY: MOD RES
LOCATION: (1)\[-.(1)\]
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11\[-.(11)\]
OTHER INFORMATION: AMIDATION
FEATURE:
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OTHER INFORMATION: D-amino acid
US-09-909-164-9
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 11
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OTHER INFORMATION: AMIDATION
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Sequence 6, Application US/09909164

Sequence 6, Application VS.02002068702A1

Sequence 6, Application No. USZ0020068702A1

SEDELCANT: Lin-Whilby, Marguerita

APPLICANT: Lin-Whilby, Marguerita

APPLICANT: Lin-Whilby, Marguerita

APPLICANT: Levy, Odile B

APPLICANT: Lin-Whilby, Marguerita

APPLICANT: Lin-Whilby, Marguerita

STILE REPRENCE: INO1192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: 60/220,101

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 11
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEDATITIS C
FILE REPERBNCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
                                             Gaps
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ORGANISM: artificial sequence
PERATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
LOCATION: (6)..(6)
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       Pred. No. 0.0014; ; Mismatches 0; Indels
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NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
FEATURE:
               100.08;
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LOCATION: (11)...(11)

CTHER INFORMATION: AMIDATION

US-09-909-164-6
       Best Local Similarity 100.
Matches 11; Conservative
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Sequence 49, Application US/09909164
; Sequence 49, Application US/09909164
; Sequence 49, Application No. US2002068702A1
; GENERAL INFORMATION:
; APPLICANT: Corvas International, Inc.
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Lim-Wilby, Marguerita
; APPLICANT: Levy, Odile E
; APPLICANT: Levy, Odile E
; APPLICANT: Erence K
; TITLE OF INVENTION: NOVER PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; TITLE OF INVENTION NUMBER: US/09/909,164
; CURRENT APPLICATION NUMBER: 60/220,101
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PATENTIN VERSION 3.1
; SEQ ID NO 49
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                                                                                                                                                                                CHER INFORMATION: 11-mer synthesized according to example FEATURE:
NAME/KEY: MOD_RES
NAME/KEY: MOD_RES
NOTHER INFORMATION: (1). (1)
OTHER INFORMATION: ACETYLATION
NAME/KEY: MOD_RES
LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
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; LOCATION: (6)...(6)
; OTHER INFORMATION: norleucine-(CO)
US-09-909-164-49
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 11
TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAMEKEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: leucine-(CO)
US-09-909-164-48
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OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: AMIDATION
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Best Local Similarity 100.
Matches 11, Conservative
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Sequence 47, Application No. US20020068702A1

Publication No. US20020068702A1

Publication No. US20020068702A1

APPLICANT: Lim-Wilby, Marquerita

FILE REFERENCE: 1001.92-US

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 47

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Sequence 48, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
TILE APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: IN01192-US
CURRENT APPLICATION NUMBER: 2003-03-25
PRIOR PILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
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NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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                                                                                   Query Match 96.2%; Score 50; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels
        ; CTHER INFORMATION: D-amino acids JS-09-909-164-10
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ORGANISM: artificial sequence
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NAME/KEY: MOD RES
LOCATION: (11)...(11)
OCHER INFORMATION: AMIDATION
FEATURE:
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Best Local Similarity
Matches 11; Conserva
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US-09-909-164-48
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Sequence 52, Application US/09909164
Sequence 52, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
COTAS INTERIAL TETERACE
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
ITILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: 1N01192-US
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 5: 52
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100.0%; Pred. No. 0.0014;
iive 0; Mismatches 0.
                                                                                                                                                     NAME/KEY: MISC_PEATURE

LOCATION: (6)...(6)

CTHER INFORMATION: (8,8)-allothreonine-(CO)
US-09-909-164-51
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; OTHER INFORMATION: propynyl glycine-(CO)
US-09-909-164-52
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US-09-909-164-8
; Sequence 8, Application US/09909164
; Publication No. US20020068702A1
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NAME/KEY: MOD RES
LOCATION: (1) ..(1)
OTHER INFORMATION: ACETYLATION
OTHER INFORMATION: ACETYLATION
NAME/KEY: MOD RES
LOCATION: (11) ..(11)
OTHER INFORMATION: AMIDATION
             NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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                                                                  FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OCTHER INFORMATION: AMIDATION
FEATURE:
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserv
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Sequence 51, Application US/0909164

Publication No. US20020068702A1

GENERAL INPORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Error, Voile E
APPLICANT: Error, NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-00-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE Patentin version 3.1

SEQ ID NO 51

LENGTH: 11
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FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(1)
COCHIEN: NORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
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LOCATION: (6)...(6)

CHER INFORMATION: 2-amino-butyric acid-(CO)
US-09-909-164-50
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ORGANISM: artificial sequence
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Sequence 13, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION

APPLICANT: Corvas International, Inc.

APPLICANT: Lewy, Odile E

APPLICANT: Lewy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEBATITIS C

FILE REFERENCE: INJUNISATION NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTING DATE: 2000-07-21

MUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTING DATE: 2000-07-21

MUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTING DATE: 2000-07-21

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SOFTWARE: PATENTING DATE: 2000-07-21

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MUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTING DATE: 2000-07-21

MUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTING DATE: 2000-07-21

MUMBER OF SEQ ID NOS: 62
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Pred. No. 0.0091;
0; Mismatches 1; Indels
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Pred. No. 0.0091;
0; Mismatches 1; Indels
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)...(11)
LOCATION: AMIDATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
FEATURE:
LOCATION: (8)...(8)
OTHER INFORMATION: D-amino acid
US-09-909-164-12

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NAME/CRY: MOD RES
LOCATION: (1) .. (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KRY: MOD RES
LOCATION: (11)... (11)
OTHER INFORMATION: AMIDATION
FEATURE:
NAME/KRY: MISC FEATURE
LOCATION: (6)... (6)
OTHER INFORMATION: NOTVALING-(CO)
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Publication No. US20202068702A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFRENCE: IN01192-US
FILE REFRENCE: 1001192-US
FILE REFRENCE: 2003-03-25
PRIOR PLILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PLILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 11
TYPE: PRI
                                 APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: 1001192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENT OF SEQ ID NOS: 62
SOFTWARE: PATENT OF SEQ ID NOS: 62
IENGTH: 11
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Pred. No. 0.0091;
0; Mismatches 1; Indels
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LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FRATURE:
LOCATION: (6) ... (6)
OTHER INFORMATION: NOTVALINE-(CO)
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LOCATION: (1) (1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.9%;
Matches 10; Conservative
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86.5%; Score 45; DB 12; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.015;

Matches 10; Conservative 0; Mismatches 1; Indels
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (8)..(8)
CTHER INFORMATION: D-amino acid
US-09-909-164-11
NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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NOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
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        Sequence 7. Application US/09909164

| Sequence 7. Application US/09909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc.
| APPLICANT: Levy, Odile E
| APPLICANT
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Publication No. US20020068702A1

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Willy, Marguerita

APPLICANT: Lim-Willy, Marguerita

APPLICANT: Lerne E

APPLICANT: Lerne E

TILE REFERENCE: INO1192-18

CURRENT FILIS OF INVENTION: NUMBER: US/09/909,164

FILE REFERENCE: 100192-25

FILE REFERENCE: 2003-03-25

FILE REFERENCE: 2000-07-21

PRIOR PILING DATE: 2000-07-21

PRIOR PILING DATE: 2000-07-21

SEQ ID NO: 62

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OTHER INFORMATION: 11-mer synthesized according to example 1
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NAME/KEY: NOD RES
OCHION: (1) . (1)
OCHIER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6) . (6)
OTHER INFORMATION: norvaline-(CO)
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NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
FEATURE:
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; LOCATION: (11)...(11)

OTHER INFORMATION: AMIDATION

US-09-909-164-7
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                                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 EEVVPXGMSYS 11
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A;cross-references: EMBL:281109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
A;Experimental source: clone R10D12
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                                                                                                                                                                                                                                                                                                                     C.Species: Lycopersicon esculentum (tomato)
C,Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C,Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C,Accession: S5781
E,Milligan, S.B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
A,Fithe: Nature and regulation of pistil-expressed genes in tomato.
A,Reference number: S57808; MUID:95375233; PMID:7647301
A,Accession: S57810
A,Molecule type: mRNA
A,Residues: 1-225 <MIL>
A,Residues: 1-225 <MIL>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: $22293; I788 #sequence revision C;Richanore, C;I Traboni, C;Cortese, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein R10D12.10 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL:U20592; NID:9924625; PIDN:AAA80497.1; PID:9924626
C; Superfamily: plant Kunitz-type proteinase inhibitor
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Score 36; DB 2; Length 1498;
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2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.3%; Score 35; DB 2;
50.0%; Pred. No. 26;
rative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, October 1996 A;Reference number: 219842 A;Accession: T24111
                                                                                                                                                                                                                                                                                                               hypothetical protein precursor (clone TPP11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: 5
A,Introns: 23/3; 56/3; 113/3; 257/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%;
54.5%;
        69.2%;
ilarity 60.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 54.5.,
G, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                          1276 EQKIPMGMSY 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 ÉQIVÈGGLQY 344
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Best Local Similarity
' - - - - - - 5; Conserva
                                                                                                                     1 EEVVPXGMSY
                                   Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T24111
              Query Match
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C;Species Clostification acetobutylicum
C;Accession: B97355 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: B97355 #setcon, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, S;Nolling, J.; Benrett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
J. Racteriol. 183, 4823-4838, 2001
J. Reference number: Aspect Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: Asp6900; MUID:2135925; PMID:21359225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4

A42452

A42452

A12452

A12452

A12452

A12452

A12452

C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Accession: A42452

B;McCris, BA.M.; Fichardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992

A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA segregation ATPase, FtsK/SpoIIIE family, YUKA B. subtilis ortholog [imported] - Clos
                                                                                                                                                                                                                                                                A,Accession: Tanglar A, A, Accession: Tanglated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rolecule type: DNA
A,Residues: 1-877 <LYN>
A,Residues: 1-877 <LYN>
A,Residues: BMBL:AL031261, PIDN:CAA20298.1; GSPDB:GN00067; SPDB:SPBC3H7.02
A,Experimental source: strain 972h-; cosmid c3H7
C,Genetics:
A,Gene: SPDB:SPBC3H7.02
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A; Molecule type: DNA
A; Mesidues: 1-1498 «KUR»
A; Mesidues: 1-1498 «KUR»
A; Cross-references: GB: AE001437; PIDN: AAK81629.1; PID: g15026814; GSPDB: GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics: A; Gene: CAC3709
                                                                                                                        C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40413
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
submitted to the EMBL Data Library, August 1998
A;Reference number: 221926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-102 <MOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ore 37; DB 2; Length 877; ed. No. 22; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 2; Length 102;
Pred. No. 3.5;
3; Mismatches 1; Indels

    fission yeast (Schizosaccharomyces pombe)
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Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative

Accession: A42452

|||| |::|| 7 QVVPSGINYS 16

g

2 EVVPXGMSYS 11

Score 37; Pred. No.

71.2%; 77.8%;

Query Match 71.2 Best Local Similarity 77.8 Matches 7; Conservative

A; Map position: 2

148 VVPOGMSYA 156

g

3 VVPXGMSYS 11

Gaps

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A,Title: A DNA-binding protein containing two widely separated zinc finger motifs that z A,Reference number: A34203; MUID:90169514; PMID:2106471
A,Rocession: A34203
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: L-2717 (FRN)
A,Residues: L-2717 (FRN)
A,Residues: L-2717 (FRN)
A,Residues: BEBL: S51435, NID:938017; PIDN:CAA35798.1; PID:938018
A,Residues: BBL: 10, 1466-144, 1990
A,Title: A large protein containing zinc finger domains binds to related sequence elemen A,Reference number: A34779; NUID:90205817; PMID:2108316
A,Accession: A34779
A,Reteus: preliminary; nucleic acid sequence not shown
A,Rocession: A34779
A,Reteus: Brelintinary; nucleic acid sequence not shown
A,Rocession: A34779
A,Reteus: Brelintinary; nucleic acid sequence not shown
A,Roceuse: 801-1072, NV, 1074-1168, NY, 1170-1225, VV, 1227-1434, NV, 1436-1607, I', 1609-16
A,Cross-references: GBS:M32019
C,Superfamily: HIV-EP2 enhancer-binding protein
C,Keywords: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
C;Accession: H64491
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: DNA
A, Residues: 1-156 < DBH3
A, Residues: 1-156 < DBH3
A, Creatences: BMBL: X87331; NID: 91041652; PIDN: CAA60762.1; PID: 9829123
A, Creatences: BMBL: X87331; NID: 91041652; PIDN: CAA60762.1; PID: 9829123
B, de Haan, M.; Grivell, L.A.; Maarse, A.C.
B, Akeference number: 866877
A, Accession: 866879
A, Molecule type: DNA
A, Residues: 1-156 < DEM>A, Accession: 86879
A, Molecule type: DNA
A, Cross-references: BMBL: Z74920; NID: 91420109; PIDN: CAA99201.1; PID: 91420111; MIPS: YOR01
A, Experimental source: strain $288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein O2612; hypothetical protein YOL303.3
C;Species: Saccharomyces cerevisiae
C;Date: O8-Jul.1995 #sequence_revisiae
C;Accession: S54619; S66879
R;Ge Han, M.; Maarse, A.C.; Grivell, L.A.
R;Reference number: S54617
A;Reference number: S54617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.3%; Score 35; DB 2; Length 2717; 66.7%; Pred. No. 1.9e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.4%; Score 34;
illarity 66.7%; Pred. No. .
Conservative 1; Mismatcl
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C, Superfamily: hypothetical protein YOR013w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2405 VVPAGLTYS 2413
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nes 6; Conserva
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Matches
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H69491
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) Accession: H8-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000

) Accession: H8-Aug-2000

A; anonymous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 200

A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A; Accession: H82691

A; Accession: Preliminary

A; Cross-reference S; CB:AE003967; GB:AE003849; NID:g9106347; PIDN:AAF84162.1; GSPDB:GN001
                4,Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-Xeference number: IS8280, MUID:91187610; PMID:1901405
4,Accession: 822293
4,Status: nucleic acid sequence not shown
4,Modecule type: mRNA
4,Residues: 1-670 cMIT>
4,Cross-references: BMBL:X54250; NID:957519; PIDN:CAA38151.1; PID:957520
5,Modecule tha authors did not translate the codon for residue 1
5;Superfamily: HIV-BP2 enhancer-binding protein
5;Superfamily: HIV-BP2 enhancer-binding protein
5;Keywords: DNA binding; transcription regulation; zinc finger
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A:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Barloose, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H

38-Neto, E.; Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

Submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.E.; Laigr

Ando, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.

B. S. S. Nures, Markins, B.M.F.; Mateukuma, A.Y.; Manck, C.F.M.; Miraca, B.C.; Mayaki, C.Y.;

F. G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Sawasak, A.J. Tsuhako, M.H.; Vallada, H.; Van Silva, P.M.; Silva Jr., W.A.; da Silva, A.

A; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A; Contents: annotation
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NAlternate names: major histocompatibility complex enhancer-binding protein 1
2;Species: Homo sapiens (man)
2;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
2;Accession: A34203; A34779
3;Fan, C.M.; Maniatis, T.
3enes Dev. 4, 29-42, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     opoisomerase IV subunit XF1353 [imported] - Xylella fastidiosa (strain 9a5c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.3%; Score 35; DB 2; Length 670; Best Local Similarity 66.7%; Pred. No. 43; Matches 6; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 VVPAGLTYS 384
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Search completed: June 3, 2004, 12:00:00 Job time: 9 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein 1 - Campylobacter jejuni (fragment)
C:Speciaes Campylobacter jejuni
C:Speciaes Campylobacter jejuni
C:Speciaes Campylobacter jejuni
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C:Accession: 140758, 847317
R:Hani, E.K.; Chan, V.L.
R:Hani, E.K.; Chan, V.L.
A:Title: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd A:Reference number: 140758; MUID:95247673; PMID:7730270
                                                                                                                                                                     A; Status: preliminary, nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-22 < Kml. A; Residues: 1-22 < Kml. A; Residues: 1-22 < Kml. A; Cross-references: GB: AE000970; GB: AE000782; NID: G2689293; PIDN: AAB89318.1; PID: G264866 C; Superfamily: cell division inhibitor minD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Residues: 1-544 <GLA>
;Cross-references: GB:AE002133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001
;Experimental source: serovar 3; biovar 1
Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.X.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUD:98049343; PMID:9389475

A;Accession: H69491
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Pred. No. 14;
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A,Molecule type: DNA
A,Residues: 1-94 <RES>
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Best Local Similarity 70.0%;
Matches 7; Conservative
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26 DIFPSGMSY 34
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A;Genetic code: SGC3
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Status: preliminary
Molecule type: DNA
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C,Accession: E90544
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pull A;Reference number: A99512; MUID:21267165; PMID:11353084
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A;Status: preliminary
A;Molecule type: DNA
A;Redidues: 1-116 <KUR>
A;Cross-references: GB:AL445566; PID:g14089674; PIDN:CAC13434.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
508 ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
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0; Mismatches 2; Indels
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C,Superfamily: Escherichia coli ribosomal protein L20
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Best Local Similarity 77.8%;
Matches 7; Conservative
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P45489 campylobact
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074377 schizosacch
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Copyright (c) 1993 - 2004 Compugen Ltd
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## ALIGNMENTS

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Y11K_TYDVA
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Matches
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                                                                                                                                                                                                  OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
Pfam, PF02142; MGS; 1.
PRINTS, PR00099, CPSASE.
TIGRFAMS; TIGR01369; CPSASE11_1rg; 1.
PROSITE; PS00866; CPSASE_2; 2.
PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Repeat; Arginine biosynthesis; Complete proteome.
ATP-binding; Manganese; Complete Droteome.
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                                                                                                                                                                                                                                                                                                                                                                                   2 (BY SIMILARITY) SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 1; Length 1058; Pred. No. 7; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MW; ED7037AF77C1E339F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable sulfate permease C3H7.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117451 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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190 EIVPNGLNYS 199
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                                                                                                                                                                                                                                                                                                                  153
302
302
284
298
300
820
832
1058 AA;
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Best Local Similarity
Matches 6; Conserv
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074377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
SEQUENCE
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NP_BIND
METAL
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DOMAIN
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REPEAT
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SULH SCHPO
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Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
"The nucleotide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
infecting monocotyledonus plants.";
Virology 187:633-642(1992).
                                                                              -i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
Nature 415:871-880(2002).
-!- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.2%; Score 37; DB 1; Length 877; 77.8%; Pred. No. 9.4; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56995A8493371E43 CRC64;
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Viruses, ssDNA viruses, Geminiviridae, Mastrevirus.
NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y11K TYDVA STANDARD; FRT; 102 AA. P31619; 01-UUL-1993 (Rel. 26, Created) 01-UUL-1993 (Rel. 26, Last sequence update) 01-CTT-1993 (Rel. 27, Last annotation update) Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                       -! - SIMILARITY: Contains 1 STAS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Geneba Spombe; SPBC3H7.02; -...
InterPro; IPR0012645; STAS.
InterPro; IPR001902; Sulph_transpt.
Pfam; PP001740; STAS; 1.
Pfam; PP00916; Sulfate_transp; 1.
TIGREAMS; TIGR00815; Sulfate_transp; 1.
PROSITE; PS01130; SLC26A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL031261; CAA20298.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96373 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 VVPQGMSYA 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; T40413; T40413.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Glison R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                               Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                           69.2%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 1.6; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                             ll protein. -
102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypotherical protein CAC3709.
                                                                                                                                                                                                                                                                                                                                                                                                                                               1498 AA
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PIR; B97355; B97355.
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InterPro; IPR002543; FtsK_SpolliE.
                                                                                                                                                                       InterPro; IPR002621; Gemini mov. Pfam; PF01708; Gemini mov; I. Hypothetical protein. SEQUENCE 102 AA; 11178 MW; A
                                                                                                                                             EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE007866; AAK81629.1;
                                                                                                                                                                                                                                                                         Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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7 QVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                             2 EVVPXGMSYS 11
                                                                                                                                                                PIR; A42452; A42452.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLOAB
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1- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE 5'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMBENCHS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1. IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLUTAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MHC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES: IT MAY ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-binding protein 1) (HIV-EP1) (Major histocompatibility complex binding protein 1) (MBP-1) (Positive regulatory domain II binding factor 1) (PRDII-BF1).
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "High-resolution, three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Biochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IN T-CELL ACTIVATION.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- INDUCTION: By mitogen and phorbol ester.
-!- DOWAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIJUE=90169514; PubMed=2106471;
Pan C.M., Maniatis T.;
A DNA-binding protein containing two widely separated zinc finger
motifs that recognize the same DNA sequence.";
Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                         ö
Pfam; PF01580; FtsK SpoIIIE; 2.
PROSITE; PS50901; FTSK; 2.
Hypochetical protein; ATP-binding; Complete proteome; Repeat.
DOMAIN 655 857
FTSK 1.
DOMAIN 1001 1188
                                                                                                                                                                                                                                                                Score 36; DB 1; Length 1498; Pred. No. 27;
                                                                                                                                                                      675 682 ATP (POTENTIAL).
1498 AA; 168968 MW; FF42037A335A9649 CRC64;
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MEDLINE=91064333; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 2717 AA.
                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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-!- SIMILARITY: STRONG, TO HIVEP2.
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                                                                                                                                                                                                                                                                69.2%;
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Best Local Similarity 60.0-
Best Local Similarity
Conservative
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P15822;
                                                                                                                                       DOMAIN
NP BIND
SEQUENCE
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ZEP1_HUMAN
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               M MINI 1949-10; Tages 1. C: nucleus; TAS.

R GO; GO:0003671; F:DNA binding; TAS.

R InterPro; IPRO00096; zd. C2H2; B.

R PROSITE; PS000026; ZINC FINGER C2H2 1; 4.

R PROSITE; PS000028; ZINC FINGER C2H2 2; 4.

R PROSITE; PS000028; ZINC FINGER C2H2 2; 4.

R PROSITE; PS000028; ZINC FINGER C2H2 2; 4.

R PROSITE; PS000028; ZINC FINGER C2H2 1; 4.

R Nuclear protein; Repeat; 3D-structure.

ZN FING 406 428 C2H2-TYPE.

ZN FING 959 981 C2H2-TYPE.

T ZN FING 2087 2109 C2H2-TYPE.

T ZN FING 959 QS7 2109 C2H2-TYPE.

T ZN FING 959 PS1 C2H2-TYPE.
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Sandal N.N., Marcker K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
MEDLINE-91129256; PubMed=1825178;
Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recognition
"Nucleotide sequence, messenger RNA stability, and bla recognition
"Nucleotide sequence," messenger RNA stability, and DNA recognition
"Nucleotide sequence," messenger RNA stability, and RNA stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.3%; Score 35; DB 1; Length 2717; 66.7%; Pred. No. 80; 1; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297217 MW; D45D3CA951FEA561 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sulfate permease II.
                                                                                                                                             EMBL; X51435; CAA35798.1; -.
                                                                                                                                                              PIR, A34203; A34203.
PDB, 3ZNF, 15-JAN-92.
PDB, 4ZNF, 15-JAN-92.
PDB, 1800, 31-OCT-93.
TRANSPAC, T00497; --
Genew; HGNC,4920; HIVEPI.
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2123
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P23622;
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SEQUENCE
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CY14 NEUCR
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        HAPPEN SERVICE SERVICE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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permease II and a putative human tumour suppressor.";

Trends Biochem. Sci. 19:19-19(1994).

-!- FUNCTION: UPPARE OF SULFATE INTO THE CELL.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- INDUCTION: Highly expressed, but only in cells subject to sulfur limitation, and it is turned on by the positive-acting Cys-3 sulfur regulatory protein.

-!- MISCELLANGOUS: SULFATE PERMEASE II IS MAINLY FOUND IN MYCELIA.

-!- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
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MEDILINE-21225279; PubMed=11326269;
MEDICOM., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S.,
Oshimuza M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome."; Nat. Genet. 28:19-20(2001).
[2] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Potential phospholipid-transporting ATPase VA (EC 3.6.3.1) (ATPVA)
(Aminophospholipid translocase VA).
ATP10A OR ATP10C OR ATPVC OR KIAA0566.
Homo sapiens (Human).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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36;
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PIR, A37956, A37956.
InterPro; IPR001902; Sulph transpt.
Pfam; PF0916; Sulfate_transp; 1.
TIGRFAMs; TIGR00815; Sulf.; 1.
PROSITE; PS01130; SLC26A; 1.
Transport; Transmembrane; Glycoprotein.
TRANSMEM 71
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POTENTIAL.
POTENTIAL.
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Pred. No.
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578
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Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,

Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,

Ra Nomura N., Ohara O.;

Rr The complete sequences of unidentified human genes. IX.

The complete sequences of 100 new cDNA clones from brain which can code for large proteins in Virco.";

DNA Res. 5:31-39(1998).

--- CATALYTIC ACTIVITY: ATP + H(2) = ADP + phosphate.

--- CATALYTIC ACTIVITY: ATP + H(2) = ADP + phosphate.

--- CATALYTIC ACTIVITY: Midely expressed, with highest levels in kidney, followed by lung, brain, prostace, testis, ovary and small intestine.

--- DISEASE: Defects in ATP10A are a cause of Angelman syndrome (AS)

--- CHARLYTIC ACTIVITY: Midely expressed, with highest levels in characterized by leatures of severe motor and intellectual characterized by features of severe motor and intellectual retardation, microcephaly, ataxia, frequent jerky limb movements and flapping of the arms and hands, hypotonia, hypotonia, hypotonia, hypotonia, hypotonia, hypotonia, hypotonia, hypotonia, and episodes of paroxysmal laughter, and an unusual facies characterized by macrostomia, a large mandible and open-mouthed characterized by and an occipilatel groove.

--- SIMILARITY: Belongs to the cation transport ATPases family (P-type
                                                                                                                                                                    SECTIONS FROM N.A.

TISSURESKIN,

MEDLINE=22388257; PubMed=12477932;

REDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Riauaner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshlykik S., Carninoi D., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Morley K.C., Hale S., Garcia A.M., Galy L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbb R.A.,

Rahas S., Maring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Stalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Stalska U., Smailus D.E.,

Chuman and mouse CDNA sequences.
     Herzing L.B.K., Kim S.-J., COOK B.H. Jr., Ledbetter D.H.;
"The human aminophospholipid-transporting ATPase gene ATP10C maps adjacent to UBE3A and exhibits similar imprinted expression.";
Mm. J. Hum. Genet. 68:1501-1505(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
MEDLINE=21313119; PubMed=11353404;
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MEDLINE=98290545; PubMed=9628581;
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                                                                                                                                                         SEQUENCE FROM N.A.
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RL20 MYCPU ID RL20 MYCPU AC Q960\forallo 0 DT 28-FEB-2003 ( DT 28-FEB-2003 ( RESULT 8 요 EMBL; AR051358; BAB47392.1; -.
EMBL; AY029504; AAX33100.1; -.
EMBL; AY02948; AAX33100.1; JOINED.
EMBL; AY02948; AAX33100.1; JOINED.
EMBL; AY02949; AAX33100.1; JOINED.
EMBL; AY02949; AAX33100.1; JOINED.
EMBL; AY029491; AAX33100.1; JOINED.

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R MIN, 605855; -
R MIN, 105830; -
R MIN,
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MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY).
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Pred. No. 70;
0; Mismatches 3; Indels
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1499 AA; 167687 MW; D4996A4D0635A68D CRC64;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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EMBL; AY029493; AAK33100.1; JOINED.
EMBL; AY029494; AAK33100.1; JOINED.
EMBL; AY029494; AAK33100.1; JOINED.
EMBL; AY029496; AAK33100.1; JOINED.
EMBL; AY029497; AAK33100.1; JOINED.
EMBL; AY029497; AAK33100.1; JOINED.
EMBL; AY029499; AAK33100.1; JOINED.
EMBL; AY029500; AAK33100.1; JOINED.
EMBL; AY029501; AAK33100.1; JOINED.
EMBL; AY029503; AAK33100.1; JOINED.
EMBL; ABOIL138; BAAS5492.1; ---
EMBL; ABOIL138; BAAS5492.1; ---
EMBL; ABOIL138; EARSE492.1; ---
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Local Similarity 72.7%;
Les 8; Conservative 0
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Venter J.C.;
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                                                                                                                                                                                                                                                                              Mycoplasma pulmonis.";

Nucleic Acids Res. 29:2145-2153(2001).

-I-FUNCTION: This protein binds directly to 23s ribosomal RNA and is necessary for the in vitro assembly process of the 50s ribosomal subunit. It is not involved in the protein synthesizing functions of that subunit (By similarity).

-I- SIMILARITY: Belongs to the L20P family of ribosomal proteins.
                                                                                                                                                 STRAIN-UAB CTIP;
MEDLINE-21267165; PubMed=11353084;
MEDLINE-21267165; PubMed=11353084;
MEDLINE-21267165; PubMed=11353084;
Mostar I., Petlig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
                                                                                                                                                                                                                                                            "The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodgern R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Rerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
508 ribosomal protein L20.
RPLT OR MYPU 2610.
Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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**HANAP, MF 00382; -; 1.

**INTERPOSE TO THE OOD TO 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 77.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; E90544; E90544.
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                           NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2234;
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O28330;
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Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeck R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDIATRE-2015 PubMed=10688204;
MEDIATRE-20150912; PubMed=10688204;
Parkhill J. Wren B.H., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quall M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE OF 160-253 FROM N.A.
STRAIN-ATCC 43431 / TGH 9011;
STRAIN-ATCC 43431 / TGH 9011;
MEDLINE-95247673; PubWed=7730270;
Hani E.K., Chan V.L.;
Expression and characterization of Campylobacter jejuni
"Expression and characterization benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 161 POTENTIAL.
165 AA; 17588 MW; BBC17054810ADBF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y990 CAMJE STANDARD; PRT; 253 AA.
AC P45489; Q9PNVO;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-CCT-2001 (Rel. 40, Last annotation update)
DF Hypothetical protein Cj0990c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000968; AAB89307.1; -. PIR; D69493; D69493.
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Matches
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SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

STRAIN-SCTOBLOGI TISSUB-Embryonic head,
MEDLINE-21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Pikunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Ashburnar M., Batalov S., Casawant T.,
A Kadora K., Matsuda H.A., Ashburnar M., Batalov S., Casawant T.,
A Kach P., Lewis S., Matsuo T., Gissi C., King B., Kochiwa H.,
Kuchl P., Lewis S., Matsuo T., Nikaido I., Pesole G., Quackehbush J.,
A Chriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barahi G.,
Blake J., Bolinga N., Carninci P., de Bonaldo M.P.,
Brownstein M.J., Bolinga N., Carninci P., de Bonaldo M.P.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Havsehizel Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Mammary fibroblast;

MEDLINE=2238825; PubMed=12477932;

MEDLINE=2238825; PubMed=12477932;

Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunararne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                       63.5%; Score 33; DB 1; Length 253; 55.6%; Pred. No. 18; 2; Indels iive 2; Mismatches 2; Indels
                                                                                                                                  EMBL; AL139076; CAB73246.1; -.
EMBL; Z36940; CAA85392.1; -.
PIR; C81374; C81374.
PIR; 140758; CATTA Complete proteome.
Hypothetical protein; Complete proteome.
SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTX3 MOUSE STANDARD; PRT; 280 AA. 095387; 09C404; 28-FEB-2003 [Rel. 41, Created) 28-FEB-2003 [Rel. 41, Last sequence update) 10-CCT-2003 [Rel. 42, Last annotation update) Protein C20orf103 homolog precursor.
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                         185 DIFPSGMSY 193
                                                                                                                                                                                                                                                                                                                                                                              2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9D387-2; Sequence=VSP_003820;
CAUTION: Ref.1 sequence differs from that shown due to frameshifts
in positions 174 and 239.
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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AROA VIBCH
AROA STANDARD; PRT; 426 AA.

LO AROA VIBCH
AROA STANDARD; PRT; 426 AA.

CONTRIED.

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 38-FEB-2003 (Rel. 41, Last annotation update)

DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-

DE enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.

CYTOPLASNIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MASSING (In isoform 2).
/FTIG=VSP 003820.
E -> V (IN REF. 1; BAB31124).
P -> A (IN REF. 1; BAB31124).
P -> A (IN REF. 1; BAB31124).
P -> A (IN REF. 1; BAB31124).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.5%; Score 33; DB 1; Length 280; llarity 75.0%; Pred. No. 20; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
PROTEIN C20ORF103 HOMOLOG.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AK014127; BAB29169.1; -.
EMBL; AK016222; BAB31124.1; ALT_FRAME.
EMBL; BC004791; AAH04791.1; -.
MGD; MGI:1920368; 31100351033k.
MGD; MGI:1923411; 6330527006Rik.
Transmembrane; Signal; Alternative splicing.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1;
IsoId=Q9D387-1; Sequence=Displayed;
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238 238 P
280 AA; 31721 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 6; Conserv
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: : | | | | | DSAIPGGMSY 107
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SEQUENCE FROM N.A.
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MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Godson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Fead T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Fraser C.M.;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-Cr-2003 (Rel. 42, Last annotation update)
15-FEB-2003 (Rel. 41, Last annotation up
                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000)
-!- CATANTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyviny1)-3-phosphoshikimate.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; VC1732; -...
HAMAP; MF 00210; -; 1.
InterPro; IPR006264; AroA.
InterPro; IPR001966; EPSP synth.
InterPro; IPR001966; EPSP synthase; 1.
Propon; PD001967; EPSP syntase; 1.
Propon; P00101467; EPSP syntase; 1.
PROSITE; PS00104; EPSP SYNTHASE 1; 1.
PROSITE; PS00104; EPSP SYNTHASE 2; 1.
Aromatic amino acid biosynthesis; Transferase; Complete proteome. SEQUENCE 426 A3; 46101 MW; 38852D6483EFEIC3 CRC64;
                                                                                                                                                                                                                                                                                                                                               'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Westwood D.K., Preston N.C., Fantes P.A.;
"Schizosaccharomyces pombe cdc37 gene.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sixth step.
-!- SUBUNIT: Monomer (By similarity)
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the EPSP synthase family.
-!- SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE004251; AAF94882.1; -. PIR; D82163; D82163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 EFVIPAGQŚY 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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094740;
                                                                                                                                                                                                                                                                                                                                                                                     cholerae."
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RA WOOD V. GWilliam R., Rajandream M.A., Lyme M., Lyme R., Stewart A.,
RA Squoros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Squoros J., Peat N., Hayles J., Chillingworth T., Churcher C.M.,
RA Gollins M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Collins M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Comnor R., Cronin N., Harris D., Hidalgo J., Hodgson G.,
RA Gollroyd S., Hornby T., Howarth S., McDonald S., McLean J.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Noney P., Moule S., Sauders R., Seeger K., Sharp S.,
Rutherford K., Rutter S., Sauders R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Trvey A., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Trvey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
ROCHART M., Frizc C., Holzer E., Mosetl D., Hilbert H.,
RA Gable C., Fuchs M., Frizc C., Holzer E., Mosetl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mortier S.M.,
A Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mortier S.M.,
A Locas M., Rochet M., Gaillardin C., Moore K., Hurst S.M.,
A Corrutti L., Lowe T., McCombie W.R., Paulsen I., Potsburg S.L.,
RA Shpakovski G.V., Useery D., Barrell B.G., Nurse P.,
RA Shpakovski G.V., Useery D., Barrell B.G., Nurse P.,
RA The Genome sequence of Schizosaccharomyces pombe.",
RA Malue 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PP03234; Cdc37, 1.
Chaperone; Cell division; Cell cycle; Nuclear protein.
SEQUENCE 466 AA; 52554 MW; 647238B34CABB3C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3,
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                                                                      STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ132377; CAB38758.1; -. EMBL; AJ132376; CAB38757.1; -. EMBL; AL049769; CAB42371.2; -. PIR; 143653; T43653. GeneDB_SPombe; SPBC986.10; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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SEQUENCE FROM N.A.
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478 AA; 54417 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.5
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium perfringens.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1502;
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146
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                                                                                                                                                                                                                                                                                605691; -
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CONFLICT
CONFLICT
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BCNS CLOPE
ID BCNS CLO
AC P08696;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE=22388257; PubMed=12477932;
MININE=22388257; PubMed=12477932;
MININE=22388257; PubMed=12477932;
MININE=22388257; PubMed=12477932;
MININE=22388257; PubMed=12477932;
MININE=22388257; MININES E.S., Wangmer L., Schemer C.R., Schuler G.D.,
MININES E.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
MININES E.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
MININES E.F., Jordan H., Patrers A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
MININES E.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
MINING D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Millalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mithing M., Madan A., Young A.C., Shevchenko Y., Smailus D.E.,
Mithing M., Madan A., Young A.C., Shevchenko Y., Salake B.,
Mithing M., Madan A., Young A.C., Shevchenko Y., Smailus D.E.,
Mithing M., Madan A., Young A.C., Shevchenko Y., Smailus D.E.,
Mithing M., Madan A., Schmin J.E., Jones S.J.M., Marra M.A.;
McGneration and initial analysis of more than 15,000 full-length
M. Human and mouse CDNA sequences."
M. Film M. Madal M. Wangelen W. M. Marra M.A.;
M. Madal M. Madal M. M. Madal M. Ma
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MEDLINE=99214318; PubMed=10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins ICP22 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after
                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.,
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                GSR2_HUMAN STANDARD; PRT; 478 AA.
Q9N2M5; Q9BTC6; Q9HAX6; Q9NPP1; Q9NPR4; Q9UF12;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 12-478 FROM N.A.
Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=9606;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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/FTIG-VAR. 011496.

/FTIG-VAR. 011496.

G -> HEG (IN REF. 2; AAH04229).

G -> R (IN REF. 3).

FRREQUIMPACKQEDELENEVRAQARLIANPSATRAKFGFQD

TVERP -> SGSYGRSWPERASSASFGGAQGPGFFCN

KOPNPAPGHRIAA (IN REF. 3).
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REIQ -> VLTVSCRGAPCPVMTPSLLPVPPRGYGRHHGCP
WAGPVGPWFRG (IN REF. 5).
GUILADREKSFQRRMIEPRERAKFKRKYKVKLVEKRAFR
BIQL -> RQQHSFRTGSRAFRGGI (IN REF. 3).
7F18923E348CB52B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDNPLDRPLVGQDEFFLE -> LNNPDKPVVWPGCLFPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garnier T., Cole S.T.; "Characterization of a bacteriocinogenic plasmid from Clostridium
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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A -> S (IN REF. 2; AAH04229)
D -> H (IN REF. 3).
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01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mulia 000041; ...
GO, GO:0005622; C:intracellular; NAS.
Nuclear protein; Polymorphism.
VARIANT 389 389 R -> Q.
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MEDLINE=87057020; PubMed=2877971;
                                                                                                                                                                                                    EMBL; AF182076; AAF62873.1; EMBL; BC004229; AAH04229.1; EMBL; BC006311, AAH06311.1; EMBL; BC010095; AAH10095.1; EMBL; AF296124; AAG30413.1; EMBL; AL359335; CAB94786.1; EMBL; AL359335; CAB94787.1; EMBL; AL122063; CAB94787.1; EMBL; AL122063; CAB94787.1; GMRS, ALG2063; GONZMS; HUMAN. Genew; HGNC;4333; GLTSCR2.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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SEQUENCE FROM N.A.
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MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDRINE=21082930; PubMed=11214968;
Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Matanabe A., Idesawa C., Kohara M., Matsumoto M., Matsuno A.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
Tomplete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22608415; PubMed=12721630;
MEDLINE=22608415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Ivanova N., Sorokin A., Anderson I.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova M., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.;
Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
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Pred. No. 13;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium loti (Megorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriacae; Megorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 AA; 38539 MW; C55268ACB7225995 CRC64;
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MDA Res. 7:331-338 (2000).

EMBL, AP003002; BABSO445-1; -

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0006237; F:merallopeptidase activity; IEA.

GO; GO:0006508; F:proteolysis and peptidolysis; IEA.

InterPro; IPR002933; Peptidase M20.
                                                                                                                                                                                                                          PRT; 344 AA.

Q815A7;
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
ABC transporter substrate-binding protein.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 423:87-91(2003).
EMBL, AE017015, AAP12123.1; -. InterProc. IPPR000437; Prok lipoprot S.
PROSITE, PS00013, PROKAR LIPOPROTEIN; 1.
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843 EEVLPNGIGYS 853
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152 EEIAPLGLSY 161
1 EEVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=226900;
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OOSBEY

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Q815A7
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J. Bacterich. 180:5003-5003 (1998).
EMBL; AF083072; AAC2669-1;
PIR; T31308; T31308.
GO; GO:001600; Cimembrane; IEA.
GO; GO:0016215; Pirransport: IEA.
GO; GO:0006810; Pirransport: IEA.
InterPro; IPR001680; WD40.
InterPro; IPR001680; WD40.
EMBRT; SM00320; WD40; 2...
                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Crenarchaeota; Thermoprotei; Cenarchaeales; Cenarchaeaceae;
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MEDINE=99422450; PubMed=9748430;
Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
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                                                                                                                                                                  73.1%; Score 38; DB 16; Length 387; 60.0%; Pred. No. 15;
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Pfam; PF01546; Peptidase M20; 1.
Hydrolase; Complete proteome.
SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
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Bukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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-01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Probable sulfate permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Hypothetical protein.
SEQUENCE 3472 AA; 367058 MW: 37FBA77777
                                                                                                                                                                                                                                                            2; Mismatches
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Best Local Similarity 54.5'
Local Similarity 6, Conservative
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2294 EDVIPRGISFS 2304
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Best Local Similarity 60.0
Matches 6; Conservative
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NCBI_TaxID=4896;
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SEQUENCE FROM N.A.
STRAIN=NOD; IISSUE=Thymus;
MEDLINE22354683; PubMed=12466851;
The PAINTOM Consortium.
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I annotation of "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MRA-2002 (TrEMBLrel. 20, Created)
01-MRA-2002 (TrEMBLrel. 20, Last sequence update)
01-MRA-2003 (TrEMBLrel. 23, Last annotation update)
01-MRA-2003 (TremBrel. 23, Last annotation update)
Similar to glioma tumor suppressor candidate region gene 2.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                           69.2%; Score 36; DB 11; Length 471; 60.0%; Pred. No. 51; tive 2; Mismatches 2; Indels
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01-MR-2003 (TrEMBLrel. 23, Last sequence update)
01-MR-2003 (TrEMBLrel. 24, Last senotation update)
01-UTN-2004 (TREMBLrel. 24, Last senotation update)
Similar to gliona tunor suppressor CANDIDATE region gene
                                                                                                                            Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025810; AAH25810.1; -.
MGD; MG1:2154441; Gltscr2.
Hypothetical protein.
NON_TER
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                                                                                                                                                                                                                                                                                                        471 AA; 54506 MW; B0DA685C374A9760 CRC64;
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                                                                                                                                                                                                                                                                                                                                  Query Match
Beet Local Similarity 60.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.2
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 EVIPAGASYN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||:| | ||:
239 EVIPAGASYN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EVVPXGMSYS 11
                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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               NCBI_TaxID=10090;
                                                                                                      TISSUE=Liver;
                                                                                                                                                                                                                                                                                                           SEQUENCE
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Q8VD18;
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            STARRES
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"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.2%; Score 37; DB 16; Length 1123; 70.0%; Pred. No. 81; tive 1; Mismatches 2; Indels C
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
R FMBL; AL132779; CAB60015.1; -.
PIR; T39116; T39116.
GenebB SPombe SPAC869.05c; -.
R GO; GO:0008271; F:sulfate porter activity; IEA.
GO; GO:0008271; F:sulfate transport; IEA.
R InterPro; IPR002645; STAS.
R InterPro; IPR01902; Sulph_transpt.
R Pfam; PF01740; STAS; 1.
R Pfam; PF01740; STAS; 1.
R Pfam; PF01740; STAS; 1.
R PROSTER PROSONOS; SULFATE (TANSP) 1.
R PROSTER PSSONOS SULFATE (TANSP) 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 71.2%; Score 37; DB 3; Length 840; Best Local Similarity 77.8%; Pred. No. 59; Matches 7; Conservative 1; Mismatches 1; Indels
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AP004171; BAC44062.1; -.
InterPro; IPR008985; ConA like lec gl.
InterPro; IPR007326; Lipoprotein 17.
Complete proteome: SEQUENCE 1123 AA; 123636 MW; A4D70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22354719; PubMed=12466555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, MYPE 2560 paralog, 57%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVPXGMSYS 11
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Q8R126

RESULT 7

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QBEWD4;

Q8EWD4

ESULT 6

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Gaps

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"Role of mobile DNA in the evolution of vancomycin-resistant
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MEDLINE=22354683; PubMed=12466851;
The FRANTOM Consortium,
The FRANTOM Consortium,
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:53-53-573(2002).
EMBL; AKO77341; BAC36760.1; -
MGD; MGI:2154441; Gltscr2.
SEQUENCE 484 AA; 55792 MM; EB67949BCBE92D44 CRC64;
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STRAIN-VS37 ATCC 700802;
MEDLINE=22550857; PubMed=12663927;
MEDLINE=22550857; PubMed=12663927;
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Unayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madugu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCEL_TaxID=1351;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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OL-MAR-2003 (TrEMBLrel. 23, Created)

01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

Similar to glioma tumor suppressor CANDIDATE region gene 2
60,770 full-length cDNAs.";
Nature 420.563-573(2002).
BMB., AKO88461.; BAC40367.1; -.
MGD, MGI: 2154441.; Gltscr2.
SEQUENCE 484 AA, 55806 MW; B3056425B5EECAD8 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pheromone binding protein, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 484 AA
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Best Local Similarity 60.0%
Best Local Similarity - 60.0%
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239 EVIPAGASYN 248
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08BK3
AC 08BK3
AC 08BK3
DT 01-MA
DT 01
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RC STRAIN-DC3000;

RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,

RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,

RA Brinkac L., Beanan W., Haft D., Selengut J., Madupu R., Daugherty S.,

RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,

RA White O., Fraser C., Collmer A.;

R. Complete sequence of Pseudomonas syringae.";

R. Complete sequence of Pseudomonas syringae.";

R. Momited (MAR-2003) to the EMBL/GenBank/DDBJ databases.

R. EMBL, AR016688, AA054162.1;

DR ROG, GO:0005634; C:nucleus; IRA.

GO; GO:0005634; C:nucleus; IRA.

BR GO; GO:0005634; C:nucleus; IRA.

BR GO; GO:0005639; F:DNA-binding; IEA.

BR GO; GO:0005639; P:DNA-directed RNA polymerase activity; IEA.

BR GO; GO:000530; P:Lanacription; IRA.

DR InterPro; IPR007081; RNA_pol_Rpbl_3.

BR InterPro; IPR007081; RNA_pol_Rpbl_3.

BR InterPro; IPR007081; RNA_pol_Rpbl_3.

BR Pfam; PR04993; RNA_pol_Rpbl_3; 1.

BR Pfam; PR04993; RNA_pol_Rpbl_3; 1.

BR Pfam; PR04998; RNA_pol_Rpbl_3; 1.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 69.2%; Score 36; DB 16; Length 559; Best Local Similarity 66.7%; Pred. No. 62; Marches 6; Conservative 2; Mismatches 1; Indels
Enterococcus faccalis.";
L Science 299:2071-2074(2003).
ENEL, AEOLGS17.
R GO, GO.0005215; Firansport, IRA.
R GO, GO.000515; Firansport, IRA.
R GO, GO.000510; Piransport, IRA.
R GO, GO.0006810; Piransport, IRA.
R HIGEPTC: IPRO00913; Prok lipoprot_S.
R HROSTIS; PSO0013; PROKAR_LIPOPROTEIN; 1.
R PROSITS; PSO0013; PROKAR_LIPOPROTEIN; 1.
R COMPLETE FIRECHOME.
SEQUENCE 559 AA; 61476 MM; CC15418D33D53DE7 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DNA-directed RNA polymerase, beta' subunit.
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60.0%; Pred. No. 41; tive 2; Mismatches

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6; Conservative
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                                                                   2 EVVPXGMSYS 11
Best Local Similarity
Matches 6; Conserva
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                                                                              040129;
01-NOV-1996 (TERMELE) 01, Created)
01-NOV-1996 (TERMELE) 01, Last sequence update)
01-OCT-2003 (TERMELE) 25, Last annotation update)
10-OCT-2003 (TERMELE) 25, Last annotation update)
Hypothetical protein precursor.
Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,

Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,

Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,

Rocap G., Larimer F.W., Lander D., Fost A.F., Regala W., Shah M.,

Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,

Webb E.A., Zineer E.R., Chisholm S.W.;

"Genome divergence in two Prochlorococcus ecotypes reflects oceanic

niche differentiation...'

Nature 424:1042-1047(2003).

Bmbl; BSZ72098; CAE21267.1;

Acyltransferase; Transferase; Complete proteome.

SEQUENCE 245 AA; 26907 MW; 106F7C4CBE2C6427 CRC64;
                                                                                                                                                                                                                                                                                                                                   Q7V6Q4;
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipid and glycerol acyltransferase (From 'motifs_6.msf').
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Bacteria, Cyanobacteria, Prochlorophytes, Prochlorococcaceae,
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SEQUENCE 225 AA, 25188 MW; 1074C261D20CFDAD CRC64;
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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E. Science 281:2012-2018 [1998].

E. Science 281:2012-2018 [1998].

E. Science 281:2012-2018 [1998].

E. Science 281:2011-2018 [1998].

E. Science 281:2011-12-2018 [1998].

E. Science 281:2011-17-2018 [1998].

E. Science 281:2011-17-2018 [1998].

E. PRIST [1998]. Tatalil. "ATP binding, IEA.

GO; GO:0006468; Piprotein kinase activity; IEA.

GO; GO:0006468; Piprotein kinase activity; IEA.

GO; GO:0006468; Piprotein amino acid phosphorylation; IEA.

E. TEROROWIP: Prot. kinase.

E. Probom; PD000001; Prot. kinase.

E. Probom; PD00001; Prot. kinase.

E. Probom; PD00001; Prot. kinase.

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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
R10D12.10 protein.
425 AA
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Job time : 29.8667 secs
PRT;
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MEDLINE=99069613; PubMed=9851916;
PRELIMINARY;
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                                                                June 3, 2004, 11:31:01; Search time 45.9333 Seconds (without alignments) 67.664 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                  Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                      DB 5; Length 11; 0.00071;
                                                                                       96.4%; Score 54; DB 100.0%; Pred. No. 0.0 iive 0; Mismatches
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus Claim 17; Page 65; 69pp; English.

Sequence 11 AA

ö ö /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7" ingredient ō The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of invention are alpha-ketcamide peptide analogues. The peptides have viruside activity, and are useful for treating and in the manufacture a medicament to trat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredicts useful for treating disorders associated with hepatitis C virus Gaps Gaps Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40. ö ö DB 5; Length 11; 0.00071; hes 0; Indels Length 11; 0; Indels 96.4%; Score 54; DB 5; Le 100.0%; Pred. No. 0.00071; ive 0; Mismatches 0; Query Match
96.4%; Score 54; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 11; Conservative 0; Mismatches note= "N-terminal acetyl" /note= "C-terminal amide" notes "D-form residue" note= "D-form residue" note= "Oxymethionine" Location/Qualifiers Brunck TK; ABB80560 standard; peptide; 11 AA. Claim 17; Page 65; 69pp; English. 19-JUL-2001; 2001WO-US023169 21-JUL-2000; 2000US-0220101P (first entry) Query Match
Best Local Similarity 100.
Matches 11; Conservative 17 1 EEVVPXGMHYS 11 Levy OE, (CORV-) CORVAS INT INC WPI; 2002-361643/39. Misc-difference Misc-difference WO200208251-A2 Key Modified-site Modified-site Modified-site Modified-site Lim-Wilby M, 31-JAN-2002. 08-OCT-2002 Synthetic virucide. protease. ABB80560; RESULT 셤 ò

RESULT 4 **BB80527** 

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                      /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17.
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Best Local Similarity
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                                                                                                                                                                                              Key
Modified-site
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activity usefu
                                                                                                                                                                                                                                                                                                                              Modified-site
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                                             08-OCT-2002
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                                                                                                                                                              Synthetic
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               ABB80537;
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                                                                                                                                                                                                                                                                                                                                                                                               note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7
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0.00071;
hes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                 note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "D-form residue"
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                                                                                                                  11 AA
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                                                                                                                ABB80527 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                    residue 7"
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                             EEVVPXGMHYS 11
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EEVVPXGMHYS
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                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                  virucide.
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                                                      /note= "Norvalyl carbonyl forming keto-amide linkage with residue ?"
                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #26.
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Pred. No. 0.0069;
0; Mismatches 1; Indels
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                                               'note= "N-terminal acetyl"
                                                                                                         /note= "C-terminal amide"
                                                                                        'note= "D-form residue"
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                               Location/Qualifiers
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                                                                                                                                                                                                           Brunck TK;
                                                                                                                                                                                                                                                                             Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                              87.5%;
90.9%;
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Best Local Similarity
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Modified-site
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                 Synthetic.
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virucide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have viruidide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                        /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                             (CORV-) CORVAS INT INC
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Brunck TK

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The sequence represents a peptide compound of the invention having hepatitis C virus (RCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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virucide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80550 standard; peptide; 11 AA.
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          19-JUL-2001; 2001WO-US023169.
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Best Local Similarity 90.9
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                                                                                Lim-Wilby M, Levy OE,
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                                                        (CORV-) CORVAS INT INC
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(first entry)

/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"

/note= "C-terminal amide" note= "D-form residue"

Brunck TK;

Levy OE,

/note= "N-terminal acetyl"

Location/Qualifiers

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                                                                                                               The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV procease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                              virus
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                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #35.
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                                                                                        Claim 17; Page 65; 69pp; English.
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           WPI; 2002-361643/39.
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                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                               Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
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                                                    activity uprotease.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80555;
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Gaps

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1; Indels

0; Mismatches

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Score 48; DB 5; Length 11; Pred. No. 0.011;

85.7%; 90.9%;

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Gaps

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Indels

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ABB80532 standard; peptide; 11
                                                                                                                                                                                                                                                  19-JUL-2001; 2001WO-US023169
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                                                                              1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                     (CORV-) CORVAS INT INC
                                                                                        1 EEVVPXGSHYS
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                                                                Local Similarity
nes 10; Conserv
                                                                                                                                                                                                        Misc-difference
                                                   Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                 Novel peptide
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Modified-site
                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                               Lim-Wilby M,
                                                                                                                                  08-OCT-2002
                                                                                                                                                                                                                                         31-JAN-2002
                                                                                                                                                                                                                                                                                                      activity protease.
                                                                                                                                                                   Synthetic
                                                                                                                         ABB80532;
                                                                                                                                                         virucide
                                                             Query Match
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Matches
                                                                                                      RESULT 11
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Norvalyl carbonyl forming keto-amide linkage with
pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide compound having hepatitis C virus protease inhibitory
ity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11.
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                                                                                       Length 11;
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Pred. No. 0.027;
                                                                                       Score 46; DB 5;
Pred. No. 0.027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                               ABB80531 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 64; 69pp; English.
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                                                                                           82.1%;
90.9%;
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1 Similarity 90.9%;
10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 residue 7"
                                                                                                                                  Conservative
                                                                                                                                                                    1 EEVVPXGMHYS 11
                                                                                                                                                                                                       EEVVPXGGHYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORV-) CORVAS INT INC
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Best Local Similarity
Matches 10; Conserv
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nes 10; Conserv
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                                                          Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200208251-A2
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Modified-site
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activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virucide.
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                                                                                             Query Match
                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Norvalyl carbonyl forming keto-amide linkage with
                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #12.
                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                              Length 11;
                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                              Score 48; DB 5;
Pred. No. 0.011;
); Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunck TK;
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                           Claim 17; Page 65; 69pp; English.
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                                                                                                                                                                                                                                                85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residue 7"
                                                                                                                                                                                                                                                                                     Conservative
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Gape

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Indels

1 EEVVPXGMHYS 11

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note= "Norvaly1 carbony1 forming keto-amide linkage with

residue 7"

Misc-difference

Modified-site

Modified-site

/note= "C-terminal amide" 'note= "D-form residue" 'note= "Oxymethionine"

WO200208251-A2

31-JAN-2002

Brunck TK;

Lim-Wilby M, Levy OE, (CORV-) CORVAS INT INC

WPI; 2002-361643/39

virus

19-JUL-2001; 2001WO-US023169 21-JUL-2000; 2000US-0220101P

'note= "N-terminal acetyl"

Location/Qualifiers

Key Modified-site Modified-site

Synthetic

virucide

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41

08-OCT-2002

ABB80561;

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides havingide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
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Pred. No. 0.042;
0; Mismatches 1; Indels
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                                               ABB80525 standard, peptide, 11
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illarity 90.9%;
Conservative (
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                                                                                                                                               (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORV-) CORVAS INT INC
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Best Local Similarity
Matches 10; Conserv
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Modified-site
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                                                                                                                                               08-OCT-2002
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                                                                                                  ABB80525;
                                                                                                                                                                                                                                                                          virucide.
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
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Pred. No. 0.042
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.4%;
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Matches
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Gaps

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RESULT 14 ABB80561 ID ABB80561 standard, peptide; 11 AA. XX

EEVVPXGMSYS 11

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                        /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                               'note= "N-terminal acetyl"
                                                                                                                                                                  /note= "C-terminal amide"
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    Lim-Wilby M, Levy OE, Brunck TK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11 AA;
                                                                                                                                                                                             WO200208251-A2
                                                                      Key
Modified-site
                                                                                                            Modified-site
                                                                                                                                                     Modified-site
                                                                                                                                                                                                                         31-JAN-2002.
                                         Synthetic
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Gaps . 0 80.4%; Score 45; DB 5; Length 11; 90.9%; Pred. No. 0.042; 1; Indels iive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.9
Matches 10; Conservative

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Search completed: June 3, 2004, 11:48:23 Job time: 45.933 sece

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PCT US93 05000-4
PCT US93 05000-6
US 08-646-517-23
US 08-246-361A-6
US 08-246-361A-23
US 08-246-361A-23
US 08-246-361A-23
US 08-64-517-19
US 08-46-517-19
US 08-46-517-19
US 08-246-361A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 4
Pred. No. 24;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT / ORGANISM: Staphylococcus epidermidis US-09-134-001C-4794
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Best Local Similarity 63.6%;
Matches 7; Conservative 5
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US-09-134-001C-4794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                     (without alignments)
48.399 Million cell updates/sec
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-21444
US-08-821-119-19
US-08-821-119-19
US-08-821-118-2
US-09-252-991A-26615
US-09-252-991A-27834
US-09-252-991A-27834
US-09-134-001C-4
US-09-621-976-6096
US-08-80-988A-23
US-08-80-988A-23
US-08-80-988A-23
US-08-460-654-4
US-08-460-771-21
US-08-246-361A-21
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US-08-464-517-22
US-08-246-361A-22
US-08-463-772-22
PCT-US93-05000-22
US-08-464-517-6
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  UM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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56
1 EEVVPXGMHYS 11
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Match Length
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Perfect score:
Sequence:
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No.
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RESULT 2

US-09-252-991A-21444

Sequence 21444 Application US/09252991A

Sequence 21444 Application US/09252991A

Sequence 21444 Application US/09252991A

Sequence 21444 Application US/09252991A

SEQUENCE 20195

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOWONAS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21444

LENGTH: 856

TYPE: PRI
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Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/064, 964
PRIOR APPLICATION NUMBER: US 60/065, 779
PRIOR APPLICATION NUMBER: US 60/065, 779
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
ILENGTH: 1037
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Sequence 2. Application US/08821118
Sequence 2. Application US/08821118
Sequence 3. Application US/08821118
Settle No. 5989889
GENERAL INFORMATION:
APPLICANT: RO!ightly, Elizabeth
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
TITLE OF INVENTION: AATIVITY
NUMBER OF SEQUENCES: . 7
CORRESPONDENCE ADDRESS:
ADDRESSES: No. 59898890 No. 5989889th America, Inc.
STREET: 405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTHARE: FESTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CIASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REGISTRATION NUMBER: 33,728
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                               Score 34; DB 2;
Pred. No. 1.2e+02
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                                          TELEX:
INFORMATION FOR SEQ ID NO: 19:
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Best Local Similarity 75.0%;
Matches 6; Conservative (
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Best Local Similarity 75.0%;
Matches 6; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 212-867-012
TELEFAX: 212-878-9655
TELEX:
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FRAGMENT TYPE: internal
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                             ) MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-821-119-19
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7304
LENGTH: 323
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APPLICANT: Rammssen, Grethe APPLICANT: Lehnbeck, Jan
APPLICANT: Lehnbeck, Jan
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
NUMBER OF SEQUENCES: 23
CORRESSED: No. 58211040 No. 5821104th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.7%; Score 34; DB 4; Length 323; 55.6%; Pred, No. 63;
                                                               DB 4; Length 856;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICAMION DATA:
APPLICATION NUMBER: US/08/821,119
FILING DATE: 19-WAR-1997
CLASSIFICATION: 435
ATTONEY, AGENT INFORMATION:
NAME: Lambiris, Blias J
REGISTAMION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107.204-US
TELECOMMUNICATION INFORMATION:
                                                                                                            Mismatches
                                                               Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                        Sequence 7304, Application US/09543681A
Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO. 58211040 NO. 58
CITY: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: TATE
    ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21444
                                                               Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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75 DVCPAGVHY 83
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Best Local Similarity
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10174
RF
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APPLICANT: UND BOOKSTEE STARM ET AL
APPLICANT: LYAND DOUGETTE-STARM ET AL
APPLICANT: LYAND DOUGETTE-STARM ET AL
TITLE OF INVENTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EDIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERRNCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/054,964
PRIOR PILING DATE: 1997-11.08
PRIOR FILING DATE: 1997-11.08
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3:50
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) Sequence 4, Application US/09408020
| Sequence 4, Application US/09408020
| Patent No. 6632937
| GENERAL INFORMATION:
| APPLICANT: Seldmen, Robert A. |
| APPLICANT: Schleper, Christa |
| APPLICANT: Schleper, Christa |
| TILL OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REFERENCE: DCORP.002A |
| CURRENT APPLICATION NUMBER: US/09/408,020 |
| CURRENT APPLICATION NUMBER: 60/102,294 |
| PRIOR PLIING DATE: 1998-09-29 |
| PRIOR PLIING DATE: 1998-09-29 |
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.105001
CURRENT PELLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11.28
FRIOR PELLING APPLICATION NUMBER: U.S. No. 6380362 60/171,678
FRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 747
TYPE PRT.
TYPE PRT.
TYPE PRT.
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                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.9%; Score 33; DB 4; Length 747; Best Local Similarity 71.4%; Pred. No. 2.5e+02; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.9%; Score 33; DB 4; 1
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 4; Mismatches 2.
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SOFTWARE RattSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
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; Sequence 3950, Application US/09134001C
; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2294 EDVIPRGISFS 2304
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Batent NO. 6551795

GENERAL INFORMATION:
APPLICANT: Marc V. Rubenfield et al.
APPLICANT: Marc V. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27834

LENGTH: 385
                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PAPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-7
NUMBER OF SEQ ID NOS: 33142
LENGTH: 277
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APPLICANT: Murison, James G.
IITLE OF INVENTION: Polynucleotides, polypeptides expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 4; Length 277;
Pred. No. 83;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.9%; Score 33; DB 4; Length 385; 44.4%; Pred. No. 1.2e+02; tive 3; Mismatches 2; Indels
                                                                                                        US-09-252-991A-26615
; Sequence 26615, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application US/09724864 Patent No. 6380362 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EEVVPXGMHYS 11
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201 EILPAALHY 209
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     VPKGWHYS 38
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US-09-724-864-36
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TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A
STREET: 8011 (2-2-2)
CITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Xaa = * ,Ala,Glu,Gly,1le,Lys,Leu,Arg,Ser,Thr,Val
US-09-621-976-6096
                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.1%; Score 32; DB 4; Length 101; 83.3%; Pred. No. 43;
                                                       Score 32; DB 4; Length 70;
Pred. No. 29;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                          Sequence 6096, Application US/09621976
Fatent No. 6639063
GENERAL INFORMATION
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: Glordano, Jr.
TITLE OF INTENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 6096
LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 77071

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/580,988A FILING DATE: January 3, 1996
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-08-580-988A-23
Sequence 23, Application US/08580988A
Patent No. 5856161
GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
                                                         Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                  4 VPXGMHYS 11
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STATE: Texas
COUNTRY: USA
ZIP: 77071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: UNSURE
                                                                                                                                                                                                                                                           -09-621-976-6096
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AUTONREY, MARKET INFORMATION:

NUMBER | SERVE | MARKET INFORMATION:

REFERENCE | MARKET INFORMATION:

REFERENCE | MARKET | MARKET
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                                                                                                                                                          Indels
                                                                                                                                                                                                                                             Sequence 3, Application US/09215096
; Sequence 3, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUWAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STRATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
                                                                                                                  57.1%; Score 32; DB 66.7%; Pred. No. 55; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
FILING DATE: 08/879,995
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LACY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-855-055
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.1
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                   28 EQVVPGGGH 36
; TOPOLOGY: linear; IMMEDIATE SOURCE:
; LIBRARY: GenBank; CLONE: 163590
US-08-879-9958-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                             1 EEVVPXGMH 9
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) CLONE: 163590
US-09-215-096-3
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CLASSIFICATION:
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Gaps
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68;
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Date of Application US/08460694

Patent No. 5858655

GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF UNEXTION:
PARDICANT: Arnold, Andrew
TITLE OF UNEXTION:
PRADICANT: Arnold, Andrew
TITLE OF SEQUENCES:
CORRESPONDENCES:
ADDRESSES: STEREY, GOLDSTEIN & FOX P.L.L.
STREET: 1100 New York Avenue, N.W., Suite 600
CITTY: Washington
STREET: 100 New York Avenue, N.W., Suite 600
COUNTRY: USA
ZITE: 20005
COUNTRY: USA
ZITE: PROBE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBH PC COMPATA:
COMPUTER: IBH PC COMPATA:
MEDIUM TYPE: PatentIn Release #1.0, Version #1.30
CURRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION UNDERR: 35,279
REFERENCE/DOCKET NUMBER: 36,279
REFEREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 2
Pred. No. 68;
1; Mismatches
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linear
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Best Local Similarity 60.0
Matches 6; Conservative
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MOLECULE TYPE: peptide
US-08-460-694-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMHY 10
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RESULT 15

28 EQVVPGGGH 36

1 EEVVPXGMH 9

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Sequence 7, Appli
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                                                                                                                                                                              June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US07 NBW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US06 NBM PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US06 NBM PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US07 NBW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US07 NBW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US07 NBW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US08 NBW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US09 NBW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US09 NBW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US09 NBW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US09 NBW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US09 NBW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US00 NBW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-21
US-09-909-164-25
US-09-909-164-36
US-09-909-164-38
US-09-909-164-38
US-09-909-164-39
US-09-909-164-39
US-09-909-164-42
US-09-909-164-42
US-09-909-164-45
US-09-909-164-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1155919 segs, 281338677 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seg length: 0
Maximum DB seg length: 200000000
                                                                                                                                                                                                                                                                                                              US-09-909-164-11
56
1 EEVVPXGMHYS 11
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Match Length
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Perfect score:
Sequence:
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No.
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Sequence 9,	t concerns	- -	_	4	4	4	Ŋ	ß	ß	equence 1	equence 2	4	equence 2	N	N	Sequence 2,	equence 2	(4	equence 3	Sequence 3:	m	m	m	m	4	4,	4	ヸ	4
US-09-909-164-9 IIS-09-909-164-3	1-407-606-60-	-08-808-16	19-909-164	-606-60	1-606-60	09-909-164-	91-606-60	09-909-164-5	09-909-164-5	US-09-909-164-19	09-909-164-2	09-909-164-2	09-909-164-2	09-909-164-2	09-909-164-2	6	09-909-164-2	09-909-164-	09-909-164-3	09-909-164-3	09-909-164-3	09-909-164-3	09-909-164-	09-909-164-3	09-909-16	09-909-164-4	09-909-164-4	6	09-909-164-4
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16	•	18	19	0	21 4	01	23 4	4	ı	26 4	27 4	80	6	•	31	32 4	33	34	ın.	9		80		0				44	

## ALIGNMENTS

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ASPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile E
APPLICANT: Lavy, Odile E
APPLICANT: BANGA, Tereance K
TILE REFERENCE: INOIL92-US
FILE REFERENCE: INOIL92-US
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQUENCE: PARENT PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQUENCE: PARENT PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQUENCE: PARENT PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQUENCE: PARENT PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQUENCE: PARENT PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQUENCE: PARENT PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQUENCE: PARENT PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQUENCE: PARENT PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQUENCE: PARENT PRILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                           FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 11-mer synthesized according to example 1 FRATURE: NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
87.5%; Score 49; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0067;
Matches 10; Conservative 0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 21
LENGTH: 11
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NAME/KEY: MISC FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC_FEATURE
COCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
US-09-909-164-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: artificial sequence
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NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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OTHER INFORMATION: AMIDATION
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US-09-164-11

Sequence 11, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
GENERAL INFORMATION:
Hallow, Marguerita
APPLICANT: Corves International, Inc.
APPLICANT: Lievy, Odile E
APPLICANT: Lievy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT PELING DATE: 2003-03-25
PRIOR PRING PATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
LENGTH: 11
TYPE: PRI
TY
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US-09-064-21
US-09-06-164-21
Sequence 21, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Corvae International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Voile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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                                                                                                   Ouery Match 96.4%; Score 54; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0007; Matches 11; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: D-amino acid
US-09-909-164-11
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
; OTHER INFORMATION: AMIDATION
US-09-909-164-7
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OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC_FEATURE
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FEATURE:
NAME/KEY: MOD RES
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Sequence 38, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Leav, Odile E

ITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN101192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR PILIAGE DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

LENGTH: 11

LENGTH: 11
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OTHER INFORMATION: 11-mer synthesized according to example 1
PEATURE:
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Pred. No. 0.01;
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENT VEXEION 3.1
LENGTH: 11
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COTHER INFORMATION: D-amino acid
US-09-909-164-34
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OTHER INFORMATION: ACETYLATION
PRATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: artificial sequence
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NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC_FEATURE
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NAME/KEY: MISC_FEATURE
LOCATION: (8)...(8)
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Matches
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile B
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PELING DATE: 2000-07-21
WUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT:
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                                                                                                                                                                                                                                                                                              1; Indels
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Pred. No. 0.0067;
0; Mismatches
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Pred. No. 0.01;
0; Mismatches
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CTHER INFORMATION: norvaline-(CO)
US-09-909-164-30
   OTHER INFORMATION: norvaline-(CO) FEATURE:
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LOCATION: (1)...(1)
COCATION: (1)...(1)
PEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(111)
OTHER INFORMATION: AMIDATION
                                                                NAME/KEY: MISC_FEATURE

LOCATION: (8)..(8)

COTHER INFORMATION: D-amino acid

US-09-909-164-25
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Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: artificial sequence
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Best Local Similarity 90.5
Matches 10, Conservative
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LENGTH: 11
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APPLICANT: Levy, odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE REFERENCE: IN0192-WS
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 42
LENGTH: 11
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US-09-909-164-44

Publication No. US20020068702A1

Sequence 44, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Evy, Odile B

APPLICANT: Brunck, Terence K

TILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEFATITIS C

FILE REFERENCE: 101192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR APPLICATION DATE: 2000-07-21
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Best Local Similarity 90.9%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
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OTHER INFORMATION: ACETYLATION
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SOFWARE: Patentin version 3.1
SEQ ID NO 44
LENGTH: 11
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ORGANISM: artificial sequence
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LOCATION: (8)..(8)
OTHER INFORMATION: Met(0)
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lievy, Odile B
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TILE REPREMENCE: INO192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PRILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENT VERSION 3.1
SEQ ID NOS: 62
SOFTWARE: PATENT VERSION 3.1
SEQ ID NOS: 62
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                                                                                                                                                                            Score 48; DB 12; Length 11;
Pred. No. 0.01;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 11;
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85.7%; Score 48; DB 12
Best Local Similarity 90.9%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-909-164-42
Sequence 42, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.,
APPLICANT: Lim-Wilby, Marguerita
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
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OTHER INFORMATION: norvaline-(CO)
FEATURE:
                                                        NAME/KEY: MISC_FEATURE

LOCATION: (6)...(6)

COTHER INFORMATION: norvaline-(CO)

WIS-09-909-164-38
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| LOCATION: (8)..(9)
| OTHER INFORMATION: D-amino acids
US-09-909-164-39
            OTHER INFORMATION: D-amino acid FEATURE:
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                               Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMHYS 11
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Sequence 5 Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lewy, Odile B

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: INO1192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SED ID NO 5

LENGTH: 11
               GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Inim Wilby, Marguerita
APPLICANT: Linim Wilby, Marguerita
APPLICANT: Linim Wilby, Marguerita
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Evy, Odile B
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NOS: 62
LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 12;
Pred. No. 0.026;
0; Mismatches
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: D-amino acid US-09-909-164-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
  Publication No. US20020068702A1
                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD RES
LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
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NAME/KEY: MOD_RES
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APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Lovy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES: US/09/909,164
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 15
LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                               Score 48; DB 12; Length 11; Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
82.1%; Score 46; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.026;
Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
                                                                                                                           NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
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; LOCATION: (6)...(6)
; OTHER INFORMATION: norvaline-(CO)
US-09-909-164-15
                       FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)..(9)
OTHER_INFORMATION: D-amino acids
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
PEATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: artificial sequence
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OTHER INFORMATION: AMIDATION
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                              | LOCATION: (8)...(8)
| OTHER INFORMATION: Met(0)
US-09-909-164-44
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LOCATION: (11)..(1
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OTHER INFORMATION: 11-mer synthesized according to example 1

RESULT 12 US-09-909-164-16 ; Sequence 16, Application US/09909164

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GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: NOUSE NOUSE
STILE OF INVENTION: NOUSE 
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ORGANISM: artificial sequence
FRATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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LOCATION: (1):.(1)
COTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6):.(6)
OTHER INFORMATION: NOTVALINE-(CO)
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LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
US20020068702A1
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LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
US-09-909-164-8
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APPLICANT: Lim-wilby, Marguerita
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Beruck, Terence
APPLICANT: Brunck, Terence
ATITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 6
SEQ ID NO
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ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 12; Length 11; Pred. No. 0.041; 0; Mismatches 1; Indels
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US-09-909-164-8
; Sequence 8, Application US/09909164
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Publication No. US20020068702A1
GENERAL INFORMATION:
                                                  FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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NAME/KRSY: MISC FEATURE
LOCATION: (9)..(9).
OTHER INFORMATION: D-amino acid
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NAME/KEY: MOD RES
LOCATION: (1) 7. (1)
OTHER INFORMATION: ACETYLATION
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.4%;
Best Local Similarity 90.9%;
Matches 10; Conservative
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DOCATION: (11)...(11)
HER INFORMATION: AMIDATION
US-09-164-6
                                                                                                                                                                                                                             FEATURE:
NAMEN KEX: MOD RES
LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
US-09-909-164-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
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Matches 10; Conserva
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T518.1 protein - A
diphthine synthase
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hypothetical prote
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amino acid antipor
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117.567 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                          June 3, 2004, 11:35:47 ; Search time 9 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283366
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           283366 segs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM protein - protein search, using sw model
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F89892
AE2001
S69892
AE2001
S69894
S9894
D92618
H7021818
H702181
H7021
H702
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
                                                                                                                                                                                                                                                                    US-09-909-164-11
56
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Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
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Perfect score:
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Maximum DB s
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                                                                                                                                                             Run on:
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DNA mismatch repai	C1489.8 profein -	L-shaped tail fibe	hypothetical 367K	tachykinin B precu	heme exporter prot	hypothetical prote	ribosomal protein	ribosomal protein	probable ThuA prot	hypothetical prote	cyclin D2 - rat	cyclin D2 - rat	cyclin D2 - mouse	cyclin D2 - human
A69663	S44754	836851	T31308	A25905	D71640	S57810	E97120	T07215	C95881	T25737	JC4011	158372	A41984	A42822
01 -	٦ ،	10	0	~	0	N	ď	N	7	~	0	~	7	0
627	1257	1396	3472	126	197	225	233	267	270	283	288	288	289	289
		58.9 1396												
	, a	0.00	58.9	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1

## ALIGNMENTS

RESULT

A/220) fraff proteinase activity modulator HflK - Thermotoda maritima (strain MSB8)
C;Species: Thermotoga maritima
C,Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
CACCESSION: A7220.
KiMelson, K.E.; Cladyton, K.A.; Galli, S.K.; Gwrini, M.L.; Dodson, K.D.; mart, M.L.; m. mart, M.L.; m. m. stewart. A M.: Cotton, M.D.; Fratt, M.S.; Phillips, C.A.; Richardson, D.,
W.O.
Nature 399, 323-329, 1999
A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sec
A; Reference number: A72200; MUID:99287316; PMID:10360571
A; Accession: A72207
A;Status: preliminary
A; Molecule type: DNA
A;Residues: 1-308 <arn></arn>
A;Cross-references: GB:AE001819; GB:AE000512; NID:94982396; PIDN:AAD36885.1; PID:9498240
A;Experimental source: strain MSB8
C, Genetics:
A;Gene: TM1822
C;Superfamily: erythrocyte band 7 integral membrane protein
Query Match 66.1%; Score 37; DB 2; Length 308;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 3 VVPXGMHY 10
Db 41 VVPSGIHY 48

Cipacies: Staphylococcus aureus
Cipacies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
Cipacies: 10-May-2001
Cipacies: 10-May-2001
Cipacies: 1.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
Cipacies: 1.; Ohta, T.; Hattori, M.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
Cipacies: 157, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Reference number: A89758; MUID:21311952; PMID:11418146
A; Accession: F9882
A; Aimolecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: SNA
A

C;Genetics: A;Gene: pyrAB C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin

carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N315

0

Score 37, DB 2, Length 1057; Pred. No. 39, 2, Mismatches 2; Indels

Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative 7.

|:| |:||| 190 EIVSNGLHYS 199 2 EVVPXGMHYS 11

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V1 protein - tobacco yellow dwarf virus (strain Australia)

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Conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Species: Xylella fastidiosa
C/Species: Xylella fastidiosa
C/Species: Sylella fastidiosa
C/Species: DAGE
C/Species: DAGE
C/Species: DAGE
C/Species: The Supervolot #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Species: DAGE
C/Species: The Second Fastidiosa Consortium of the Organization for Nucleotide Seque
Nature 406, 151-157, 2000
A/Title: The Genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Rocession: DBGE
A/Reture: preliminary
A/Rocession: DBGE
A/Reture: preliminary
A/Rocession: DBGE
A/Residues: 1-156 <SIN
A/Ross-references: GB:ABC04014; GB:ABC03849; NID:g9107044; PIDN:AAF84752.1; GSPDB:GNO
A/Rosi-references: GB:ABC04014; GB:AEC03849; NID:g9107044; PIDN:AR84752.1; GSPDB:GNO
A/Rosi-references: GB:AEC03849; NID:GPDB:GNO
A
                                 A; Accession: S69046
A; Molecule type: DNA
A; Restdues: 1.460 «HAL»
A; Cross-references: EMBL: U43703; NID: g1244769; PIDN: AAB68221.1; PID: g1244776; MIPS: YPL1
C; Genetics: A; Gene: SGD: UME1
A; Cross-references: SGD: S0006060; MIPS: YPL1390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-43 «VAB»
A; Cross-references: BBB: 228292; NID: 9486536; PIDN: CAA82146.1; PID: 9486537; MIPS: YKR067
A; Experimental source: strain S288C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Saccharomyces cerevisiae
C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C; Accession: 538143
R; Van Vliet-Reedijk, J.C.; Planta, R.J.
submitted to the Protein Sequence Database, March 1994
A; Reference number: 538130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            C, Superfamily: Saccharomyces cerevisiae transcription modulator WTM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.3%; Score 36; DB 2; Length 460; 62.5%; Pred. No. 25; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.3%; Score 36; DB 2; Length 743; 75.0%; Pred. No. 43; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 62.5%;
tes 5; Conservative
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C, Keywords: transmembrane protein
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A,Gene: SGD:GPT2
A,Cross-references: SGD:S0001775
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Best Local Similarity 75.0°
Matches 6; Conservative
A; Reference number: $69040
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R.Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A.Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A.Fitcle: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
A.Reference number: A42452; MUID:92188538; PMID:1546458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C)Accession: AE2001
R)Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, B DNA Res. 8, 205-213, 2001
A;Fitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: Ab1807; MUID:21595285; PMID:1159840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein YPL139c - yeast (Saccharomyces cerevisiae)
()Species: Saccharomyces cerevisiae
()Species: Saccharomyces cerevisiae
()Date: 2-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 17-Mar-2000
()Accession: S69046
(*S.Hall, J.; Deballo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K. submitted to the EMBL Data Library, December 1995
A)Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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A;Status: preliminary
A;Nolecule type: Dreliminary
A;Rosidues: 1-75: CAUR>
A;Rosidues: 1-75: CAUR>
A;Cross-references: GB:BA000019; PIDN:BAB77929.1; PID:g17135383; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: tobacco yellow dwarf virus
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-102 <MOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
```

64.3%; Score 36; DB 2; Length 102; 60.0%; Pred. No. 5; tive 3; Mismatches 1; Indels

Query Match Best Local Similarity 60.07 Thea 6; Conservative

A;Accession: A42452

1||| |::|| 7 QVVPSGINYS 16

2 EVVPXGMHYS 11

; 0

64.3%; Score 36; DB 2; Length 252; 50.0%; Pred. No. 13; Live 3; Mismatches 2; Indels

Query Match
Best Local Similarity 50.0
Matches 5; Conservative

235 EMIVPAGLHF 244

1 EEVVPXGMHY 10

3:Genetics: A:Gene: XF1950

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Till protein - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: G86430
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; V.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Aki, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Aitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1.425 <WIL>
A;Cross-references: EMBL;Z81109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
A;Experimental source: clone R10D12
C;Genetics: A;Gene: CESP:R10D12.10
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A;Molecule type: DNA
A;Residues: 1-510 <STO>
A;Cross-references: GB:AE005172; NID:g4587512; PIDN:AAD25743.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                         hypothetical protein R10D12.10 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T24111
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C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 25-Aug-2003
C;Accession: G69117
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diphthine synthase - Methanobacterium thermoautotrophicum (strain Delta H)
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Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 2; Indels
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C;Superfamily: hexose phosphate transport protein uhpT
                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, October 1996 A; Reference number: 219842 A; Accession: T24111
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A;Introns: 23/3; 56/3; 113/3; 257/2
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Best Local Similarity 50.0
Matches 5; Conservative
              219 EEVVESGLHES 229
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EEVKPPGIHF 21
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4, Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunse, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palnieri, D.A. Sodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A, Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, H.; Yanlada, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z., Contents: annotation
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R.)Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
R.) Oiu, D.; Spadafora, R.; Wanie, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A; Reference number: A69000; MUID:98037514; PMID:9371463
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-311 «ATH»
A; Cross-references: GB: AE000850; GB: AE000666; NID: G2621794; PIDN: AAB85215.1; PID: G262179
A; Experimental source: strain Delta H
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Syspecies: Nicotiana tabacum (common tobacco)
Sybate: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000
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*Residues:1.-23 <OHM>
A;Cross.references: EMBL:D38126; NID:g790362; PIDN:BAA07324.1; PID:g1208498
A;Experimental source: strain BY4; tissue-type leaf
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Pred. No. 19;
1; Mismatches 3; Indels
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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EEILPQGVH 127
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Best Local Similarity
Matches 7; Conserv
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A;Start codon: GTG
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A;Cross-references: GB:AE001932; GB:AE000513; NID:g6458481; PIDN:AAF10353.1; PID:g64584
A;Experimental source: strain R1
C;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 1
C;Superfamily: 3-dehydroquinate synthase; 3-dehydroquinate synthase homology
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R;Seeger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21565
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;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
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Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels
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60.7%; Score 34; DB 2; Length 355;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 1; Indels
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Molecule type: DNA
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A;Molecule type: DNA
A;Residuss: 1-279 <#HT.
A;Crosa-references: GB:AE001889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795
A;Experimental source: strain Rl
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Ospecies: Deinococcus radiodurans
C;Daces: Ospecies: Osp
                                                                                                                                                                                                                                                                                                                                                                                                                       |Residues: 1-264 <MTH>
|Cross-references: GB:AE000940, GB:AE000666, NID:G2623011; PIDN:AAB86340.1; PID:G262301
|Reperimental source: strain Delta H
|Genetics:
                     R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
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A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DR0271
```

Length 264;

A,Gene: WTH1874 C,Superfamily: diphthamide biosynthesis methyltransferase

1; Indels

Score 34; DB 2; Pred. No. 35; 2; Mismatches 1

Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative 2

ò 셤 C,Accession: B75478
C;Accession: B75478
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
R, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma. S.; Smith, H.O.; Venter, V.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

3-dehydroquinate synthase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

- Deinococcus radiodurans (strain R1)

ö

Gaps

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Length 279; 2; Indels

Score 34; DB 2; Pred. No. 38; 0; Mismatches

Match 60.7%; Local Similarity 75.0%; les 6; Conservative

Query Match

Accession: C75538

100 VPLGRHYS 107

4 VPXGMHYS 11

A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A,Reference number: A75250; MUID:20036896; PMID:10567266

A, Residues: 1-350 < WHI: A; Status: preliminary A; Molecule type: DNA Accession: B75478

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                                                                                                                                                                                                                                                                                                                                                                                               Q9vwp4 drosophila Q89a96 buchnera ap P32784 saccharomyc O74377 schizosacch Q9kv29 vibrio chol P15822 homo sapien P20273 homo sapien P17280 chimpanzee P97885 rattus norv
                                                               saccharomyc
schizosacch
vibrio chol
homo sapien
                          bacillus an
drosophila
                                                                                                                                                                                                                                                                                15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR SE0879.
P39948
P40595
P19887
                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                        ALIGNMENTS
  CGDI, RAT
HYPE AZOVI
128A BACAN
SUNC DROME
MILE BUCEP
SCTI, YEBAC
SULH SCHPO
RPOC VIBCH
ZEPI, HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE01646; AA004476.1; -.
HAMAP; MF 01210; -; 1.
InterPro; IPR006275; Card Lglu.
InterPro; IPR005493; CPase L.
InterPro; IPR005493; CPase L. D2.
InterPro; IPR005491; CPase L. D3.
InterPro; IPR005491; CPase L. D3.
InterPro; IPR004941; CPase L. D3.
InterPro; IPR004562; MGS llke.
InterPro; IPR001691; SHPTC acsite.
Fam; PF02786; CPSase L. D2; 2.
Ffam; PF02786; CPSase L. D2; 2.
Ffam; PF02786; CPSase L. D2; 2.
Ffam; PF02142; MGS; 1.
Fram; PF02142; MGS; 1.
  295
341
353
353
573
759
1401
2717
847
124
    STAEP
  QBCPJ4;
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CARE STAEP
ID CARE S'
    0817x9 vibrio para
099ur5 staphylococ
P31619 tobacco yel
003586 mesocricetu
02586 mesocricetu
02586 mesocricetu
02586 mesocricetu
02586 mesocricetu
02581 methanobact
027912 methanobact
027912 methanobact
027912 methanobact
027912 methanobact
027912 methanobact
027313 parcowia 11
P46513 vibrio para
07853 canorhabdi
P1339 bacteriopha
078176 clostridium
0781778 clostridium
078178 conopus lae
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gallus gall
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homo sapien
mus musculu
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Q8rg86 fusobacteri
                                                                                                        (without alignments)
117.693 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                             3, 2004, 11:32:06 ; Search time 4.86667 Seconds
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                           141681 seqs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YK47_YEAST
GAAB METTH
DPHB METTH
DPHB METTH
DPHB METTH
YIL5 VIBBA
PHSL DESBA
MUTL_BACSU
WPBA_CABEL
YLTE BUTS
TKNK_BOVIN
PBL ANGGA
MSR_CABEL
YLTE BUTS
TKNK_BOVIN
RS2_CALON
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CARB_FUSNN
AROA_VIBPA
CARB_STAAM
                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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BRARE
XENLA
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STAAW
TYDVA
YEAST
YEAST
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                               4inimum DB seq length: 0
4aximum DB seq length: 2000000000
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56
1 BEVVPXGMHYS 11
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Match
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Perfect score:
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XX Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bartana A., Gardner W., Grechkin G., Zhu L., Anderson I., Rogan Y., Chaga O., Gottsman B., Bernal A., Asieva O., Chu L., Kogan Y., Chaga O., Gottsman B., Bernal A., Arguides N., Overbeek R.; Asonstein M., Kyrpides N., Overbeek R.; Tonone sequence and analysis of the oral bacterium Fusobacterium arrain ATCC 25586 "; Tonone sequence and analysis of the oral bacterium Fusobacterium Tonoleatum strain ATCC 25586 "; Tonone sequence and analysis of the oral bacterium Fusobacterium Tonoleatum strain ATCC 25586 "; Tonoleatum strain Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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TIGRFAMS; TIGR01369; CPSasell_lrg; 1.

PROSITE: P800866; CPSASE_1; 2.

PROSITE: P800867; CPSASE_2; 2.

Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

DOMAIN 402 S46 OLDEANYPHOSPHATE SYNTHETIC DOMAIN.

DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

DOMAIN 30 1057 ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
                                                                                                                                                                                            10 ATP (POTENTIAL).
52 ATP (POTENTIAL).
84 MANGANESE 1 (BY SIMILARITY).
86 MANGANESE 1 (BY SIMILARITY).
80 MANGANESE 2 (BY SIMILARITY).
80 MANGANESE 2 (BY SIMILARITY).
81 MANGANESE 3 (BY SIMILARITY).
82 MANGANESE 3 (BY SIMILARITY).
817391 MW; 8944D7D8DBBICAES9 CRC64;
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Pred. No. 7.3;
2; Mismatches 2; Indels
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Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1058 AA
                                                                                                                                                                                                                                                                                                                                                          69.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | | | : | | | : | | | 189 KEVVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EEVVPXGMHYS 11
                                                                                                                           929
1057
546
1057
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1057 AA;
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                153
302
284
298
300
820
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ID CARB FUSNN
AC Q8RGB6;
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SEQUENCE
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                                                                                                                                                                             REPEAT
NP_BIND
NP_BIND
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METAL
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REPEAT
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Matches
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Gaps
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STRAIN=RING 2210633 / Serotype O3:K6;

MEDLINE=22568454; PubMed=12620739;

MEDLINE=22568454; PubMed=12620739;

Makino K., Oshima M., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Tijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";

Lancet 361:743-749(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.
--- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q87QX9;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
12-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
enolpyruvylshikimate-3-phosphate synthase) (EPSPS)
AROA OR VP1020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
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Pred. No. 12;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio parahamolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sixth step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.9%;
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les 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 EIVPNGLNYS 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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Matches
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Lancet 359:1819-1827(2002).

-i- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP phosphate + Leglutamate + carbamoyl phosphate.

-i- COACTOR: Binds 3 manganese ions per subunit (By similarity).

-i- PATHWAY: Arginine biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=22040717; Pubmed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Baba T., Tawan N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamanoto K., Alramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (82 SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                               Complete protecme.
CARDAXYPHOSPHATE SYNTHETIC DOMAIN.
OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain)
                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 2; 2.
Arguinne biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
ATP-binding; Manganese; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1; Length 1057;
Pred. No. 19;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1057 AA.
                           EMBL; AP003361; BAB57365.1; --
PIR; PR9922; PB9892.
HSSP; P00968; 1CSO.
HANAP; MF 01210; --; 1.
InterPro; IPR005493; CPase_L.
InterPro; IPR005493; CPase_L.
InterPro; IPR005493; CPase_L.
InterPro; IPR005481; CPase_L.D2.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
Pfam; PF00289; CPase_L.D3.
send an email to license@isb-sib.ch)
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Best Local Similarity
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: 2 ATP a Lightramine + CO(2) + H(2)O = 2 ADP +
phosphate + L-glutamate + carbamoyl phosphate.

-!- COFACTOR: Binds 3 manganese ions per subunit (By similarity).

-!- PATHWAY: Arginine biosynthesis.

-!- PATHWAY: Pyrimidine biosynthesis, first step.

-!- PATHWAY: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21311952; PubMed=1114146;
MEDLINE=21311952; PubMed=1114146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta Y., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hizakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanashita M., Vamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramateu K.,
Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
26-Tabmoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthase ammonia chain).
CARB OR PYRAB OR SAVI203 OR SAVI046.
Staphylococcus aureus (strain Muso / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                           HAMAP, MF 00210; -; 1.
InterPro; IRROD1986; ERSP synth.
Pfam; PF00275; ERSP synthase; 1.
PROSITE; PS00104; EFSP-SYNTHASE 1; 1.
PROSITE; PS0085; ERSP SYNTHASE 2; 1.
Aromatic amino acid blosynthasis; Transferase; Complete proteome.
SEQUENCE 426 AA; 46094 MW; 373D39CC5BA1F70F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                         66.1%; Score 37; DB 1; Length 426; 60.0%; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
  SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the carB family.
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                                                                                                                                                                                               EMBL; AP005076; BAC59283.1; -.
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28-FEB-2003 (Rel. 41, Last seq
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Best Local Similarity 60.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Query Match
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                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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REAL PRO142; MGS; 1.

REAL PRO142; PRO1098; CPSASE.

REAL TIGREAMS; TIGREAGE; CPSASE 1; 2.

DR PROSITE; PS00866; CPSASE 1; 2.

EN PROSITE; PS00866; CPSASE 2; 2.

EN REAL PRO11E; PS00866; CPSASE 2; 2.

EN REAL PROSPHATE SYNTHETIC DOMAIN.

A 10 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
PATHWAY: Pyrimidine biosynthesis; first step.
SUBUNIT: Composed of two Chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
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MEDLINE-92188538; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).

ATP (POTENTIAL).

AMNGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

117185 MW, D8E3B09F9BGGF152 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tobacco yellow dwarf virus (strain Australia) (TYDV) Viruses; ssDNA viruses; Geminiviridae; Mastrevirus. NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                  similarity).
SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                             HAWAP; MF 01210; -; 1.
InterPro; IPR006275; CarA L glu.
InterPro; IPR005483; CPase L.
InterPro; IPR005483; CPase L. D2.
InterPro; IPR005480; CPase L. D3.
InterPro; IPR005481; CPase L. D3.
InterPro; IPR005481; CPase L. D3.
InterPro; IPR005481; CPase L. D3.
InterPro; IPR005482; MSS 11ke
Pfam; PP02786; CPSase L. Chain; 2.
Pfam; PP02786; CPSase L. D3; 1.
Pfam; PP02142; MGS; 1.
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HAMAP; MF_01210; -; 1.
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01-JUL-1993 (Rel. 26, Last seq
01-OCT-1993 (Rel. 27, Last ann
Hypothetical 11.2 kDa protein.
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60.0%;
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es 6; Conservative
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153 21'
284 284 298 298 300 820 82 82 83 83 1057 AA;
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ID YIIK_TYDVA
AC P31619;
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SEQUENCE
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SECURATE FROM N.A.

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SECURATE FROM N.A.

SEA BESSER AB972;

RATAIN=22886 / AB972;

RATAIN=32886 / AB972;

RATAIN CAPERTY J.M. Conter F., Davis K., Davis R.W., Cherry J.M., ABP Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duetry J.M., Rottin M., Friesen J.D., Fritz C., Goffeau A., Rottin M., Friesen J.D., Fritz C., Goffeau A., Ratin S., Hamann K., Johnston M., Kalman S., Kleine K., Amper S., Mesenguy F., Mewes H.-W., Mirtipati S., Mosetl D., RA Hunicke-Smith S., Mamath R., Johnston M., Schafe M., Wambutt R., Wang Y., Wedler E., Wedle
                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL Gustation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this eratement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants."; Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMEL YEAST STANDARD; PRI; 460 AA.

Q03010; P87330;

01-NOV-1997 (Rel. 35, Last sequence update)

10-OCT-2003 (Rel. 42, Last and annotation update)

Moiosis negative regulator UMEL.

UMEL OR WIM3 OR YPL139C OR LP17C.

Saccharomyces cerevisiae (Baker's seat).

Saccharomyces cerevisiae, Saccharomyceties;

Saccharomycetales; Saccharomycetas;
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Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al protein. To AA, 11178 MW; A40BCF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M81103; AAA47947.1; -.
PIR; A42452; A42452.
InterPro; IPR002651; Gemini mov.
Pfam; PF01708; Gemini mov; I.
Hypotherical protein.
SEQUENCE 102 AA; 11178 MW; A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.08;
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Local Similarity
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SEQUENCE FROM N.A.
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035586;
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TRANSMEM
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Matches
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=S288c;
van Vliet-Reedijk J.C., Planta R.J.;
submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELINIAR LOCATION: Integral membrane protein (Probable).
-!- SUBCELINIAR STRONG, TO YEAST YBL011W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                              PIR; S69046; Separamonline; 144121; --

R GENTOMINE; 144121; --

R GENTOMINE; SERVICE STRUCTURE; SERVICE STRUCTURE; SERVICE STRUCTURE; SERVICE STRUCTURE; SERVICE STRUCTURE; SERVICE STRUCTURE; SROOTS STRUCTURE; SERVICE STRUCTURE STRUCTURE; SERVICE STRUCTURE STRUCT
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YK47_YEAST STANDARD; PRT; 743 AA.
1956.48;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NUV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kDa protein in CCPI-MET1 intergenic region.
YKRO67W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.3%; Score 36; DB 1; Length 460; 62.5%; Pred. No. 13; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 451 WD 4.
460 AA; 51022 MW; AAGF60448B7BCBA9 CRC64;
                                                                                                                                                                EMBL; U10280; AAB40937.1; -. EMBL; U43703; AAB68221.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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85 IVPLGLHY 92
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Paton V.G., Shackelford V.E., Krieans S.K.;
Paton V.G., Shackelford V.E., Krieans S.K.;
Cloning and subcellioral localization of hamster and rat isopentenyl diphosphate dimethylallyl diphosphate isomerase. A PTSI motif targets the enzyme to peroxisomes.";
J. Biol. Chem. 272:18946-18950(1997).
J. PHOLI CHALYZES THE 1,3-ALLYLIC REARRANGEMENT OF THE HOMOALLYLIC SUBSTRATE ISOBERTENT IN THE THIGHLY ELECTROPHILIC ALLYLIC ISOMEN DIMETHYLALLYL DIPHOSPHATE (DMAPP).
--- CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
130opentemyl-diphosphate delta-isomerase 1 (EC 5.3.3.2) (IPP isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00293; NVDIX; 1.
Probom; PD004109; IPP isomerase; 1.
Carotenoid biosynthesis; Cholesterol biosynthesis;
Isoprene biosynthesis; Sterol biosynthesis; Isomerase; Peroxisome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranidaa; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0004366; F:glycerol-3-phosphate O-acyltransferase acti.
GO; GO:000864; P:phospholipid biosynthesis; IDA.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; PlaC; 1.
Hypothetical protein; Transmembrane.
TRANSMEM 31 55
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                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 1; Length 743;
Pred. No. 21;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                               84B9946E56B82F15 CRC64;
                                                                                                                                                                                    Transmembrane.
SPOTENTIAL.
POTENTIAL.
POTENTIAL.
4 POTENTIAL.
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interPro; IPR000086; NUDIX_hydrolase.
                                                                                                                                                                                                           31 55 PO
69 85 PO
502 524 PO
539 555 PO
743 AA; 83644 MW;
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                                                                                                                                                                                                                                                                                                                                                                                            64.3%;
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1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                   DPHB OR MTH1874.
                                                                                                                                                             DPHB METTH
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                                                                                                                 RESULT 11
DPHB_METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAINE-BELEA H;

A SMITH D.R., DOUCETEE-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
Addredge T., Bashirzadeh R., Blackelly D., Cook R., Gilbert K.,
Addredge T., Bashirzadeh R., Blackelly D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
A gadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jamin N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
McDougall S., Shimer G., Goyal A., Patwell D., Prabhakar S.,
McDougall S., Shimer G., Goyal A., Petrovski S., Church G.M.,
McDougall S., Shimer G., Goyal A., Petrovski S., Church G.M.,
McDougall S., Shimer G., Goyal A., Petrovski S., Church G.M.,
McDougall S., Shimer G., Goyal A., Petrovski S., Church G.M.,
McDougall S., Shimer G., Goyal A., Petrovski S., Church G.M.,
McDougall S., Shimer G., Goyal A., Petrovski S.,
McDougall S., Shimer Composed of a glutamine amidotransferase
C. -- PATHWAY: GMP synthase subunit (B) (Potential).
C. -- SIMILARITY: Belongs to the GMP synthase family.
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (EC 6.3.5.2) (GMP
                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_00345; -; 1.
InterPro; TRR001674; GMP_synth_C.
Pfam; PF00958; GMP_synt_C; 1.
LigRPAMs; TIGR00884; guaA_Cterm; 1.
Ligase; GMP blosynthesis; Purine blosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 63.6%; Pred. No. 13; 7; Conservative 1; Mismatches 3; Indels
                                                                                                                 Score 35; DB 1; Length 227; Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 184 GMP-BINDING (BY SIMILARITY).
29 35 ATP (BY SIMILARITY).
308 AA; 34403 MW; F2DCF6ED202CAEC1 CRC64;
86 BY SIMILARITY.
148 148 BY SIMILARITY.
225 227 MICROBODY TARGETING SIGNAL.
227 AA; 26317 NW; FSOOA6586385E803 CRC64;
                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                      308 AA.
                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GÜAAB OR MTH710.
Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000850; AAB85215.1; ALT_INIT.
HSSP; P04079; 1GPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 40, Created)
                                                                                                                      62.5%;
                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                     121 EEVDPNEMHY 130
                                                                                                                                                                                                                      1 EEVVPXGMHY 10
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Best Local Similarity
Matches 7; Conserv
                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Delta H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetase)
                                                                                                                                                                                                                                                                                                                                                                                      GAAB METTH
ACT_SITE
ACT_SITE
SITE
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                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                026806;
                                                                                                                                                                                                                                                                                                                                          RESULT 10
GAAB_METTH
                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
Aldredge T., Bashirzadeh R., Blakely D., Cock R., Gilbert K.,
A Adredge T., Bashirzadeh R., Blakely D., Cock R., Gilbert K.,
A Adredge T., Bashirzadeh R., Blakely D., Cock R., Gilbert K.,
A Spadafora R., Vicare R., Wange Y., Wierzbowski J., Gibson R.,
A Jwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
Daniels G.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
T. Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
J. FUNCTION: Required for the methylation step in diphthamide
Diosynthesis (By similarity).
C. I. CARALYIIC ACTIVITY: S-adenosyl-L-henthionine + 2-(3-carboxy-3-aminopropyl)-L-histidine = S-adenosyl-L-homocysteine + 2-[3-carboxy-3-(methylammonio)propyl]-L-histidine.
C. I. PATHWAY: Diphthamide biogynthesis, second step.
J. SIMILARITY: Belongs to the diphthine synthase family.
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                                                                                                                                                                                                                                                        10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last amnotation update)
Probable diphthine synthase (RC 2.1.1.98) (Diphthamide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanobacterium thermoautotrophicum.
Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales,
Methanobacteriaceae, Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.7%; Score 34; DB 1; Length 264; 62.5%; Pred. No. 18; 1; Indels iive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Methyltransferase; Complete proteome.
SEQUENCE 264 AA; 28858 MW; 366BAB4B4D992C21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426 AA.
                                                                                                                                                                                    264 AA
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PIR, 669117; 669117.
HAMAP; MF 01084; -; 1.
InterPro; IPR000878; Cor/por_Metransf.
InterPro; IPR004551; Dphthn_gynthase.
Pfam; PF00590; TP methylase; 1.
IIGRFAMS; TIGR00522; dph5; 1.
                                                                                                                                                                                    PRT;
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SLS1_YARL1
ID SLS1_YARL1 STANDARD; 1
AC Q99158;
DT 01-NOV-1997 (Rel. 35, Created)
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216 EEVVESGLHES 226
                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 VVPAGLHF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                    methyltransferase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=187420;
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Jancet 361:743-749(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363
419
441 AA;
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                                                                                                                    McCarter L.L.;
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TRANSMEM
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TRANSMEM
TRANSMEM
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PHSL DESBA
           SOLUTION STATEMENT OF STATEMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                               STRAIN-ATCC 20460 / W29;
MEDLINE=96216076; PubMed=8662639;
MEDLINE=96216076; PubMed=8662639;
Boistane A., Beckerich J.-M., Gaillardin C.;
Boistane A., Beckerich J.-M., Gaillardin C.;
Boistane A., Beckerich T.-M., Gaillardin C.;
Brotein translocation process in the yeast Yarrowia lipolytica.";
J. Biol., Ghem. 271-11668-11675(1996).
-i- FUNCTION: Involved in the protein translocation process. May interact directly with translocating polypeptides to facilitate their transfer and/or help their folding in the ER. It is not required for viability but is essential for optimal growth at elevated temperatures.
-i- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=RIMD 210633 / Serotype 03:K6;
MEDLINE=22508454; PubMed=12620739;
MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasuunaga T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLS1 PROTEIN.
PREVENT SECRETION FROM ER (POTENTIAL).
, 0ACD7EF17540B8E2 CRC64;
                                                                                   Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales;
Vibrionaceae, Vibrio.
VCBL_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.7%; Score 34; DB 1; Length 426; 44.4%; Pred. No. 30; ive 4; Mismatches 1; Indels
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SLS1 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein VP2115 (ORF3) VP2115.
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InterPro; IPR00886; ER target_S.
PROSITE; PS00014; ER TARGET; 1.
Endoplasmic reticulum; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47201 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z50154; CAA90516.1; -. PIR; S58132; S58132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 44...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::|:| |:|
52 DQVIPAGLH 60
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426 AA;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=4952;
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01-03N-1990 (Rel. 13, Created)
10-03N-1990 (Rel. 13, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Periplasmic [NiFeSe] hydrogenase large subunit (EC 1.12.99.6) (NiFeSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hydrogenlyase large chain).
Besulfoblemicrobium baculatus).
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfomicrobiaceae; Desulfomicrobium.
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                                                                                                                  "Moty, a component of the sodium-type flagellar motor.";
d. Bacteriol. 176:4219-4255(194).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: STRONG, TO H.INFLUENZAE H10325.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513 AA.
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EMEL; U06949; AAAA271.1; -.
InterPro; IPR004770; Antiport nhac.
InterPro; IPR001991; Na/dico Symport.
Pfam, PF03523; Na Hantiporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS, PROOL/3; EDTRNSPORT.
Hypothetical protein; Transmembrane;
TRANSMEM 21 41 POTENTIA
                                                            MEDLINE=94292449; PubMed=8021208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45961 MW;
SEQUENCE OF 1-140 FROM N.A.
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Best Local Similarity 54.5
Matches 6; Conservative
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297 PGGLHYS 303
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513 AA;
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                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                        MEDLINE=99306038; PubMed=10378275;

MEDLINE=99306038; PubMed=10378275;

MEDLINE=99306038; PubMed=10378275;

MEDLINE=99306038; PubMed=10378275;

Fontecilla-Camps J.C.;

"Removal of the bridging ligand atom at the Ni-Fe active site of linkel hydrogenase upon reduction with H2, as revealed by X-ray structure analysis at 1.4-A resolution.";

Structure 7:557-566(1999);

-!-COPALYITIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor.

-!-COPACTOR: Nickel, 2 irrom and selenocysteine. Iron 1 has three cyanide and carbon monoxide ligands. Iron 2 has three water ligands.

-!-COPACTOR: Nickel, 2 irrom and selenocysteine. Iron 1 has three cyanide and carbon monoxide ligands. Iron 2 has three water ligands.

-!-COPACTOR: Nickel, 2 irrom and selenocysteine. Iron 1 has three cyanide and carbon monoxide ligands. Iron 2 has three water ligands.

-!-SUBUNIT: Heterodimer of a large and a small subunit.

-!-SUBCELIANEOUS: PERHAPS THE LEADER OF THE SMALL SUBUNIT SERVES AS A TRANSPORT VEHICLE FOR BOTH SUBUNITS.

-!-SIMILARITY: Belongs to the [NiFe]/[NiFeSe] hydrogenase large subunit family.
                                                                                                                                                                                                                                                                                                                                           EMBL; M18271; AAA23375.2; -.
DR EMBL; M18271; AAA23375.2; -.
DR PIR; A33101; HQDVLB.
DR PDB; 1CC1; 01-JUN-99.
DR InterPro; IPR001501; Ni hdi.
DR Pfam; PF00374; NiFeS Hases; 1.
DR PROSITE; PS00509; NI HGENASE L 1; 1.
W Oxidoreductase; Periplasmic; Metal-binding; Nickel; Iron; Selenium; T INIT MET 51 -.
T METAL 51 -.
T METAL 51 -.
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NICKEL.
IRON 1.
NICKEL.
IRON 2 (VIA CARBONYL OXYGEN).
NICKEL.
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 Bacteriol. 170:4429-4429(1988)
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58.9%; Score 33; DB 1; Length 513;
Best Local Similarity 71.4%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                               MUTL BACSU

1D MOTL BACSU

AC P49850,
DT 01-0CT-1996 (Rel. 34, Created)
DT 01-0CT-2096 (Rel. 42, Last sequence update)
DT 10-0CT-2096 (Rel. 42, Last sequence update)
DE DNA mismatch repair protein muth.
GN MUTL OR BSU17050.
GN BSU111us subtlise.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
56683 MW; AC8285A6F80576FC CRC64;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: This protein is involved in the repair of mismatches in DNA. It is required for dam-dependent methyl-directed DNA mismatch repair. May act as a "molecular matchmaker", a protein that promotes the formation of a stable complex between two or more promotes the formation of a stable complex between two or more DNA-binding proteins in an ATP-dependent manner without itself being part of a final effector complex (By similarity). SIMILARITY: Belongs to the DNA mismatch repair mutl/hexB family.
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PROSITE; PS00058; DNA MISMATCH_REPAIR_1; 1.
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EMBL; 299112; CAB13578.1; -.
PIR; A69663; A69663...
HSSP; P23367; 1BKN.
Subtilist; BG11402; mutL.
HAMAP; MF 00149; -; ITPbind AFPase.
InterPro; IPR002999; DNA_mis_repair.
PFam; PP01119; DNA_mis_repair; 1.
PFam; PP01119; DNA_mis_repair; 1.
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RA KUNDINES 9044031; Pubmace3384377;
RA KUNBILLES 9044031; Pubmace3384377;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boussier L., Brans A., Braun M., Briganell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brington J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Broizot P., Devine K.M., Dusterhoft A., Erhlich S.D., Emmerson P.T.,
RA Brian K.D., Errington J., Funes C., Galizzi A., Galleron N.,
RA Eritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Eritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Eritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Eritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Eritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mallado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Ropoport G., Rey M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
A Tasato V., Uchiyama S., Vandenbol M., Vanneberger T.,
RA Tosato V., Uchiyama S., Vandenbol M., Vanneberger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane C., Yamanoto R., Yamanoto R., Yamanoto B., Nobikawa H., Danchin A.,
RA Woshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H.P., Zumstein B., Roylius R., Waller B., Waller R., Waller R.
                                                                                                      MEDLINE=96349107; PubMed=8760914;
Ginetti F., Perego M., Albertini A.M., Galizzi A.;
"Bacillus subtilis mutS mutL operon: identification, nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                 sequence and mutagenesis:";
Microbiology 142:2021-2029(1996).
SEQUENCE FROM N.A.
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Score 33; DB 1; Length 627;
Pred. No. 71;
1; Mismatches 4; Indels
DNA repair; Complete proteome.
SEQUENCE 627 AA; 70431 MW; 068A0509CC265343 CRC64;
                                                                                                                                                                                                                              Search completed: June 3, 2004, 11:49:53 Job time: 4.86667 seca
                                                    Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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O8621 caenorhabdi
O8631 caenorhabdi
O8652 aspergillus
O990yc drosophila
O990yc drosophila
O990yc drosophila
O8911 brucella me
O8911 brucella me
O8052 mus musculu
O8711 drosophila
O12479 eaccharomyc
Q8ppg xanthomonas
O8444 candidatus
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Q8pib0 xanthomonas
O99011 prototheca
Q96n44 homo sapien
                 29xvk4 caenorhabdi
29sa71 arabidopsis
Q8tz07 methanopyru
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SEQUENCE FROM N.A.
Strouberg R.;
Strouberg R.;
Strouberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032195; AAH32195.1; -
MGD; MG1.1915724; Tada31.
MG2; GO:0003515; F:lada31.
GO; GO:0005515; F:protein binding; IPI.
SEQUENCE 413 AA; 46621 MW; A9BBA1DC70CDA0D5 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 22, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence A1987856.
TADA31 OR 1110004819RIK.
TADA31 OR 110004819RIK.
Bukaryota, Metazoa, Ghordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae; Musinae
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Last sequence update)
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                                                                                                                                                                                  Q9KBA1
Q8CAL1
O16912
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Q9VQL7
Q12479
Q8P6P8
Q8KTQ4
Q9KDC1
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Q9RXN9
Q98HU6
Q9RW92
Q9XAM3
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(TrEMBLrel. 23, I
(TrEMBLrel. 25, I
 168 EEIPPLGKHYS 178
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                                                                         NCBI_TaxID=10090;
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01-MAR-2003
01-MAR-2003
01-OCT-2003
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ID Q8CP,
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DT 01-M
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 Q8K289
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Q8x2e2 thermocoga
Q9hlh8 thermocolasm
Q8dih0 synechococc
Q8ywp1 anabaens sp
Q3avk4 pisum sativ
Q5avk4 pisum sativ
Q5pc35 xylella fas
Q9pc35 xylella fas
Q9pc35 xylella fas
Q40479 nicotiana t
Q3wb7 hordetella
Q7wb7 bordetella
Q7wb23 bordetella
Q38317 lactobacilla
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q8K2B4
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Q8KWP1
Q9KWP1
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Q9PC35
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length: 2000000000
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1 EEVVPXGMHYS 11
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Match Length DB
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Maximum DB
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Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                             66.1%; Score 37; DB 16; Length 308; 75.0%; Pred. No. 34; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.1%; Score 37; DB 17; Length 322; 75.0%; Pred. No. 36; ative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
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Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                              Protease, Complete proteome.
SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 AA; 36918 MW; BBC239E71009D167 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Multidrug efflux transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9HIM8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last agquence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Glucose-fructose oxidoreductase related protein.
TA0250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 407:508-513 (2000).

EMBL, AL445063; CAC11395.1; -.

GO; GO:0016491; F:oxaldoreductase activity; IEA.

GO; GO:006118; P:oxalectron transport; IEA.

InterPro; IPR000683; GFO_IDH_MocA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 AA.
                                                                                                         GOO, GO:0016020; C:membrane; IEA.
GOO; GO:0016020; F:peptidase activity; IEA.
InterPro; IPR001107; Band 7.
InterPro; IPR001972; Stomatin.
PRINTS; PR00721; STOMATIN.
SMO0244; PHB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
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                EMBL, AE001819; AAD36885.1; -. PIR; A72207; A72207. TIGR; TM1822; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 75.0
Les 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
Nature 399:323-329(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VVPXGMHY 10
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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08DIHO
1D 08DIH
AC 01-M
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MEDLINE-99287316; PubMed=10360571;
MEDLINE-99287316; PubMed=10360571;
MERDINE-99287316; PubMed=10360571;
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., McHart D.H., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D. Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg B.L., Smith H.O., Venter J.C., Fraser C.M., Mite O., Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                     STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBL_TaxID=2336;
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                                                                                                                                                                                                                                                                                          Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AE016746; AA004476.1; -.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0004086; F:Carbamoyl-phosphate synthase activity; IEA.

GO; GO:0004086; F:Carbamoyl-phosphate synthase activity; IEA.

GO; GO:0004086; F:Carbamoyl-phosphate synthase activity; IEA.

GO; GO:0004867; F:Carbamoyl-phosphate synthase activity; IEA.

GO; GO:0004867; F:Carbamoyl-phosphate synthase activity; IEA.

GO; GO:0006876; P:nitrogen metabolism; IEA.

GO; GO:0006508; P:nitrogen metabolism; IEA.

GO; GO:0008866; P:nitrogen metabolism; IEA.

GO; GO:0018866; P:nitrogen metabolism; IEA.

GO; GO:0018866; P:nitrogen metabolism; IEA.
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Pred. No. 49;
2; Mismatches 2; Indels C
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UTV-2003 (TrEMBLrel. 24, Last annotation update)
FTSH protease activity modulator HFLK.
                             Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
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      Carbamoyl-phosphate synthase large chain
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TIGREAMS; TIGREDISS; CPSASE11_1rg; 1.
PROSITE; PSODS6; CPSASE 1; 2.
PROSITE; PSOD667; CPSASE 2; 2.
PROSITE; PSOD639; THIOL_PROTEASE_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR00543; Cara Lglu.
InterPro; IPR00543; CPase L
InterPro; IPR00540; CPase L
InterPro; IPR00540; CPase LD2.
InterPro; IPR00540; CPase LD3.
InterPro; IPR00540; CPase LD3.
InterPro; IPR004162; MGS ILCAP
Ffam; PP00289; CPSase L Chain; 2.
Pfam; PP00289; CPSase L Chain; 2.
Pfam; PP002189; CPSase L Chain; 2.
Pfam; PP002189; CPSase LD3; 2.
Pfam; PP02182; MGS; I
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Best Local Similarity 63...
7; Conservative
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SEQUENCE 1057 A
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Gaps 0

Q9X2E2 RESULT 3 Q9X2E2

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RESULT 8
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MEDLINE=20194806; PubMed=10732668;
Tauch A., Krieft S., Kalinowski J., Puhler A.;
Tauch A., Krieft S.,
"The 51,409-bp R-plasmid pTP10 from the multiresistant clinical
"The 50,409-bp R-plasmid pTP10 from the multiresistant clinical
"Solate Corynebacterium striatum M82B is composed of DNA segments
initially identified in soil bacteria and in plant, animal, and human
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SPECIES—C.xerosis; STRAIN=M82B;
MEDLINE=96117603; PubMed=8559800;
MEDLINE=96117603; PubMed=8559800;
Tauch A.; Kassing F., Kalinowski J., Puhler A.;
"The Corynebacterium xerosis composite transposon Tn5432 consists of two identical insertion sequences, designated iS1249, flanking the erythromycin resistance gene ermCX.";
Plasmid 34:119-131(1995).
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.1%; Score 37; DB 16; Length 10
63.6%; Pred. No. 1.2e+02;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64;
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208 AA; 23012 MW; PI504BEIECDE85A6 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (GCrA).
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EMBL; AF024666; AAG03390.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
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TIGRFAMS; TIGR00915; 2A0602; 1.
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Best Local Similarity 63.6
Matches 7, Conservative
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Pfam; PF00873; ACR
                                                                                          SEQUENCE FROM N.A.
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SEQUENCE 1044 AJ
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NCBI_TaxID=32046;
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SEQUENCE 20
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64.3%; Score 36; DB 2;

Query Match

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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X MEDIZINE-21595285; PubMed=11759840; Xuritz T., Sasamoto S., A Mareneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., A Mataneko T., Nakamura Y., Wolk C.P., Kuritz T., Kawashima K., Kimura T., A Kishida Y., Kohara M., Matsumoto M., Makazaki N., Kihmuro S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Basuda S., Sugimoto of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.", DNA Res. 8:205-213(2001).

R PIRJ, ABZ001; ABZ7729:1; -. R REMBL, ABO03806; BAB7729:1; -. R PIR, ABZ001; ABZ001.
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STRAIN=CV. Alaska;
MEDILINE=21231727; PubMed=11333309;
Sassa N., Matsushita Y., Nakamura T., Nyunoya H.;
"The Molecular Characterization and in situ Expression Pattern of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 protein; Complete proteome.
252 AA; 28831 MW; 925572DA5D1CA519 CRC64;
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Plant Cell Physiol. 42:385-394 (2001).
Plant Cell Physiol. 42:385-394 (2001).
EMBL; ABO48173; BB39155.1; -.
GO; GO:0009288; C:flagellum (sensu Bacteria); IEA.
GO; GO:000574; F:motor activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005199; P:structural molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Alr1563.
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Last sequence update)
Last annotation update)
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    Pred. No. 36;
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Best Local Similarity 50.00.
    Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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130 DVIPEGKHYA 139
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235 EMIVPAGLHF 244
                                                                                                                2 EVVPXGMHYS 11
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NCBI_TaxID=103690;
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QSYWP1
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R. Martins Gequence of the plant pathogen Xylella fastidiosa.";

R. Wanna, Adella M. Abratz. J. M. Sakars. J. M. Saya M.A., Satz M., Meidanis J., Setubal J.C., Sautal J. Sakars. J. J. Setubal J.C. Santal J. Sakars. J. J. Setubal J. Sakars. J. J.
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MEDLINE=22421331; PubMed=12533478;
Wan Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
Wan Sluys M.A., forlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
NCBI_TaxID=2371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein, Complete proteome.
SEQUENCE 156 AA, 17144 MW, D8358619C6671A5D CRC64;
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1-0TN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CO; GO:0005622; C:intracellular; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0005935; P:clemotaxis; IEA.
GO:0007165; P:signal transduction; IEA.
InterPro; IPR002545; CheW.
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Kanthomonadaceae, Kylella.
NCBI_TaxID=183190,
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Best Local Similarity
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R GO, GO:0005622; C:Intracellular; IEA.

R GO; GO:0006874; F:11gase activity; IEA.

R InterPro; IPR001357; BRCT.

R Pfan; PF005313; BRCT; 1.

R PARAT; SW00292; BRCT; 1.
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MEDLINE=96020672; PubMed=7476204;
MEDLINE=96020672; PubMed=7476204;
MOSES E.K., Good R.T., Sinistaj M., Billington S.J., Langford C.J.,
Rood J.I.;
"A multiple site-specific DNA-inversion model for the control of Ompl
phase and antigenic variation in Dichelobacter nodosus.";
Mol. Microbiol. 17:183-196(1995).
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45.5%; Pred. No. 1.5e+02;
tive 4; Mismatches 2; Indels
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Pred. No. 37;
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             InterPro; IPR001444; Flag_bb_rod.
InterPro; IPR005202; GRAS.
Pfam; PF03514; GRAS!
PF03TTE; P$00588; FLAGELLA BB ROD; 1.
SEQUENCE 819 AA; 90372 WW; 41B67BD6DC72ADFA CRC64;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-077-2003 (TrEMBLrel. 24, Last annotation update)
XF1950.
XF1950 Xylella fastidiosa.
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Bacteroides nodosus (Dichelobacter nodosus).
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55.6%;
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Best Local Similarity 45.5
Matches 5; Conservative
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hes 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     343 DDVVPTSLHFS 353
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                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMHYS 11
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21 IVPAGVHWS 29
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01-NOV-1996 (
01-JUN-2003 (
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Q57489;
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RESULT 10

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099C35 1D 099 DT 011 DT 011 DT 011 OS XF

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1 EEVVPXGMHY 10
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Q9LW50
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Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R., Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Teal S.M., Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J., Coutinho L.L., Kimura B.T., Ferro E.S., Harakava R., Kurames B.B., Marino C.L., Giglioti B., Abreu I.L., Alves L.M.C., do Amaral A.M., Bala G.S., Blanco S.R., Britco M.S., Cannavan F.S., Celestino A.W., da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T., Leoni S.G., Oliveira A.R., Rosa V.E. Ur., Sassaki F.T., Sena J.A.D., de Souza A.A., Turffi D., Tankumo P., Yanai G.M., Zaros L.G., Civerlo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids;
lamiids, Solanales, Solanaceae, Nicotiana.
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SEQUENCE FROM N.A.

STRAIN=BY4, TISSUE=Leaf;

STRAIN=BY4, TISSUE=Leaf;

MEDLINE=95276459; PubMed=7756828;

MEDLINE=95276459; PubMed=7756828;

MEDLINE=95276459; PubMed=7756828;

Tethylene-inducible DNA binding proteins that interact with an ethylene responsive element.";

Tethylene responsive element.";

Plant Coll 7:133-1821995).

R PIR; 702590; 702590.

R PIR; 702590; 702590.

R HSSP, 080337; 2GCC.

R TRANSPAC; T02654; Cinucleus; IEA.

GO; GO:0006354; Cinucleus; IEA.

GO; GO:0006355; Pirranscription of transcription, DNA-dependent; IEA.

GO; GO:0006355; Pirranscription of transcription, DNA-dependent; IEA.

R PRODA; PRO0147; APZ EMPREPELEMAT.

PRINTS; PRO0367; ETHREPELEMAT.

PROMADM: CONDENS FREEF: 1.
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                                                                                                                                                                                                                                                                   Kitajima J.P.; "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Kylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%; Score 35; DB 16; Length 156; 55.6%; Pred. No. 42; tive 3; Mismatches 1; Indels
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Tastidiosa.";

D. Bacteriol. 185:1018-1026(2003).

The Bacteriol. 185:1018-1026(2003).

GO, GO:0005622; C:intracellular; IEA.

GO, GO:0006931; P:chemotaxis; IEA.

GO, GO:000715; P:chemotaxis; IEA.

GO; GO:0007165; P:signal transduction; IEA.

Interpro; IPR002545; Chew.

PROSITE; PS30851; CHEW; I.

Hypotherical protein; Complete protecome.

SEQUENCE 156 AA; 17130 MW; D83583B9C6671A5D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
EREBP-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              llarity 55.6%;
Conservative
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Matches 6, Conservative
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SEQUENCE 233 AA; 2
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Matches 5; Conserv
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MEDLINE=22827954; PubMed=12910271;
Parkill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
Harris D.E., Holden M.T.G. Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Peltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Morberzak H., O'Neil S., Ormond D., Price C.,
Rabbinowitsch E., Rutter S., Sanders M., Seaunders D., Seeger K.,
Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005634, C:nucleus; IEA.
GO; GO:0005634, C:nucleus; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:000471; TE RRP.
Pfam; PF00847; AP2-domaIn; 1.
PRINTS; PR00367; ETHRSPELEMNT.
PRODOM; PD001423; TE FRY.
SMART; SM00380; AP2; I.K.
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.5%; Score 35; DB 10; Length 237; 60.0%; Pred. No. 66; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 AA; 26243 MW; 01BC3EB51E46298 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                   237 AA
                                                                                                                                             Created)
                                                                                                                                                                                                                                                Nicotiana sylvestris (Wood tobacco)
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                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel, 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60...
6; Conservative
                                                                                                     PRELIMINARY;
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90 OAVVPKGRHY 99
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 52 / ATCC BAA-587;

MEDLINE=2287594; PubMed=12910271;

MEDLINE=22875954; PubMed=12910271;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach T.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach T.,

A Achtman M., Atkin R., Baker S., Sander B., Doggett J.,

Relivell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Babinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Babinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Babinowitsch E., Rutter S., Sanders M., Saunders S., Stevens K.,

Bunnin L., Whitchead S., Barrell B.G., Maskell D.J.,

"Comparative analysis of the genome sequences of Bordetella pertussis,

R Bordetella parapertussis and Bordetella bronchiseptica.",

BMBL, BK640425; CAR40321.1; -.

SARABL, BK640425; CAR40321.1; -.
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Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
"Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertussis and Bordetella bronchiseptica.";
Nat. Genet. 35:32-40(2003).
EMBL: BX640440; CAE31621.1; -.
CCMD1ete proteome.
262 AA; 28907 WW; B3CA29331CB776B2 CRC64;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBL_TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 16; Length 262;
Pred. No. 73;
1; Mismatches 2; Indels
                                                                                                                                              62.5%; Score 35; DB 16; Length 262; 66.7%; Pred. No. 73;
                                                                                                                                                                                        2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative enoyl-COA hydratase.
                                                                                                                                                                                                                                                                                                                                                               262 AA
                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                             PRT;
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Best Local Similarity 66.7%
....has 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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182 QEVVPYGQH 190
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182 QEVVPYGQH 190
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Hepatitis Hepatitis Hepatitis Hepatitis

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                   Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
                                                                                                                                                                                                                                                                                                                                                                                  note= "N-terminal acetyl"
                                                                                                                                                                                                   ALI GNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Oxymethionine"
ABB80558
ABB80550
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                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                ABB80561 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-2000; 2000US-0220101P
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lim-Wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-361643/39
Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                 Synthetic
ABB80561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protease
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 Abb80561 Hepatitis
Abb80524 Hepatitis
Abb80529 Hepatitis
Abb80542 Hepatitis
Abb80543 Hepatitis
Abb80543 Hepatitis
Abb80543 Hepatitis
Abb80543 Hepatitis
Abb80548 Hepatitis
Abb80521 Hepatitis
Abb80521 Hepatitis
Abb80557 Hepatitis
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67.664 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                   otal number of hits satisfying chosen parameters:
                                                                                                                                                                 1586107 segs, 282547505 residues
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Listing first 45 summaries
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11: geneseqp1980s:*
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha **etocamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Norvaly1 carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                                            ABB80524 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                               /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
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llarity 100.0%; Pred. No. 0.0024;
Conservative 0; Mismatches 0; Indels
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Norvaly1 carbony1 forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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                                                       ABB80528 standard; peptide; 11 AA.
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RESULT 4
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.
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cive 0; Mismatches 0;
                                                                                                                                                                    'note= "N-terminal acetyl"
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Matches 11, Conservative

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ð g RESULT 5 ABB80562 ID ABB80562 standard; peptide; 11 AA.

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha **Etoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                         /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22
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90.9%; Pred. No. 0.023;
iive 0; Mismatches
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residue 7"
                                             "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.023;
0; Mismatches 1
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                       'note= "N-terminal acetyl"
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                                                             residue 7"
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Best Local Similarity 90.9
Matches 10; Conservative
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Length 11; 1; Indels Ŋ

19-JUL-2001; 2001WO-US023169

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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/note≂ "C-terminal amide"
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                             /note= "D-form residue"
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les 10; Conservative
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Misc-difference 9
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                                                                                                                      ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
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virucide.
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Pred. No. 0.036;
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                                21-JUL-2000; 2000US-0220101P
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                                                       (CORV-) CORVAS INT INC
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Claim 17; Page 64; 69pp; English.
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inhibitory activity. The peptides of the
  hepatitis C virus (HCV) protease inhibitory activity. The peptides of invention are alpha-ketoamide peptide analogues. The peptides have viruside activity, and are useful for treating and in the manufacture a medicament to trant disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredits useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.036;
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                                                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.036;
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                                                                                                                                                         Claim 17; Page 65; 69pp; English.
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                               WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 10; Conserv
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                 carbonyl forming keto-amide linkage with
                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
                                                                                                                                                                            "N-terminal acetyl"
                                                                                                                                                                                                                                                              "C-terminal amide"
                                                                                                                                                                                                                                      note= "D-form residue"
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sequence represents a peptide compound of the invention having

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ABB80547;

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virucide.

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'note= "2-aminoisobutyryl carbonyl residue forming a keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
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                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
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Pred. No. 0.036;
0; Mismatches
                                                                                                                                                                                                                                                             'note= "N-terminal acetyl"
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/note= "C-terminal amide"
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                   ABB80566 standard; peptide; 11 AA
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90.9%;
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Best Local Similarity 90.9
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                                                  ABB80566;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
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                                   Gaps
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   DB 5; Length 11; 0.036;
                                 1; Indels
   Score 46; DB E
Pred. No. 0.036
0; Mismatches
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 85.2%;
90.9%;
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                 Similarity 90.9
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketchande peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                       /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                          note= "N-terminal acetyl"
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                                                                                        Synthetic.
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is useful for treating disorders associated with hepatitis C virus

Sequence 11 AA;

Query Match

Best Local Similarity 90.9%; Pred. No. 0.036;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps

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es 10; Conservative 1 EEVVPXGMDYS 11

1 EEVVPXGMDYS 11 ||||||| ||| 1 EEVVPXGSDYS 11

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Search completed: June 3, 2004, 11:48:23 Job time: 45.9333 secs Appli Appli Appli Appli Appli Appli Appli Appli Appl

Sequence Sequence Sequence

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parent 4, Application US/08853948B

parent No. 6210943

parent OF INVENTION: THE SAME

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prize PREPRENCE: 0049-0235-0

current Print OF INVENTION NUMBER: US/08/853,948B

current Print OF THOS: 1097-05-09

current Print OF SEQ ID NOS: 10

software Parent Nos: 10

software Parent Nos: 2.1

software Parent Nos: 10

software Parent Nos: 10

software Parent Nos: 10

software Parent Nos: 10

current Nosemarion: Carlo Man, Asp,

current Nosemarion: Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe,
                                                                                                                                                                                                                                                                                                                                                                                                           ## SEQUENCE 4848 Application US/09134000C

| Sequence 4848 Application US/09134000C
| Patent No. 6617156
| GENERAL INFORMATION:
| APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
| CURRENT APPLICATION NUMBER: US/09/134,000C
| CURRENT PILING DATE: 1998-08-13
| PRIOR APPLICATION NUMBER: US 60/055,778
| PRIOR PILING DATE: 1997-08-15
| SOFFWARE PER PATENTION NUMBER: US 60/055,778
| SEQ ID NOS: 6812
| SEQ ID NO 4848
| LENGTH: 181
                                                                                                                                                                           Sequence 20, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 4
Patent No.
Sequence 2
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Sequence
Sequence
Sequence
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Pred. No. 11;
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US-08-560-584-23

US-08-460-694-4

US-08-460-744-4

US-08-19-977-7

US-08-19-977-7

US-08-46-517-21

US-08-464-517-21

US-08-464-517-21

US-08-464-517-21

US-08-464-517-22

US-08-464-517-22

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US-08-464-517-22

US-08-464-517-22

US-08-464-517-22

US-08-464-517-22

US-08-463-772-22

US-08-926-842B-21

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0; Mismatches
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Best Local Similarity 70.0%;
Matches 7; Conservative
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Sequence 9, Appli
Sequence 76, Appl
Sequence 82, Appl
Sequence 31637, A
Sequence 4, Appli
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Sequence 4, Appli
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                                                                                                                    June 3, 2004; 11:36:47; Search time 11.7333 Seconds (without alignments) 48.399 Million cell updates/sec
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3: /cgn2 = fptodata/2/iaa/6A_COMB.pep:*
4: /cgn2 = fptodata/2/iaa/6B_COMB.pep:*
5: /cgn2 = fptodata/2/iaa/PcTUS_COMB.pep:*
6: /cgn2 = fptodata/2/iaa/PcTUS_COMB.pep:*
                       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-853-9488-4
US-08-853-9488-5
US-09-697-367-24
US-09-997-367-24
US-08-718-777-7
US-08-718-777-7
US-09-934-272-8
US-09-394-272-8
US-09-394-272-8
US-09-394-272-8
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US-08-963-851-14
US-09-540-236-2677
US-09-134-000C-4318
US-08-070-165F-8
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US-08-569-147-82
US-09-252-991A-31637
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                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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54
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Match Length
                                                                                                                                                                                        litle:
Perfect score:
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                                                                                         M protein
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                                                                                                                                                                                                                          sequence:
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US-08-429-054A-11
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                                      US-09-394-272-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                           APPLICANT: AKTHAMA, TOYOTA
APPLICANT: AKTHAMA, TOYOTA
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 0049-0235-0
CURRENT APPLICATION NUMBER: US/08/853,948B
CURRENT APPLICATION NUMBER: 197-05-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
ENGTH: 348
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Pred. No. 24;
2; Mismatches 1; Indels
                                                     Length 341;
                                                                                        1; Indels
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GENERAL INFORMATION:
APPLICANT: Calmi, Perry G.
APPLICANT: Tarczynski, Mitchell
APPLICANT: Tarczynski, Mitchell
APPLICANT: Tarczynski, Mitchell
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: BB1166 US NA
CURRENT FILING DATE: 2000-10-26
PRIOR PPLICATION NUMBER: 60/084,529
PRIOR FILING DATE: 1998-MAY-07
PRIOR FILING DATE: 1998-MAY-07
PRIOR FILING DATE: 1999-WAY-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENTH: 368
; OTHER INFORMATION: Pro, Ser, Thr, Trp, Tyr, or Val
US-08-853-948B-4
                                                     Score 36; DB 3;
Pred. No. 22;
2; Mismatches
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Sequence 24, Application US/09697367
Patent No. 6323015
                                                                                                                                                                                                                                        Sequence 5, Application US/08853948B
Patent No. 6210943
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                                                     Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative ;
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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; ORGANISM: Citrus unshiu
US-08-853-948B-5
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234 VIPPGMDFS 242
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228 VIPPGMDFS 236
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; ORGANISM: Zea mays
US-09-697-367-24
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US-08-853-948B-5
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435 VIPPGMDFS 443

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                                                                                                                                                                                                                                   Score 36; DB 2; Length 1068;
Pred. No. 81;
2; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC compatible
COMPUTER: Elb PC compatible
COMPUTER: DEADLE PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,777
FILING DATE: NOT YET ASSIGNED
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/175,471
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BALDATA RAG-VENTER
REGISTRATION NUMBER: 32,750
RESTRATION NUMBER: 32,750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Unido, D.
APPLICANT: Lando, D.
APPLICANT: Lando, D.
APPLICANT: Bruneau, J. M.
APPLICANT: Gervais, M.
TITLE OF INVENTION: MODIFICATION OF SUCROSE TITLE OF INVENTION: PHOSPHATE
TITLE OF INVENTION: SYNTHASE IN PLANTS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESSES: ADDRESSES: Law Offices of Barbara Rae-Venter STRET: Eds Ableidan Avenue, Suite 440
CITY: Palo Alto
CITY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08718777
Patent No. 5981852
                         11:
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         66.7%;
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amino acid
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                LENGTH: 1068
TYPE: Amino acid
STRANDENESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
JS-08-429-054A-11
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   435 VIPPGMDFS 443
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3 VVPXGMDYS 11

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453 VIPPGMDFS 461
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; ORGANISM: Oryza sativa
US-09-394-272-9
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COUNTRY: U.S
TATE: TO S
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TOPOLOGY: 1:
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US-09-394-272-4

US-09-394-272-4

Sequence 4, Application US/09394272

Sequence 4, Application US/09394272

Sequence 4, Application US/09394272

GENERAL INSORMATION:

APPLICANT: Haigler, Candace H.

APPLICANT: Haigler, Candacy A. Scott

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT APPLICATION NUMBER: US/09-10

; SOFTWARE: PatentIn Ver. 2.0

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

LENGTH: 1081

TYPE: PRT

CREANISM: Craterostigma plantagineum
US-09-394-272-4
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Patent No. 6472586

GENERAL INFORMATION:
APPLICANT: Holdler, Candace H.
APPLICANT: Holday, A. Scott

TITLE OF INVENTION: TRANSCENIC FIBER PRODUCING PLANTS WITH INCREASED FILE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 11 Voc. 2.0
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                                                                                                                                                    Query Match 66.7%; Score 36; DB 4; Length 1068; Best Local Similarity 66.7%; Pred. No. 81; Matches 6; Conservative 2; Mismatches 1; Indels
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Pred. No. 83;
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LENGTH: 1083

TYPE: PRT

OCGANISM: Arabidopsis thaliana
US-09-394-272-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1068
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                                                             ; TYPE: PRT
; ORGANISM: Zea mays
US-09-394-272-8
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US-09-394-272-11
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Search completed: June 3, 2004, 12:03:08
Job time : 12.8 secs
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31637
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US-09-252-991A-31637
Squence 31637, Application US/09252991A
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: 10996.136
CURRENT FILING DATE: 1099-02-18
SPIOR FILING DATE: 1998-02-18
SPIOR FILING DATE: 1998-02-18
SPIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31637
LENGTH: 1065
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SEQUENCE 82, Application US/08569147

Sequence 82, Application US/08569147

PACENT NO. 6180377

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: HUMANISED ANTIBODIES

NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 61803771s, LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia Place - 46th Floor

CITY: Philadelphia Place - 46th Floor

STREET: DA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IS PROPRY disk

COMPUTER: DA

COMPUTER: Barentin Release #1.0, Version #1.25 (EPO)

SOFTWARE: Pacentin Release #1.0, Version #1.25 (EPO)

CURSENT APPLICATION DATA: 356

CLASSIFICATION STREET 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.0%; Score 34; DB 3; Length 140; Best Local Similarity 75.0%; Pred. No. 20; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
JS-08-569-147-82
                                                                                                       122 VVPTGFDY 129
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Query Match 63.0%; Score 34; DB 4; Length 1065; Best Local Similarity 85.7%; Pred. No. 2e+02; Matches 6; Conservative 0; Mismatches 1; Indels
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FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
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                                                                                                                              June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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Sequence 26,
Sequence 27,
Sequence 5,
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Sequence 31,
Sequence 32,
Sequence 35,
Sequence 40,
Sequence 40,
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Sequence 13
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Sequence 9,
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/NEW_PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-12
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US-09-909-164-25
US-09-909-164-26
US-09-909-164-5
US-09-909-164-5
US-09-909-164-9
US-09-909-164-10
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                                                                                                                                                                                                                                                                                                                                                                                              1155919 seqs, 281338677 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
Sequence:
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45	46	47	48	49	20	57	22	,	17	17	18	13	20	23	24	21	25	28	29	33	36	37	43	30	34	38	9	42	44
Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence		Sequence	Sequence	Seguence	Seguence	Sequence	Seguence
-09-909-164-4	-09-909-164-4	US-09-909-164-47	19-909-164-4	i.	39-909-164-5	19-909-164-5	39-909-164-	19-909-164-	19-909-164-	31-606-60	19-909-164-1	19-909-164-	19-909-164-2	19-909-164-	19-909-164-2	-909-16	19-909-164-2	09-909-164-2	19-909-164-2	19-909-164-3	09-909-164-3	-909-164-3	19-909-164-	39-909-164-3	9-1	-09-909-164-3	-09-909-1	US-09-909-164-42	-09-909-164-4
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## ALIGNMENTS

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Sequence 8, Application US/0990164
; Sequence 8, Application US/0990164
; Publication No. US20020068702A1
; Publication No. US20020068702A1
; GENERAL INPORMATION:
; APPLICANT: Lim-wilby, Marguerita
; APPLICANT: Lim-wilby, Marguerita
; APPLICANT: Lim-wilby, Marguerita
; APPLICANT: Brunck, Terence K
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; TITLE OF INVENTION NUMBER: US/09/909,164
; CURRENT APPLICATION NUMBER: 00/220,101
; RICR APLICATION NUMBER: 60/220,101
; RICR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
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NAME/KEY: MOD RES
LOCATION: (1) . (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6) . (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC FEATURE
LOCATION: (9). . . (9)
OTHER INFORMATION: D-amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: artificial sequence
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US-09-909-164-22

Sequence 22, Application US/0909164

Sequence 22, Application NG/0909164

Sequence 22, Application NG-02020068702A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: NGVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
FRIOR PILING DATE: 2003-07-21
FRIOR PILING DATE: 2000-07-21

NUMBER OF SEC ID NOS: 62

SOFTHAMER: PATCHIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 96.3%; Score 52; DB 12; Length 11; 1 Similarity 100.0%; Pred. No. 0.00097; 11; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VETRION 3.1
LENGTHARE: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
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CTHER INFORMATION: D-amino acids
US-09-909-164-13
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OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
PEATURE:
                                                                                                                                                                                                                 TYPE: PRT ORGANISM: artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMDYS 11
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NAME/KEY: MISC FEATURE
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Matches 11, Conserva
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FEATURE:
NAME/KEY: MOD RES
TON: (11)...(1
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NAME/KEY: MOD_RES
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LENGTH: 11
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US-09-909-164-12

Sequence 12, Application US/09909164

Sequence 12, Application No. US20020068702A1

SEDENAL No. US20020068702A1

SENERAL Timeraminomal, Inc.

APPLICANT: Lim-Wilby, Marguerita

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PatentIn version 3.1

SEQ ID NO 12

LENGTH: Lim-Wilby, Marguerita

Marguerita Marguerita

SEQ ID NO 12

LENGTH: Lim-Wilby, Marguerita

Marguerita Marguerita

SEQ ID NO 12
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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                                                                             Query Match 96.3%; Score 52; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.00097; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 96.3%; Score 52; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.00097; Matches 11; Conservative 0; Mismatches 0; Indels
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(WS-09-909-164-13
(S-09-909-164-13)
(Sequence 13, Application US/09909164
(Publication No. US20020068702A1
(GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE
LOCATION: (8) ...(8)
CTHER INFORMATION: D-amino acid
US-09-909-164-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) ...(1)
OTHER INFORMATION:
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ORGANISM: artificial sequence
; OTHER INFORMATION: AMIDATION
US-09-909-164-8
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Sequence 5, Application US/09909164

Sequence 5, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Corvae International, Inc.
APPLICANT: Lim-whibby, Warguerita
APPLICANT: Lim-whibby, Warguerita
APPLICANT: Lim-whibby, Warguerita
APPLICANT: Lim-whibby, Warguerita
FPLE NOT INVENTION: NOVEL PEFTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENCE: IN01129-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTH VERSION 3.1
SEQ. ID NO 5:
FILE REVERSED TO NOS: 62

SOFTWARE: PATENTH VERSED TO NOS: 62

SOFTWARE: PATENTH VERSED TO NOS: 62

MANGER OF SEQ ID NOS: 62
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PELING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 27
LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.0%; Score 47; DB 12; Length 11; 90.9%; Pred. No. 0.0097; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KRY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: D-amino acids US-09-909-164-27
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NAME/KEX: MOD RES
LOCATION: (1) ~ (1)
OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORWATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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US-09-909-164-26

US-09-909-164-26

Sequence 26, Application US/09909164

Publication No. US20020068702A1

Publication No. US20020068702A1

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby,
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11) ...(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                        Score 47; DB 12; Length 11; Pred. No. 0.0097; 0; Mismatches 1; Indels
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87.0%; Score 47; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 1; Indels
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
                OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                         FEATURE:
| NAME/KEY: MISC FEATURE
| IOCATION: (9).7(9)
| OTHER INFORMATION: D-amino acid
| US-09-909-164-22
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                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: artificial sequence
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ASQUENCE 10, Application US/09909164

Sequence 10, Application US/09909164

Publication No. US20200068702A1

GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Morel PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION NUMBER: US/09/909,164

PILE REFERENCE: IN01192-US
PRICA PILING DATE: 2003-03-25
PRICA PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 11
FYEE: PRT
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN version 3.1
SEQ ID NO 9
LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 11-mer synthesized according to example 1
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85.2%; Score 46; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC FEATURE LOCATION: (6)...(6) OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD_RES
LOCATION: (1)...(1)
CTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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1.OCATION: (8)..(8)

OTHER INFORMATION: D-amino acid

US-09-909-164-9
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: artificial sequence
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APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: 1001192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 11
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ORGANISM: artificial sequence
PEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
PEATURE:
NAME/KEY: MOD_RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
PEATURE:
NAME/KEY: MISC_PEATURE
LOCATION: (6) ... (6)
OTHER INFORMATION: norvaline-(CO)
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Pred. No. 0.015;
0; Mismatches 1; Indels
                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                       Score 46; DB 12;
Pred. No. 0.015;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, IT
APPLICANT: Lim-Wilby, Marguerita
       OTHER INFORMATION: norvaline-(CO) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KRY: MISC. PEATURE
LOCATION: (9) ...(9)
OTHER INFORMATION: D-amino acid
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                                                                                                                                                                  Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
US-09-909-164-6
                                                    NAME/KEY: MOD RES

LOCATION: (11)..(11)

CTHER INFORMATION: AMIDATION
US-09-909-164-5
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Best Local Similarity 90.9
Matches 10; Conservative
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US-09-909-164-9
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APPLICANT: Levy, Odile E

APPLICANT: Brunck, Terence K

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN01192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PLING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PATENTIN VEXEION 3.1

SEQ ID NO 32

TURNOTH: 11
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Sequence 35, Application US/09909164
Sebication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lin-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Extuck, Terence K
TITLE OF INVENTION: NOWEER: US/09/909,164
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ.ID NO 35
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COTHER INFORMATION: 11-mer synthesized according to example 1 FEATURE:
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , LUCATION: (9)...(9); OTHER INFORMATION: D-amino acid US-09-909-164-32
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: artificial sequence
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ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
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NAME/KEY: MOD RES
LOCATION: (11)..(:
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GENERAL INFORMATION:
Publication No. US20020068702A1
GENERAL INFORMATION:
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INOLY NUMBER: 00/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 46, DB 12, Length 11;
Pred. No. 0.015;
0, Mismatches 1; Indels
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Publication No. US20020068702A1
GENERAL INPORMATION:
APPLICANT: Corvas International, International
                                                                                                                                                                       FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                ; LOCATION: (8). (9); OTHER INFORMATION: D-amino acids JS-09-909-164-10
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPXGMDYS 11
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                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE
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LENGTH: 11
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas international, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lavy, Odile E
APPLICANT: Lavy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: 1001192-US
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 41
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) \( \text{L} \). (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) \( \text{L} \). (1)
OTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6) \( \text{L} \). (6)
OTHER INFORMATION: norvaline-(CO)
OTHER INFORMATION: norvaline-(CO)
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; OTHER INFORMATION: D-amino acids
US-09-909-164-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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| Sequence 40, Application US/09909164
| Sequence 40, Application US/09909164
| Sequence 40, Application US/2020068702A1
| Sequence 40, Application No. US20020068702A1
| Septicant No. Us20020068702A1
| APPLICANT: Lin-Whilby, Marguerita CURRENT APPLICATION NUMBER: US/09/909.164
| CURRENT APPLICATION NUMBER: 60/220,101 PRIOR APPLICATION NUMBER: 60/220,101 PRIOR FILING DATE: 2000-07-21 | NUMBER OF SEQ ID NOS: 62 | SOFTWARE: Patentin version 3.1 | SEQ ID NO 40 | LENCTH: LIN-WHILD APPLICATION NUMBER: CONTINUE APPLICATION NUMBER: CONTINUE APPLICATION NUMBER: MARGUERICA DE LA LENCTH: LIN-WHILD NO 40 | LENCTH: LENCTH: LIN-WHIL
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ORGANISM: artificial sequence
PRATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                            FEATURE:
NAME/KEY: NISC FEATURE
LOCATION: (8)..(8)
OTHER INFORMATION: D-amino acid
US-09-909-164-40
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; OTHER INFORMATION: D-amino acid
US-09-909-164-35
                                   OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.5
Matches 10; Conservative
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RESULT 15 US-09-909-164-41 ; Sequence 41, Application US/09909164

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sucrose-phosphate
                                                                   3, 2004; 11:35:47 ; Search time 9 Seconds
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117.567 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                         Potal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Match 1
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disease resistance	RND multidrug effl	hypothetical prote	hypothetical 367K	partial transposas	hypothetical prote	fibroblast growth	hypothetical prote	hypothetical prote	conserved hypothet	unknown protein [i	transposase ISC105	transposase ISC105	hypothetical prote	pantoate-beta-alan	transposase ISC105
T48899	F83335	T30830	T31308	A99427	A90471	S27021.	E90335	857810	A96001	A96546	F90298	C90307	C64417	G83055	E90487
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908	1062	1062	3472	97	128	172	184	225	247	257	262	267	276	283	299
63.0	63.0	63.0	63.0	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1
34	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33
30	31	32	33	34	35	36	3.7	38	9	40	41	42	43	44	45

## ALIGNMENTS

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                                        hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein O2612; hypothetical protein YOL303.3
(Species: Saccharomyces cerevisiae)
C.Species: O8-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
                                                                                                                                                                                                                   A;Accession: S54619
A;Accession: S54619
A;Molecule type: DNA
A;Residues: 1-156 - ODEH-
A;Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
R;Cross-references: ABRE:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
B;de Haan, M.; Grivell, L.A.; Maarse, A.C.
Submitted to the Protein Sequence Database, July 1996
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                                                                                                                                     C,Accession: S54619; S66879
R,de Haan, M.; Maaree, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A,Reference number: S54617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Superfamily: hypothetical protein YOR013w
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A; Map position: 15R
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Matches 7; Conser
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RESULT 1
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Conserved hypothetical protein AF2411 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: OS-Dec-1997 #sequence_revision OS-Dec-1997 #text_change 22-Oct-1999
C;Accession: D69551
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, G; Rischann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
A;Attle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

D69551

A,Accession: D69551 A,Status: preliminary, nucleic acid sequence not shown; translation not shown

Score 38; DB 2; Pred. No. 6.8; 3; Mismatches

Query Match Best Local Similarity 54.5%; Matches 6; Conservative

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Cipace: Usermar-Zoll meaguence_revision of particles of the Constant of States of Stat
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C; Superfamily: sucrose-phosphate synthase; sucrose-quorose-phosphate synthase homology
C; Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
                                                                                                                                         R;Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
wol. Gen. Genet. 252, 346-351, 1996
A;Title: Cloning and molecular analysis of CDNAs encoding three sucrose phosphate synth
A;Reference number: S72648; MUID:96439842; PMID:8842155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Cross-references: EMBL:AB006660; NID:g2351059; PIDN:BAA22071.1; PID:g2351060; Bxperimental source: fruit, cv. Miyagawa-Wase, Bxperimental source: fruit, cv. Miyagawa-Wase, Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
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C;Genetics:
                 sucrose-phosphate synthase (EC 2.4.1.14) isoform 3 - Citrus unshiu (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown protein F25P22.17 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                             0;Species: Citrus unshiu
2;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
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Pred. No. 23;
0; Mismatches 3; Indels
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234 VIPPGMDFS 242
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA; Residues: 1-348 < KOM>
                                                                                                                                                      C, Accession: S72650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetica:
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Matches
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A,Residues: 1-363 «KLE»
A,Cross-references: GB:AE001109, GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tobacco yelld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Pathway: sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Reywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;1-341/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Experimental source: fruit, cv. Miyagawa-Wase
Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VI protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A;Title: The nucleotide sequence of the infectious cloned DNA component of the factories number: A42452; MUID:92188538; PMID:1546458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A;Residues: 1-102 <MOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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Pred. No. 4.3;
3; Mismatches 1; Indels
                                                                                                                                                               Length 363;
                                                                                                                                                                                                                                            Indels
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Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative

A; Accession: A42452

2 EVVPXGMDYS 11 

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Best Local Similarity 66.7 Matches 6; Conservative

|:| |||:| 228 VIPPGMDFS 236 3 VVPXGMDYS 11

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Sucrose-phosphate synthase homolog F28Mil.40 - Arabidopsis thaliana C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: A.Apr.1999 #sequence_revision 30-Apr.1999 #text_change 16-Jul-1999
C'Accession: T04062
R'Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X Bubmitted to the Protein Sequence Database, March 1999
A'Reference number: Z15184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Accession: T04103
R;Sakamoto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Fujimura, T.
A;Title: Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS) gene that A;Reference number: 215212
                                                                                                                                                                                                                       A; Residues: 1-1081 <ING>
A; Residues: 1-1081 <ING>
A; Cross-references: EMBL:Y11795; NID:g2130349; PIDN:CAA72491.1; PID:g2130350
A; Experimental source: ABA-treated callus
C; Genetics:
A; Genetics: Bp2
C; Function:
C; Function: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
A; Pathway: sucrose biosynthesis
C; Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology
C; Reywords: glycosyltransferase; haxosyltransferase; sucrose-biosynthesis
F;176-674/Domain: sucrose-phosphate synthase homology <885>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 4
A; Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3; 9
A; Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3; 9
A; Note: PSSM11.40
C; Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology
F; 230-714/Domain: sucrose/sucrose-phosphate synthase homology <85PS>
lant Physiol. 115, 113-121, 1997
Title: Analysis of cDNA clones encoding sucrose-phosphate synthase in relation to suga
*Reference number: 216874; MUID:97451773; PMID:9306694
*Accession: T09837
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Pred. No. 60;
2; Mismatches 1; Indels
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A,Rebidues: 1-1083 <BEV>
A,Cross-references: EMBL:AL049487
A,Experimental source: cultivar Columbia; BAC clone F28M11
                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1081 <ING>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Cross-references: EMBL:D45890; PIDN:BAA08304.1
A;Experimental source: subsp. Japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.78;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 66.7
les 6, Conservative
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                              NyMolecule type: mRNA
NyResidues: 1-1049 <NDL>
NyResidues: 1-1049 <NDL>
NyMores references: GBL033175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
NyMores references: CBL033175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
NyMore: UDPGJucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDPglucosylt
Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          );Species: Zea maye (maize)
);Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
);Accession: JQ1329; PQ0260
];Accession: JQ1329; PQ0260
];Accession: JQ1329; PQ0260
];Accession: JQ1329; PQ0360
];Accession: JQ1329; PQ0338837; PMID:1840396
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!Residues: 71-74;206-212/471-481;872-892 <WOR1>
!Residues: 71-74;206-212/471-481;872-892 <WOR1>
!Comment: This enzyme transfers the glucosyl group from UDBglucose to fructose-6-phosph
;Comment: This enzyme is involved in the regulation of carbon partitioning in the leave
                                                                          \'valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella
sane 170, 217-222, 1996
\'variable for rice sucrose-phosphate synthase-encoding gene.
\variable richaracterization of a rice sucrose-phosphate synthase-encoding gene.
\variable rence number: JC4783; MJID:96235138; PMID:8666248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description: catalyzes the formation of sucrose-6-phosphate from UDFglucose and D-fruc Pathway: sucrose biosynthesis
Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
180-663/Domain: sucrose/sucrose-phosphate synthase homology <8SPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fru
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.)Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
.)Keywords: glycosyltransferase; hoxosyltransferase; sucrose biosynthesis
?;178-666/Domain: sucrose/sucrose-phosphate synthase homology <8SPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: Sps1
Introns: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3;
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.Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999
.Accession: JC4783
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v;Molecule type: mRNA
v;Residues: 1-1068 <MOR>
v;Cross-references: GB:M97550; NID:g168625; PIDN:AAA33513.1; PID:g168626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Length 1068;
Pred. No. 59;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ucrose-phosphate synthase (EC 2.4.1.14) - maize
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Best Local Similarity 66.7
Matches 6; Conservative
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436 VIPPGMDFS 444
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C; Species: Aeropyrum pernix
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C; Accession: H7279
R; Kawarabayasi, Y: Hino, Y: Horikawa, H: Yamazaki, S: Haikawa, Y:, Jin-no, K.; Takalawa, H: Takaniya, M.; Masuda, S: Funahashi, T:; Tanaka, T:; Kudoh, Y:, Yamazaki, J:;
DNA Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A; Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 5
A;Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AjStatus: preliminary
AjMolecule Vype: DNA
AjResidues: 1-440 «KAW»
AjRosaleues: 1-440 «KAW»
AjCross-references: DDBJ:APO00058; NID:g5103388; PIDN:BAA79178.1; PID:g5103657
AjExperimental source: strain Kl
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A;Molecule type: DNA
A;Residues: 1-1150 WA
A;Cross-references: EMBL:Z78015; PIDN:CAB01437.1; GSPDB:GN00023; CESP:C53A5.2
A;Experimental source: clone R02D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1150 <WIL>
A;Cross-references: EMBL:Z81486; PIDN:CAB03994.1; GSPDB:GN00023; CESP:C53A5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C53A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Apte: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20173; T23857
R;Mortimore, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                          probable alkaline proteinase APB0263 - Aeropyrum pernix (strain K1)
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64.8%; Score 35; DB 2; Length 1150;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h. Samilarity 64.8%; Score 35; DB 2; Length 440; Similarity 66.7%; Pred. No. 35; 6; Conservative 2; Mismatches 1; Indels
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submitted to the EMBL Data Library, August 1996
AFFefernece number: Z19808
A;Accession: T23857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: APE0263
C;Superfamily: subtilisin; subtilisin homology
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A; Accession: T20173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: H8760
C;Accession: H8760
B;Nicerman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, W.T.; DeBoy, R.T.; Dodson, R.J.; Dispiro, L.; Venter, J.C.; Fraser, C.M.
J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
A.Map position: 1
A.Introns: 120/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
A.Introns: 120/3; 200/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
C.Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C.Keywords: glycosyltransferase; hexosyltransferase
F:196-680/Domain: sucrose/sucrose-phosphate synthase homology <85PS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL: Z81109; PIDN: CAB03241.1; GSPDB: GN00023; CESP: R10D12.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein R10D12.10 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C.Accession: T24111 submitted to the EMBL Data Library, October 1996 A.Reference number: Z19842 A.Accession: T24111
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0
                                                                                                                                                                                                                         Query Match 66.7%; Score 36; DB 2; Length 1084; Best Local Similarity 66.7%; Pred. No. 60; Matches 6; Conservative 2; Mismatches 1; Indels
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64.8%; Score 35; DB 2; Length 425;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 <WIL>
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A;Map position: 5 A;Introns: 23/3; 56/3; 113/3; 257/2

A; Gene: CESP:R10D12.10

335 EQIVPGGLQY 344

RESULT 13

1 EEVVPXGMDY 10

Best Local Similarity 54.5 Matches 6; Conservative

A; Status: H87560
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-433 < STO>
A; Cross-references: C; Generin

A; Gene: CC3322

Query Match

266 EVILPPGFDYS 276

1 EEVVPXGMDYS 11

ò

Experimental source: clone R10D12

453 VIPPGMDFS 461

g

3 VVPXGMDYS 11

escherichia

thermotoga rattus norv homo sapien mus musculu brachydanio xenopus lae gallus gall xenopus lae

gallús gall homo sapien

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SEQUENCE FROM N.A.

SITAIN=ATCC 25586;

WEDITE=21886394; PubMed=11889109;

WEDITE=21886394; PubMed=11889109;

WEDITE=21886394; PubMed=11889109;

WEAPTIME=21886394; PubMed=11889109;

WEAPTIME=21886394; PubMed=11889109;

WEAPTIME V., Anderson I., Ivanova N., Grechkin G., Los T., Lykidis A., Battacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu La., Nogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein A., Kyrpides N., Overbeek R., Genome sequence and analysis of the oral bacterium Fusobacterium rucleatum strain ATCC 25586.";

"Genome sequence and analysis of the oral bacterium Fusobacterium plusphate + i-glutamate + carbamoyl phosphate.

"I Bacteriol. 184:2005-2018(2002).

"I CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + Diosphate + i-glutamate + carbamoyl phosphate.

"I PATHWAY: Pyrimidine biosynthesis."

"I PATHWAY: Pyrimidine biosynthesis."

"I PATHWAY: Pyrimidine biosynthesis."

"I SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRNGB6.

QB-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last sequence update)

Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).

CARB ON FN0422.

Pusobacterium nucleatum (subsp. nucleatum).

Bacteria; Fusobacteria; Fusobacterias; Fusobacteriaces;
                                          Q9wxrl
Q004821
P30279
P30280
P200459
P490755
P53786
P55169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1058 AA.
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-!- SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                CGD2_HUMAN
CGD2_MOUSE
CGD1_BRARE
CGD1_XENLA
CGD2_CHICK
                                                                                                                                                                                                                            CGD2_XENLA
CGD1_CHICK
CGD3_HUMAN
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InterPro; IPR006275; CarA L glu.
InterPro; IPR006543; CPase L D2.
InterPro; IPR005499; CPase L D2.
InterPro; IPR0054960; CPase L D3.
InterPro; IPR005491; CPase L D3.
InterPro; IPR004361; CPase L D3.
InterPro; IPR004362; MGS IIRe.
Pfam; PP002089; CPSase L Chain; 2.
Pfam; PF02786; CPSase L D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
\begin{array}{c} \mathbf{u} \, \mathbf{
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  RESULT 1
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  tobacco yel
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zea mays (m
craterostig
drosophila
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populus nig
borrelia bu
arabidopsis
arabidopsis
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homo sapien
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rattus norv
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vibrio chol
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xenopus lae
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                                                                                                                                                                               June 3, 2004, 11:32:06; Search time 4.86667 Seconds (without alignments) 117.693 Million cell updates/sec
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P31619
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P018284
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Q92bc5
Q8y6u8
Q04667
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141681 seqs, 52070155 residues
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PLAT POPNI
SYFB BORBU
SYFB ARATH
RPPB ARATH
RPSH ARATH
Y939 METJA
PANC PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARB_FUSNN
Y11K_TYDVA
SPS_ORYSA
SPS_MAIZE
SPSZ_CRAPL
FAF_DROME
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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4aximum DB seq length: 2000000000
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54
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Match 1
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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No.
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QVVPSGINYS 16

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                                                                                                                                                                                                                                                                                                                                                                                                  ö
R Pfam; PF02142; MGS; 1.

R RIGREAMS; TIGRO169; CPSase11 lrg; 1.

DR TIGREAMS; TIGRO169; CPSase11 lrg; 1.

DR PROSITE; PS00866; CPSASE 1; 2.

DR ROSITE; PS00867; CPSASE 2; 2.

KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KW Arginine biosynthesis; Complete proteome.

CARSOXYPHOSPHATE SYNTHETIC DOMAIN.

402 546 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

**TARTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92188538; PubMed=1546458;
Morits B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
"The nuclectide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                             12 ATP (POTENTIAL).
14 NANGANESE 1 (BY SIMILARITY).
18 MANGANESE 1 AND 2 (BY SIMILARITY).
10 MANGANESE 2 (BY SIMILARITY).
10 MANGANESE 3 (BY SIMILARITY).
117451 MW; ED7037AF77C1E39F CRC64;
                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Length 1058;
Pred. No. 9.4;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 1; Length 102;
Pred. No. 2.2;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, M81103, AAA47947.1; -.
PIR, A42452, A42452.
InterPro; IRR002621; Gemini_mov.
Pfan, PF01708; Gemini_mov; Ī.
Pypothetical protein.
SEQUENCE 102 AA; 11178 MW; A40ECFIEOAF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infecting monocotyledonous plants."; Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
01-GCT-1993 (Rel. 27, Last ann
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                    70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EVVPXGMDYS 11
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1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                    123033
23033
3008
2008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIIK_TYDVA
ID YIIK_TYDVA
AC P31619;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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REPEAT
REPEAT
NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                      Jene 170:217-222(1996).

-!- FUNCTION: Involved in the regulation of carbon partitioning in the leaves of plants. May regulate the synthesis of sucrose and therefore play a major role as a limiting factor in the export of photoassimilates out of the leaf.
-!- CAPALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP + sucrose 6-phosphate.
-!- ENZYME REGULATION: Activity regulated by phosphorylation and moderated by concentration of metabolites and light.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: Sucrose synthesis.
-!- SUBDNIT: Homodimer or homotetramer (By similarity).
-!- PTM: Phosphorylated. However, phosphorylation is not essential for enzyme function (By similarity).
-!- SIMILARITY: Belongs to the glycosyltransferase family 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                       (UDP-glucose-fructose-phosphare glucosyltransferase).
Oryza sativa (Rice).
Oryza sativa (Rice).
Subaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                      Herrera-Estrella L.; "Characterization of a rice sucrose-phosphate synthase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 36; DB 1; Length 1049; 66.7%; Pred. No. 24; 1; Indels 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1049 AA; 116455 MW; ED862E2819AA4B04 CRC64;
                                                                                                                                                                                                                                                      STEAIN-cv. Indica-IR36; TISSUE-Leaf;
MEDLINE-96235138; PubMed-8666248;
Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001296; Glyco trans 1.
Pfam; PF00534; Glycos transf 1; I.
Transferase; Glycosyltransferase; Phosphorylation.
DOMAIN
22
29
POLY-GLY.
                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1068 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@igb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-GLU.
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P31927;
01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U33175; AAC49379.1; -. PIR; UC4783; UC4783. Gramene; Q43802; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 VIPPGMDFS 444
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les 6; Conserv
                                 15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                        NCBI_TaxID=4530;
ORYSA
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SEQUENCE
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 SPS ORY
Q43802;
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SPS_MAIZE
                                                                                                                                                                                                                                                                                                                                                            gene.
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EVVPXGMDYS 11

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Gaps

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Lamiales; Lamiales incertae sedis; Lindernieae;

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DOMAIN
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                                                                                                                                                                                                                                                                    STRAINECV. PIONEER 3184; TISSUE=Leaf;

MEDLINE=9238837; PubMed=1840396;

MEDLINE=9238837; PubMed=1840396;

"Expression of a maize sucrose phosphate synthase in tomato alters

"Expression of a maize sucrose phosphate synthase in tomato alters

"Expression of a maize sucrose phosphate synthase in tomato alters

"Expression of a maize sucrose phosphate synthase in tomato alters

"I leaf carbohydrate partitioning.";

Plant Cell 3:1121-1130(1991).

"I plant Cell 3:1121-1130 (1991).

"I plant cell 4:1130 (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: Sucrose synthesis.
-!- SUBUNIT: Homodimer or homotetramer.
-!- DEVELOPMENTAL STAGE: Germinating seeds or mature leaves.
-!- PIM: Phosphorylated. However, phosphorylation is not essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craterostigma plantagineum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase 2 (EC 2.4.1.14) (UDP-glucose-fructose-phosphate synthase 2)
                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND 872-892.
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the glycosyltransferase family 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%; Score 36; DB 1; Length 1068; 66.7%; Pred. No. 25; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 1068 AA; 118575 MW; 074679B5E9A1D282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001296; Glyco_trans_1.
Pfam; PF00534; Glycos transf_1; T.
Transferase; Glycosyltransferase; Phosphorylation.
DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1081 AA.
                                                            phosphate glucosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M97550; AAA33513.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 6, Conservative
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435 VIPPGMDFS 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JQ1329; JQ1329.
                                                                                                                                                                                       NCBI_TaxID=4577;
                                                                                                       Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MaizeDB; 25294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPS2_CRAPL
ID SPS2_CRAPL
AC 004933;
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10.NOV-1997 (Rel. 35, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3.1.2.15)

[Ubiquitin thioleserase FAF) (Ubiquitin-specific processing protease FAF) (Debiquitin thioleserase FAF) (Ubiquitin-specific processing protease FAF) (Debiquitinating enzyme FAF) (Fat facets protein).

PAF OR BCDNA:LD22582 OR CG1945.

BLAF OR BCDNA:Anthropoda, Hexapoda; Insecta; Pterygota;

Bukaryota; Mctazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Behydroidea; Drosophilidae; Drosophila.
                                                                                                   MEDINE=97451773; PubMed=9306694; Ingram J., Bartels D.; Ingram J., Chandler J.W., Gallagher L., Salamini F., Bartels D.; Amanler G. Chandler G.W., Gallagher L., Salamini F., Bartels D.; Felation to sugar interconversions associated with dehydration in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMEL, Y11795, CAA72491.1; -.
EMEL, Y109837, T9887.
InterPro, IPR001296; Glyco_trans_1.
InterPro, IPR001396; Glycoo transf_1; 1.
Pfam; PF00534; Glycos transf_rase; Phosphorylation; Multigene family.
Transferase; Glycosyltransferase; Polyly-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 1; Length 1081;
Pred. No. 25;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     787 790 POLY-ARG.
1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 2778 AA.
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MEDLINE=93202020; PubMed=1295747;
Fischer-Vize J.A., Rubin G.M., Lehmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6, Conservative
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                                                                      FROM N.A.
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Craterostigma.
NCBI_TaxID=4153;
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                                                                            SEQUENCE
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SEQUENCE OF 1089-2778 FROM N.A. (ISOFORM 1).

SEQUENCE OF 1089-2778 FROM N.A. (ISOFORM 1).

KEDLINE=20196012; PubMed=10731138;

RUDIN G.M., Hong L., Brokstein P., Evans-Holm M., Frise B.,

Stapleton M., Harvey D.A.;

T. A Drosophila complementary DNA resource.";

"A Drosophila could play a role in pole cell determination, development or MEDLINE=22426069; PubMed=12537572;
Mistar S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Histar S., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J. Russoc S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome: a Genome Biol. 3: RESEARCH0083.1-RESEARCH0083.22(2002). REVISIONS, AND ALTERNATIVE SPLICING.

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GO; GO:0007349; P:cellularization; IMP.
GO; GO:0007456; P:cellularization; IMP.
GO; GO:0007456; P:cytoplasm; IDA.
GO; GO:0007456; P:cytoplasm; Gosta Drosophila); IMP.
GO; GO:0008583; P:mystery cell fate differentiation (sensu Dr. .; IMP.
GO; GO:0007697; P:nuclear migration; IDA.
GO; GO:000579; P:protein deubiquitination; IDA.
GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IGI. Gарв ISOId=P55824-3; Sequence=VSP 005269;
-!- TISSUE SPECIFICITY: Eye disks and ovaries.
-!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-!- SIMILARITY: Belongs to peptidase family C19. -1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0 = ubiquitin + a thiol. -1- ALTERNATIVE PRODUCTS: Event-Alternative splicing, Named isoforms=3; Comment=Experimental confirmation may be lacking for some ö Score 35; DB 1; Length 2778; Pred. No. 1.1e+02; 2; Mismatches 3; Indels 2; Mismatches IsoId=P55824-2; Sequence=VSP_005270; IsoId=P55824-1; Sequence=Displayed; InterPro; IPR001394; Peptidase C19. EMBL; L04959; AAP01345.1; -EMBL; L04958; AAP01346.1; -EMBL; L04960; AAP01347.1; -EMBL; L04960; AAF01348.1; -EMBL; AE003779; AAF57198.1; -EMBL; AE003779; AAF57198.1; -EMBL; AF19677; AAD38652.1; -MEROPS; C19.007; -Flybase; FBgn0005632; faf. PFam; PF00443; UCH; 1. PROSITE; PS00972; UCH 2 1; 1. PROSITE; PS00973; UCH 2 2; 1. PROSITE; PS50235; UCH 2 3; 1. 64.8%; 54.5%; Local Similarity 54.5 isoforms; Query Match Best Loca Matches % THE THE THE THE TRANSPERSE BEARE B

| :|| | :| 1394 EVIVPDGQDFS 1404 1 EEVVPXGMDYS 11

RESULT 7

us-09-909-164-12.rsp

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METAL
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF252283; AAF81719.1; -.

REMBL; AF252283; AAF81719.1; -.

REMBL; AB40923; BA496014.1; ALT_INIT.

REMBL; REMOSS CACCOOCTION CONTROL CO
                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Kikuno R., Ishikawa K. I., Hirosawa M., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kay M.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May play a role in organizing the actin cytoskeleton of the brain cells.
                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
MODI_TaxID=9606,
                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=20347694; PubMed=10888605;
Koob M.D., Nemes J.P., Benzow K.A.,
"The SCAS transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHLI).";
Hum. Mol. Genet. 9:1543-1551 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEICH 1.
KEICH 2.
KEICH 3.
KELCH 4.
KEICH 5.
KEICH 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Cytoplasmic.
-! TISSUB SPECIFICITY: Highly expressed in brain.
-!- SIMILARITY: Contains 1 BTB/POZ domain.
-!- SIMILARITY: Contains 6 Kelch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kelch repeat; Repeat.
SER-RICH.
             OSNRG4; OSH4X4; OSH65; OSP238; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Kelch-like protein 1. KHEL OR KIAA1490.
   748 AA
PRT;
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20277482; PubMed=10819331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [3]
SEQUENCE OF 179-409 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82680 MW;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 7:143-150(2000)
                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            649
701
748 AA;
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SEQUENCE FROM N.A.
   HUMAN
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                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee J.-S.; "Molecular cloning and characterization of plastocyanin precursor in
                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000923; BlueCu_1.
InterPro; IPR001235; Copper_blue.
InterPro; IPR001235; Copper_blue.
InterPro; IPR00127; Copper-bind; 1.
Pfam; PF00127; Copper-bind; 1.
PRINTS; PR00125; Copper_blue; 1.
PROSTER; PS00124; COPPER BLUE; 1.
Chloroplast; Copper Blue; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
63.9%; Score 34.5; DB 1; Length 748; 80.0%; Pred. No. 35; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
E45725D25B5F400D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLASTOCYANIN.
PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY)
COPPER (BY SIMILARITY)
                                                                                                                                                                                                                                                  P20423; QSBBB, Ornion, Created)
01-FEB-1991 (Rel. 17, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Plastocyanin, chloroplast precursor.
                                                                                                                                                                                                                                    154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Ilpoom; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF093636; AAC78108.1; -. HSSP; P00289; 2PCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15577 MW;
  Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                    STANDARD;
                                                                                                                            127 EEVVP-GMDF 135
                                                                                 1 EEVVPXGMDY 10
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154
139
142
                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 1
139 1
142 1
142 1
154 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 58-154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
                                                                                                                                                                                                                                                             Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae;
Triticeae, Hordeum.
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         produce 1.91.00. 277:97-104 (1993).

-1. FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.

-1. SUBCELLULAR LOCATION: Loosely bound to the inner thylakoid membrane surface in chloroplasts.

-1. SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                                                                                                                                                                                                                                                                                       BREL; VOOTO4; CAA68696.1; -.

REBL; VOOTO4; CAA68201.1; -.

REL; Z38347; CAA62201.1; -.

R PIR, S38255; S38255.

R PSP; PO0289; 2PCF.

R INTERPO; IPRO01235; Copper blue.

IN INTERPO; IPRO01235; Copper blue.

R PRINTS; PRO0127; COPPERBLUE.

R PROSTITE; PSO0196; COPPERBLUE.

R PROSTITE; PSO0196; COPPERBLUE.

R PROSTITE; PSO0196; COPPER BLUE; 1.

R CALOROPLAST.

CHLOROPLAST.

TRANSIT 1 58 CHLOROPLAST.
63.0%; Score 34; DB 1; Length 154; 54.5%; Pred. No. 8.7; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASTOCYANIN.
PLASTOCYANIN-LIKE.
                                                                                                                                                                                    01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plagtocyanin, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COPPER
                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
STRAIN=cv. NK 1558;
MEDLINE=94039081; PubMed=8223592;
                               6; Conservative
                                                                                      100 EDAVPSGVDVS 110
                                                                                                                                                              STANDARD;
                                                           1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58
155
155
140
143
143
Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                            PLAS HORVU
P08248;
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DOMAIN
METAL
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                                                                                     ö
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Italica;
Dimitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
Dimitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
"Complete amino acid sequence of poplar plastocyanin b.";
FEBS Lett. 226:17-22(1987).
-I. FUNCTION: Participates in electron transfer between P700 and the
                                                                                                                                                                                                                                                                                                                                                       Populus nigra (Lombardy poplar).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Sallcaceae; Saliceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytochrome b6-f complex in photosystem I.

-!- SUBCELLULAR LOCATION: Loosely bound to the inner thylakoid membrane surface in chloroplasts.
-!- SIMILARITY: THESE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF FOPLAR PLASTOCYANINS A AND B.
-!- SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probom; PD001235; Copper blue; 1.
PR05ITE; PS00196; COPPER BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
Transit peptide; Multigene family.
TRANSIT
                                                63.0%; Score 34; DB 1; Length 155; 54.5%; Pred. No. 8.7;
                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRALM-ev. Italian TISSUB-Leaf;
Reichert J., Jenzelewski V., Haehnel W.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
120 120 T -> N (IN CV. NK 1558).
155 Aa; 15709 MW; DAA7EABE5F6F4F91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CALLONG FLAST
PLASTOCYANIN B.
PLASTOCYANIN-LIKE.
COPPER.
COPPER.
COPPER.
                                                                                                                                                                                                                                                                         01-OCT-1989 (Rel. 12, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                             Plastocyanin B, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z50186; CAA90565.1; -.
PIR; S00210; S00210.
PIR; S62208; S58208.
HSSP; P00299; IPLC.
InterPro; IPR000923; BlueCu 1.
InterPro; IPR00135; Copper blue.
InterPro; IPR00135; Copper blue.
Pfam; PF00127; copper-blud; I.
PRINTS; PR00156; COPPERBLUE.
                                                                                     6; Conservative
                                                                                                                                         101 EDAVPSGVDVS 111
                                                                                                                                                                                                                                          STANDARD;
                                                                                                                     1 REVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 70-168.
                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                          PLAT POPNI
VARIANT
SEQUENCE
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                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELTUTAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain family. Subfamily 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 35210 / B31;
MEDLINE=9805544; PubMed=9403685;
Frager C. M., Casjens S., Hanng W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb U.-F., Fledschmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
Barbour A.G., Hinnebusch J.;
"Phenylalanyl-tRNA synthetase genes (alpha and beta subunits) and thoredoxin reductase gene of Borrelia burgdorferi.";
thioredoxin reductase gene of Borrelia burgdorferi.";
submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP diphosphate + L-phenylalanyl-tRNA(Phe).
                                                          ö
                          63.0%; Score 34; DB 1; Length 168; 54.5%; Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                          3; Indels
168 AA; 16981 MW; F20DA6EA2038AEEA CRC64;
                                                                                                                                                                                                   566 AA.
                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001153; AAC66870.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U82978; AAB41019.1; -.
             Query Match
Best Local Similarity 54.2
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 390:580-586(1997).
                                                                                                          |: || |:| |
112 EDAVPSGVDVS 122
                                                                                                                                                                                                   STANDARD;
                                                                                        1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=139;
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SEQUENCE
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                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. Columbia;

A Seki M., Iida K., Saturai T., Akiyama K., Ishida J.,

A Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,

A Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,

A Hayashizaki Y., Shinozaki K.;

I "Arabidopsis thaliana full-length CDNA.";

I Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Potential disease resistance protein.

-!- DOWAIN: The LRR repeats probably act as specificity determinant of pathogen recognition (By similarity).

-!- SIMILARITY: Belongs to the disease resistance NB-LRR family.

-!- SIMILARITY: Contains 1 NB-RR domain.

-!- DATABASE: NAME=NIB-LRRS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE=Functional and comparative genomics of disease resistance gene
                                                                         Gaps
                                                                                                                                                                                                                                                       10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable disease resistance RPP8-like protein 4.
RPP8L4 OR AT5G48620 OR KISNIS.9.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Columbia;
MEDLINE=99087489; PubMed=9872454;
Nakamura Y., Sato S., Asamizu B., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones.";
DNA Res. 5:297-308(1998).
                                                                         ö
                               Score 34; DB 1; Length 566;
Pred. No. 33;
0; Mismatches 1; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
DOMAIN 10 45 LEUCINE-ZIPPER.
566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB015468; BAB10695.1; -.
EMBL; AK117163; BAC41841.1; -.
Interzro; IPR000767; Disease_resist.
Interzro; IPR001611; LRR.
Interzro; IPR00181; NB-ARC.
Pfam; PF00560; LRR; 2.
Pfam; PF00931; NB-ARC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WWW="http://niblrrs.ucdavis.edu".
                                        63.0%;
85.7%;
                                        Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                        169 VPFGMDY 175
                                                                                                                    4 VPXGMDY 10
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    SEQUENCE
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RBL4_ARATH
ID _RBL4_A
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MEDLINE-20271766; PubMed=10810142;
Cooley M.B., Pathirana S., Wu H.-J., Kachroo P., Klessig D.F.;
"Members of the Arabidopsis HRT/RPP8 family of resistance genes confer resistance to both viral and comycete pathogens.";
Plant Cell 12:663-676(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holub E.B., Dangl J.L.;
"Intragent's recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN-cv. Columbia, Dubmed-1453172;

MEDLINE-2259850; Pubmed-1453172;

MEDLINE-2259860; Pubmed-1453172;

Samada K., Lim G., Dale J.M., Chen H., Shinn P., Falm C.J.,

Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriuni M.J.,

Chan M.M., Tang C.C., Ondera C.S., Deng J.M., Akiyama K., Ansari Y.,

Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao O., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Idda K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
                                                                                                                                                                                                                                                                                                                                         Q8W4_D9; Q8GWG5; Q9MSA1; Q9ZSY3; Q9ZSY4;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Disease resistance protein RPP8 (Resistance to Peronospora parasitica protein 8).
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Columbia;
MEDDINDE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2 RPP8-3, AND VARIANTS.
STRAIN=CV. Columbia, and cv. Landsberg erecta;
MEDLINE=99030133; PubMed=9811794;
MEDLINE=99030131, Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
                                                                                                                                                            ö
                                                                                                                         Length 908;
                                                                                                                                                            Indels
                                                                                    3111991B17239693 CRC64;
                                                                                                                     DB 1;
54;
               LRR 1.
LRR 2.
LRR 3.
ATP (POTENTIAL).
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                                                                                                                     Score 34; DB 1
Pred. No. 54;
2; Mismatches
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Arabidopsis thaliana (Mouse-ear cress
                                                                                      104448 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Cell 10:1861-1874(1998).
                                                                                                                         63.0%;
                                                                                                                                      60.08;
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                                                                                    908 AA;
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Best Local Similarity
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathogen recognition.

-!- MISCELLANEOUS: In cv. Columbia and cv. Landsberg erecta, RPPB specifically recognizes the Bacos avirulence protein (from Peronospora parasitica, while it is not the case in cv. Di-17, where it confers resistance to Turnip Crinkle Virus uppon recognition of the viral capsid protein.
-!- SIMILARITY: Bonds to the disease resistance NB-LRR family.
RPPB/HRT subfamily.
-!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
-!- SIMILARITY: Contains 1 NB-ARC domain.
-!- DATABASE: NAME-NIB-LRRS,
-!- DATABASE: NAME-NIB-LRRS,
NOTE-Functional and comparative genomics of disease resistance gene
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20496823; PubMed=11041886;
Ren T., Qu F., Morris T.J.;
PubMed T. Separation of the resistance to turnip crinkle virus.";
Plant Cell 12:1917-1926(2000).
-!- FUNCTION: Disease resistance protein. Resistance proteins guard
the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein.
That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. The interaction with TIP (TCV-interacting protein) may be essential for the recognition of the avirulence proteins, and the triggering of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isold=Q8044J9-2; Sequence=VSP_007171, VSP_007172;
Note=Has been shown to exist only in cv. Columbia so far;
Note=Has been shown to exist only in cv. Columbia so far;
DOMAIN: The LRR repeats probably act as specificity determinant of
pathogen recognition.
POLYMORPHISM: The strong polymorphisms present in cv. Di-17 and
cv. Columbia are probably due to an unequal crossing-over between
the highly related RPBs and RPHBA genes present in cv. Landsberg
erecta. Such variations probably modify the specificity of
Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y. Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., "Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                      STRAIN=CV. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Sakajima M., Enju A., Kamnya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana [ull-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                defense response.
SUBUNIT: Interacts with the NAC protein TIP.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q8W4J9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homologs;
WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2)
                                                                                                                     Science 302:842-846(2003).
                                                                                                                                                                                                                                                                                                                                     [6]
INTERACTION WITH TIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=1;
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EMBL; AY062514; AAL32592.1; -. EMBL; AK118862; BAC43449.1; -. InterPro; IPR000767; Disease_resist.

EMBL; AF089710; AAC83165.1; -. EMBL; AF089711; AAC78631.1; -.

AF234174; AAF36987.1; AB025638; BAA97426.1;

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6; Conservative
                                                                                                                                            STANDARD;
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nes 6; Conservative
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EKLVPGGEDY
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GKGV -> EKGI (in cv. Landaberg erecta).

C -> R (in cv. Landaberg erecta).

C -> R (in cv. Landaberg erecta).

F -> L (in cv. Landaberg erecta).

C -> Q (in cv. Di-17).

Q -> Q (in cv. Di-17).

Y -> S (in cv. Di-17).

R -> P (in cv. Di-17).

R -> P (in cv. Di-17).

R -> F (in cv. Di-17).

A -> V (in cv. Di-17).

C -> S (in cv. Di-17) and cv. Landaberg erecta).

C -> R (in cv. Di-17 and cv. Landaberg erecta).

C -> R (in cv. Di-17 and cv. Landaberg erecta).

C -> R (in cv. Di-17 and cv. Landaberg erecta).

C -> R (in cv. Di-17 and cv. Landaberg erecta).

C -> R (in cv. Di-17 and cv. Landaberg erecta).
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C -> S (in cv. Di-17 and cv. Landsberg erecta).

T -> I (in cv. Di-17).

S -> R (in cv. Di-17).

S -> R (in cv. Di-17).

H -> Q (in cv. Di-17).

I -> L (in cv. Di-17).

K -> M (in cv. Di-17).

K -> M (in cv. Di-17).

K -> M (in cv. Landsberg erecta).

K -> M (in cv. Landsberg erecta).
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LER 2.
ATP (POTENTIAL).
WEMLLTSRNEGVGIH -> ELLWYIHEALFLINS (in
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I -> K (in cv. Di-17 and cv. Landsberg
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Y -> F (in cv. Di-17).

S -> Y (in cv. landsberg erecta).

C -> S (in cv. Di-17 and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Landsberg erecta).

A - V (in cv. Landsberg erecta).

E -> Q (in cv. Landsberg erecta).

DATLSWQ -> NKYLRVH (in cv. Di-17).

NKLSWQ -> NKYLRVH (in cv. Landsberg erecta).

WQ -> SH (in cv. Landsberg erecta).
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DSEISTYSLFY -> YSKISAYDLFN (in cv.
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AC 053451,

COSSAGE STATE STANDARD; PRT; 276 AA.

COSSAGE STANDARD; PRT; 276 AA.

COSSAGE STANDARD; CRE1. 35, Created)

DT 01-NOV-1997 (Re1. 35, Last sequence update)

ENVOCATION (Re1. 35, Last sequence update)

ENVOCATION (Re1. 35, Last sequence update)

ENVOCATION (Re1. 35, Last sequence update)

SO Methanococcus jammaschii.

ACCT-2001 (Re1. 40, Last sequence update)

SO Methanococcus jammaschii.

Rehanococcus jammaschii.

NUCHII TAALD-2109; PUNMedes S08087;

RA MEDINES-65137999; PUNMedes S08087;

RA SULL C. MAILE O., Olean G. J. Zhou L., Fleischmann R.D., Racker S. M. Marke O., Olean G. J. Zhou L., Fleischmann J.L., Mayore D., RA Sutton G. G., Blake J.A., Fleischald L.M., Clayton R.A., Glodek A.,

RA SULL C. MAILE O., Olean G. J. Zhou L., Flainamn J.L., Mayore D., RA Sutton G. G., Blake J.A., Flainamn J.L., Mayore D., RA Sutton G. G., Blake J.A., Flainamn J.L., Mones C. R., Venter J. C., Matches R., Kirkness E.F., Weinstock K.G., Merrick J.C.,

RA Cotton M.D., Roberts K.M., Hutter M.A., Kaline B.P., Borcdowsky M.,

RA Scott J.L., Geophagen N.S.M., Maken B.P., Borcdowsky M.,

RA Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.,

RA Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.,

RA Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.,

RA Scott J.L., Geophagen Scholler Institute methanogenic archaeon, Methanococcus

FR. Schence 273:1059-1077(1996).

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Q88cc0 pseudomonas Q8Rt3 rhizobium e Q9xvk4 caenorhabdi Q9a382 caulobacter Q9yfi3 aeropyrum p Q9yfi3 eropyrum p Q9yfi3 eropyrum p Q8x25 ralstonia s Q8x25 ralstonia s Q9x67 andrographi Q95p46 carcinus ma Q17704 caenorhabdi O52673 escherichia O5266 escherichia O52673 eropyrum p Q98x29 rhizobium 1 Q8b577 homo sapien Q98x29 rhizobium 1 Q8b577 homo sapien Q9s915 thermoanaer

Qddzwg streptococc QPved4 prochloroco QPved4 prochloroco QBSSk6 mycobacteri QBT)0 agrobacteri Q9yet8 aeropyrum p Q11595 rhodopirell Q815a7 bacillus ce Q29920 archaeoglob Q29920 archaeoglob

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MEDLINE-94019318, PubMed=8413243,
Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "CYC2 encodes a factor involved in mitochondrial import of yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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De haan M., Maarse A.C., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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052666
027146
098K29
Q8TBJ7
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Q9YFI3
Q83L92
O52680
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Q855K6
Q8GP33
Q8U7J0
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095P46
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Qaesl9
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Q29920
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SEQUENCE FROM N.A.
STRAIN=FY1679;
MEDLINE=94169519; PubMed=7764548;
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
 PRELIMINARY;
                                                                                       SEQUENCE FROM N.A.
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NCBI_TaxID=4932;
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012479
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 Q12479
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030260 archaeoglob
086100 synchococc
0822b4 entercoccci
022081 citrus unsh
022096 citrus unsh
089568 arabidopsis
09917 arabidopsis
099170 arabidopsis
09910 oryza sativ
08064 oryza sativ
08xpa8 clostridium
08xpa8 clostridium
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116.206 Million cell updates/sec
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1: sp_archea:*
2: sp_bacteria:*
4: sp_human:*
5: sp_human:*
5: sp_mammal:*
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Q8ESV7
Q8ESV7
Q8DIHO
Q8ZZB4
Q2Z096
Q8ZZB7
Q9Z777
P93782
Q9SN30
Q4SN30
Q4
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Gapop 10.0 , Gapext 0.5
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54
1 EEVVPXGMDYS 11
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Match Length DB
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Local Similarity 54.5
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STRAIN=HTB831 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.,
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHS1, which complements a drug-hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Biosci. Biotechnol. Biochem. 58:391-395 (1994).
EMBL; Z74920; CAA99201.1; -.
EMBL; X74319; CAA60762.1; -.
PIRS; S54619; S54619.
SGD; S0005539; YOR013W.
SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
NCBI_TaxID=182710;
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                                                                                                                                                                                                                                                                                                                             Query Match
74.1%; Score 40; DB 3; Length 156;
Best Local Similarity 77.8%; Pred. No. 3;
Matches 7; Conservative 1; Mismatches 1; Indels
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InterPro; IPR001279; Blactmase-like.
Pfam; PF00753; Jactamase-B; I.
Hypothetical protein; Complete proteome;
SEQUENCE 319 AA; 35617 MW; 3BDAE4BF13E79E37 CRC64;
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Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical conserved protein.
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O30260;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein AF2411.
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Best Local Similarity 60.0.
Best Conservative
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189 EQLVPHGIDY 198
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MEDLINE=222214; PubMed=12240834;
Makamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
Makamura Y., Kaneko T., Sato S., Ikeuchi M., Kishida Y.,
Makamura Y., Kaneko T., Sato S., Ikeuchi M., Kabina Y.,
Miyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
Kiyokawa C., Kohara M., Takeuchi C., Yamada M., Tabata S.;
Kiyokawa C., Kohara M., Takeuchi C., Yamada M., Tabata S.;
Miship S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the thrmophilic cyanobacterium
Thermosynachococus elongatus BP-1.";
DNA Ress. 9:123-130(202).

MEMBL; AROOS374; BAC09170.1; -.
MGO; GO:0016215; Fitransporter activity; IEA.
MGO; GO:0016216; Fitransporter activity; IEA.
MGO; GO:0016216; Fitransporter activity; I
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.D., Kerlavage A.K., Graham D.E., Kyrpides N.C., Peterson G.G., Gill S., Pielschmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McMeil L.K., Badger M.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Sadow P.W., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Wenter J.C.,
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Nature 390:364-370(1997).
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBL_TaxID=32046;
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Pfam; PR00296; bac_luciferase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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PIR; D69551; D69551.
TIGR; AF2411; -.
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us-09-909-164-12.rspt

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Created)
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234 VIPPGMDFS 242
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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Q8W568;
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STRAILE-VB3 (A TCC 700802;
STRAILE-VB3 (A TCC 700802;
STRAILE-LYB (A TCC 700802;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Daugherty S., Dedson R.J., Umrkin S., Kolonay J., Madugu R.,
Daugherty S., Deboy R.T., Durkin S., Kolonay J., Madugu R.,
Vamachevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
Entercocous faecalis.";
                                                                                                                                                                                                                                                                                                 Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
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Pepermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Sapindales; Rutaceae; Citrus.
NCBL_TaxID=55188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] — SEQUENCE FROM N.A. SERVINGE Juice sacs and segment epidermis; STRAIN=cv. Miyagawa-Wase; TISSUE-Juice sacs and segment epidermis; MEDLINE-96439842; PubMed=8842155; Komatsu A., Takanokura Y., Omura M., Akihama T.; Komatsu A., Takanokura Y., Omura M., Akihama T.; Ciloning and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu Warg.).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 AA; 16127 MW; 555799BF1E47D34E CRC64;
                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Large conductance mechanosensitive channel protein.
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Last annotation update)
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GO; GO:0016020; C:membrane; IEA.

GO; GO:000216; F:non channel activity; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR001185; MS_channel.

Pfam; PF01741; MsCL; 1.
                                                                                       149 AA.
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01-JAN-1998 (TrEMBLrel. 05, Last seque)
01-JUN-2003 (TrEMBLrel. 24, Last annot
Sucrose-phosphate synthase (Fragment)
                                                                                                                                                  Created)
                                                                                    PRT;
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ProDom; PD007253; MS_channel; 1.
TIGRFAMS; TIGR00220; mscL; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE016956; AA082828.1; -. TIGR; EF3152; -.
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                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                    PRELIMINARY;
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SEQUENCE 149 AA:
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                       MSCL OR EF3152
                                                                                                           082ZB4;
01-JUN-2003 (
01-JUN-2003 (
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                          RESULT 5
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STRAIN=CV. Miyagawa-Wase; TISSUE-Juice sacs and segment epidermis; Komateu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.; "Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.)."; Plant Sci. 140:169-178 (1999).
EMBL; AB006319; BAA23215.1; -.
PIR: S72649; S72649.
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Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;

Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;

Guring sucroses accumulation in citrus fruits (Citrus unshiu Marc.).";

BMBL; AB006660; BAA22071.1;

PIR. $72550; $72550.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Sapindales, Rutaceae, Citrus.
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TISSUE-Unice sacs and segment epidermis;
MEDLINE=96439842; PubMed=8842155;
KOMATSU A., Takanokur Y., Omura M., Akihama T.;
"Cloning and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
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                                                                                                                                                                                                                                                      341 341
341 AA; 38136 MW; 61417A69C4560777 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN'1998 (TrEMBLrel. 05, Created)
01-JAN'1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Sucrose-phosphate synthase (Fragment).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                         Similarity 66.7%; Score 36; DB 10; Similarity 66.7%; Pred. No. 50; 6; Conservative 2; Mismatches 1;
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66.7%; Pred. No. 51;
tive 2; Mismatches 1;
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VIPPGMDFS 422
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A Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
A Ishida J., Jones T., Kaniya A., Karlin-Neumann G., Kawal J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
A Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis ORP Clones.",
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR13044; AAM47352.1;
EMBL; AR13044; AAM47352.1;
CO:0003824; F:catalytic activity; IEA.
GO: GO:0004508; F:prolyl oligopeptidase activity; IEA.
RO: GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro: IPR00377; Ser_estrs.
                                                                                                                                                                     SEQUENCE FROM N.A.
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Isbaida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                               Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RO ENDOPEP SER; 1.
49682 MW; A159955B21742C4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 70.0 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 EEDVPSAMDY 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EEVVPXGMDY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
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Q9C9T7;
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Q9C9T7
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Sugiharto B., Sakakibara H., Sugiyama T.,
Sugiharto B., Sakakibara H., Sugiyama T.,
In Sugiracane: Nolecular Cloning of the cDNAs and Comparative Analysis
T. Sugarcane: Nolecular Cloning of the cDNAs and Comparative Analysis
T. Gene Expres ssion.",
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

St. Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

St. GO:0046524; F:Sucrose-phosphate synthase activity; IEA.

GO:0046524; F:Sucrose-phosphate synthase activity; IEA.

GO:0005058; P:Sucrose-phosphate synthase activity.

R O: GO:0005058; P:Sucrose-phosphate synthase activity.

R InterPro: IPR001296; Glyco trans 1.

Peam, PP00534; Glycos trans 1.

R InterPro: IPR001296; Glycos trans 1.

R InterPro: IPR001296; Iransferase.

TANON TER.

1 1

SEQUENCE 1047 AA; 116379 MW; DOEDB34961E1DB3D CRC64;
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Langin-Hooper S., Lee A., Lee J.W., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Miltscher J., Miranda M., Niguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Sowley D., Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Sequence and analysis of chromosome lof the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%; Score 36; DB 10; Length 460; 70.0%; Pred. No. 70; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AC012679; AAG52073.1; -.
PIR; G96764; G96764.
G97 GO:0003287; F:catalytic activity; IEA.
G0; G0:0004287; F:prolyl oligopeptidase activity; IEA.
G0; G0:0006288; F:prolyl oligopeptidase activity; IEA.
G0; G0:0006508; F:proteolysis and peptidolysis; IEA.
InterPro; IPR000471; Pept. S9_AS.
InterPro; IPR000379; Ser_estra.
PROSTIE; PS00708; PRO_ENDOPRP_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. -
SEQUENCE 460 AA; 50564 MW; E94B27B5C4B249EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last amnotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (Fragment)
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 EEDVPSAMDY 227
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wes 7; Conserv
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PRT;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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453 VIPPGMDFS 461
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Q9GQ04;
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GO; GO:0046524; F: sucrose-phosphate synthase activity; IEA.

GO; GO:0046524; F: sucrose-phosphate synthase activity; IEA.

GO; GO:0009058; P: biosynthesis; IEA.

InterPro; IPR001296; Glyco_trans 1.

Ffam; PF00534; Glyco_trans 1.

Glycosyltransferase; Transferase;

SEQUENCE 1083 AA; 122688 MW; BFC126FCA2137BB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Japonica; Sakamoto M., Higo K., Shimada H., Sakamoto M., Satozawa T., Kishimoto N., Higo K., Shimada H., Fujimura T.; Fujimura T.; Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS) gene that is specifically expressed in the source organ."; Plant Sci. 112.207-217 (1995). EMBL, D45890; BAA03304.1; -. PIR; T04103; T04103.
                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
61-JUN-2003 (TrEMBLrel. 24, Last annotation update)
5ucrose-phosphate synthase-like protein (EC 2.4.1.14).
F28M11.40 OR A44G10120.

Rarabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
NCBI_TAXID=3702;
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL049487; CAB39764.1; -.
EMBL; AL04516; CAB78135.1; -.
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GO; GO:0004459; F:L-lactate dehydrogenase activity; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Sucrose phosphate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%; Score 36; DB 10;
66.7%; Pred. No. 1.8e+02;
iive 2; Mismatches 1;
                     PRT; 1083 AA.
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Best Local Similarity 66.7.
6; Conservative
                     PRELIMINARY;
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SEQUENCE FROM N.A.
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                     05N360
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08N36
                                            SOW REPORT OF THE PROPERTY OF 
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enthartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                             Score 36; DB 10; Length 1084;
Pred. No. 1.8e+02;
2; Mismatches 1; Indels C
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Sasaki T., Matsumoto T., Yamamoto K.;
"Orrya sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0678F11.";
Submitted (MAR-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003437; BAB86107.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 66.7%; Score 36; DB 10; Length 1100; Best Local Similarity 66.7%; Pred. No. 1.9e+02; Matches 6; Conservative 2; Mismatches 1; Indels C
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Eriocheir sinensis (Chinese mitten crab).
Eukaryota, Merazoa, Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida, Decapoda; Pleccyemata; Brachyura;
Eubrachyura; Grapsoidea; Varunidae; Eriocheir.
[11]
GO, GO:0006096; P:glycolysis; IBA.
InterPro; IPR001236; Glyco_trans_1.
InterPro; IPR001557; L. LDH.
Pfam; PF00534; Glycos_transf_1; 1.
PROSITE; PS00644; L. LDH; 1.
SEQUENCE 1084 AA, 119417 MW; 4D0D79AFEDD2F92B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1100 AA; LLDH; 1. - 084F4604BA389CAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gramene; Q88064; -...
GO; GO: 0004459; F:L-lactate dehydrogenase activity; IEA.
GO; GO: 0009058; P: biosynthesis; IEA.
GO; GO: 0006096; P:glycolyais; IEA.
InterPro; IPR001296; Glyco_trans_1.
Interpro; IPR001297; LLDH.
Pfam; PF0054; Glycos transf_1; 1.
PROSITE; PS00064; L_LDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative sucrose-phosphate synthase.
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01-WAR-2001 (TrEMBLrel, 16, Last sequence update)
01-WAR-2001 (TrEMBLrel, 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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MEDLINE=21664373; PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohehima K., Yamashita A.,
Shiba T., Ogsaswara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
Weihrauch D., Towle D.W.; Malay Market are expressed in Malfils exchanger and Nat/K+/2Cl- -cotransporter are expressed in gills of the euryhaline Chinese crab Eriocheir sinensis."; Comp. Biochem. Physiol. 126:S158-S158(2000). Malay Rangine Chinese Remail, Rangine Rangin Rangine Rangine Rangine Rangine Rangine Rangine Rangine Rangine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium perfringens.
Bacteridium, Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1502;
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                                                                                                                                                                                                                                                                                                                 Query Match

64.8%; Score 35; DB 5; Length 219;

Best Local Similarity 75.0%; Pred. No. 49;

Matches 6; Conservative 1; Mismatches 1; Indels
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GO; GO: 0003824; F:catalytic activity; IEA.
GO; GO: 0003824; F:catalytic activity; IEA.
InterPro; IPR000205; Mo.Bs.
InterPro; IPR000259; MaD.Bs.
InterPro; IPR000594; ThiF_domain.
Ffam, PF00899; ThiF; I.
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219 AA, 24159 MW, 599442DA26F0D3F1 CRC64,
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein CPE0057.
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                           Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41
                                                                                                                                                                                                                                                                                                                                                                                                  'note= "N-terminal acetyl"
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ABB80556
ABB80560
ABB805560
ABB80534
ABB80533
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  Lim-Wilby M, Levy OE,
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Misc-difference
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 Abb80561 Hepatitis
Abb80529 Hepatitis
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Abb80529 Hepatitis
Abb80562 Hepatitis
Abb80543 Hepatitis
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Abb80548 Hepatitis
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Abb80567 Hepatitis
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                                                              3, 2004, 11:31:01 , Search time 45.9333 Seconds (without alignments) 67.664 Million cell updates/sec
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                  1586107 segs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                             - protein search, using sw model
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Gapop 10.0', Gapext 0.5
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1: geneseqp1980s:*
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1 EEVVPXGMDYS 11
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
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                                                                                                                                                                 Match 96.3%; Score 52; DB 5; Length 11; Local Similarity 100.0%; Pred. No. 0.0024; les 11; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0024;
ive 0; Mismatches 0; IndelB
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"

/note= "C-terminal amide"

Brunck TK;

'note= "D-form residue" /note= "D-form residue"

'note= "Oxymethionine"

'note= "N-terminal acetyl"

Location/Qualifiers

(first entry)

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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42
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                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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Claim 17; Page 65; 69pp; English.
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                         Sequence 11 AA;
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ABB80562 standard; peptide; 11 AA.

RESULT 5 ABB80562 ID ABB8

EEVVPXGMDYS 11

1 EEVVPXGMDYS 11

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'note= "Norvalyl carbonyl forming keto-amide linkage with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.023;
0; Mismatches
                               /note= "N-terminal acetyl"
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                                                                                                                                                                                   /note= "C-terminal amide"
                                                                                                                 'note= "D-form residue"
                                                                                                                                                  'note= "D-form residue"
Location/Qualifiers
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                                                                                                                                                                                                                                                                                         19-JUL-2001; 2001WO-US023169.
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ilarity 90.9%;
Conservative
                                                                                  residue 7"
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                   Misc-difference 9
                                                                                                  Misc-difference
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 Key
Modified-site
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                      /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22.
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                                                                                                                                                                      'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                           /note= "C-terminal amide"
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                                                                                                                                     Location/Qualifiers
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90.9%;
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                                                                                                                                     Key
Modified-site
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Best Local S:
Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                  ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
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                                   /note= "C-terminal amide"
           /note= "D-form residue"
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Local Similarity 90.9%;
es 10; Conservative (
                                                                                                            19-JUL-2001; 2001WO-US023169
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                                                                                                                                                           (CORV-) CORVAS INT INC
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Misc-difference 9
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Modified-site
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activity usefu
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                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28.
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Pred. No. 0.036;
0; Mismatches 1; Indels
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                                                                                      Brunck TK;
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                                                                                                                                                                                        Claim 17; Page 64; 69pp; English.
           19-JUL-2001; 2001WO-US023169.
                                    21-JUL-2000; 2000US-0220101P.
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Best Local Similarity 90.9%;
Matches 10; Conservative
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                                                                                      Lim-Wilby M, Levy OE,
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                                                              (CORV-) CORVAS INT INC
                                                                                                            WPI; 2002-361643/39.
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ABB80548
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                 peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                     Score 46; DB 5;
Pred. No. 0.036;
                                                                                                                                                                                                                                                               0; Mismatches
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residue 7"
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                                                                                     Claim 17; Page 65; 69pp; English
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          WPI; 2002-361643/39
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les 10; Conser
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2
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                                                                                                                                    Length 11;
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                                                                                                                                 Score 46; DB 5;
Pred. No. 0.036;
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Best Local Similarity 90.9
Matches 10; Conservative
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                   note= "2-aminoisobutyry1 carbony1 residue forming a keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
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                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46
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Pred. No. 0.036;
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                               ABB80566 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
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Pred. No. 0.036;
0; Mismatches 1; Indels
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                  Query Match
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                             /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                 'note= "N-terminal acetyl"
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85.2%; Score 46; DB 5; Length 11; 90.9%; Pred. No. 0.036; 1; Indels iive 0; Mismatches 1; Indels

Query Match
Best Local Similarity 90.9
Matches 10; Conservative

1 EEVVPXGSDYS 11

Search completed: June 3, 2004, 11:48:24 Job time: 46.9333 secs

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TYPE: PRT
ORGANISM: Citrus unshiu
FEATURE:
OTHER INFORMATION: Xaa at position 109 is one of Ala, Arg, Asn, J
OTHER INFORMATION: Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met,
                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT CAGANISM: Enterococcus faecalis US-09-134-000C-4848
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Sequence 82
Sequence 31
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/cgr2_6/prodata/2/iaa/B_COMB.pep:*
/cgr2_6/prodata/2/iaa/PcTUS_COMB.pep:*
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-718-777-7
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US-08-569-147-76
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Maximum Match 100%
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Sequence 4848, Application US/09134000C

Sequence 4848, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucete-Stamm et al

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERACCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT PILING DATE: 1998-08-13

FRIOR APPLICATION NUMBER: US 60/055,778

FRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4848

LENGTH: 181
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Patent No. 6210943

GENERAL INFORMATION:

APPLICANT: AKTHAMA, TOYOTA

TITLE OF INVENTION:

TITLE OF INVENTION: THE SAME

TITLE OF INVENTION: THE SAME

FILE REFERENCE: 0049-0235-0

CURRENT FILING DATE: 1997-05-09

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 4

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 21, Appli
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 21, Appl
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Sequence
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                US-08-460-694-4

US-08-460-744-4

US-08-460-744-4

US-08-461-711B-4

US-08-464-517-21

US-08-464-517-21

US-08-463-772-21

PCT-US93-05000-21

US-08-926-842B-20

US-08-464-517-22

US-08-464-517-22

US-08-464-517-22

US-08-464-517-22

US-08-266-842B-21

US-08-926-842B-21

US-08-926-842B-21

US-08-926-842B-21
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1049
                RESULT 5
US-09-394-272-10
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Patent No. 621043

Patent No. 621043

GENERAL INFORMATION:

APPLICANT: AKIRAMA, TOYOTA

TITLE OF INVENTYON: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING

TITLE OF INVENTY PAPLICANTION: THE SAME

FILE REFERENCE: 0049-0235-0

CURRENT FILING DATE: 1997-05-09

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 5

LENGTH: 348

TYPE: PRT

TYPE: PRT

CORRANISM: Citrus unshiu

US-08-853-9488-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 3; Length 348;
Pred. No. 22;
                                                Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OCOZGO Jr., Emil M.
APPLICANT: Clami, Perry G.
APPLICANT: Clami, Perry G.
APPLICANT: Tarczynaki, Mitchell
TITLE OF INVENTION: SUGGOSE PHOSPHATE SYNTHASE
TITLE OF INVENTION: SUGGOSE PHOSPHATE SYNTHASE
TILE REFERENCE: BB1166 US DA.
CURRENT PILING DATE: 2000-10-26
PRIOR FILING DATE: 1998-MAY-07
PRIOR FILING DATE: 1999-MAY-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
LENGTH: 368
; OTHER INFORMATION: Pro, Ser, Thr, Trp, Tyr, or Val
US-08-853-948B-4
                                                  DB 3;
22;
                                                Score 36; DB 3
Pred. No. 22;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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Patent No. 6323015
GENERAL INFORMATION:
                                                Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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234 VIPPGMDFS 242
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
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US-08-853-948B-5
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US-08-429-054A-11

Sequence 11, Application US/08429054A

Sequence 11, Application US/08429054A

Patent No. 5917126

GENERAL INFORMATION:
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),
TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Sequence 10, Application US/09394272

Sequence 10, Application US/09394272

Patent No. 6472588

GENERAL INFORMATION:
APPLICANT: Halagler, Candace H.
APPLICANT: Halagler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED FILE REPERENCE: 201304/1000

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT PILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 10.
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FILING DATE: 26-APR-1995
CLASSIFCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 842,337
FILING DATE: 20-March-1992
APPLICATION NUMBER: PCT/FR 91/00593
FILING DATE: 18-Ualy-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: French 90402094.9
FILING DATE: 20-Ualy-1990
CLASSIFICATION NUMBER: French 90402094.9
FILING DATE: 20-Ualy-1990
CLASSIFICATION: 800
ATTORNEY/AGENT INFACTION
ATTORNEY/AGENT INFACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146.1137
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NAME: Charles A. Muserlian
REGISTRATION NUMBER: 19,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 14
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 600 THIRD AVENUE CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 VIPPGMDFS 444
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ORGANISM: Oryza sativa
US-09-394-272-10
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Best Local Similarity
Matches 6; Conserv
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435 VIPPGMDFS 443
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66.7%; Score 36; DB 2; Length 1068;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 6; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Law Offices of Barbara Rae-Venter STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STATE: 220 Sheridan Avenue, Suite 440
CITY: Palo Alto
STATE: California
CUNTRY: USA
ZIP: 94306
COMPUTER: CALIFORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,777
FILING DATE: NOT YET ASSIGNED
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/175,471
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BARDARA RAE-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.072.02US
TELEPHONE: (418)328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08718777
; Sequence 7, Application US/08718777
; Patent No. 5981852
; GENERAL INFORMATION:
APPLICANT: Van Assche, C.
APPLICANT: Lando, D.
APPLICANT: Bruneau, J. M.
APPLICANT: Gervais, M.
TITLE OF INVENTION: MODIFICATION OF SUCROSE
TITLE OF INVENTION: SYNTHASE IN PLANTS
NUMBER OF INVENTION: SYNTHASE IN PLANTS
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1068 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                          TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-429-054A-11
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                                                                                                                                                                                                                                                                                                                                                                                       435 VIPPGMDFS 443
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3 VVPXGMDYS 11

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Sequence 7, Application US/09051341

Fatent No. 6124528

GENERAL INFORMATION:
FATULE OF INVENTION:
FITULE OF INVENTION:
MODIFICATION OF SOLUBLE SOLIDS USING
FITULE OF INVENTION:
MURBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
IP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Delocyme PC-DOS/MS-DOS
CORPUTER: Delocyme PC-DOS/MS-DOS
COMPUTER: Delocyme PC-DOS/MS-DOS
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Sequence 8, Application US/09394272
GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: EXAMESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION UNMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,341
FILING DATE:
CLASSIFICATION NUMBER: US/09/17351
APPLICATION NUMBER: PCT/US96/17351
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 08/549,016
FILING DATE: 27-OCT-1996
APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BATDATA REA-VENTEY: Ph.D.,
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.110.02US
TELEPHONE: (415)328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 6, Conservative
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// MOLECULE TYPE: protein
US-09-051-341-7
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MOLECULE TYPE: protein US-08-569-147-76
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TYPE: PRT
CRGANISM: Oryza sativa
US-09-394-272-9
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| Sequence 11, Application US/09394272
| Patent No. 6472586
| GENERAL INFORMATION:
| APPLICANT: Haigler, Candace H.
| APPLICANT: Haigler, Candace H.
| TITLE OF INVENTION: TRANSCENCE FIBER PRODUCING PLANTS WITH INCREASED
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
| TITLE OF INVENTION: UNMER: US/08/394,272
| CURRENT PILING DATE: 1999-09-10
| WUMBER OF SEQ ID NOS: 14
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 11
| LENGTH: 1083
                                                                                                                                                                                                                                                                                                                                             US-09-394-272-4

i Sequence 4, Application US/09394272

j Patent No. 6472588

j Patent No. 6472588

j Batent No. 6472588

j GENERAL INFORMATION:

j APPLICANT: Haigler, Candace H.

j APPLICANT: Haigler, Candace H.

j APPLICANT: Haigler, Candacy, A. Scott

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT APPLICATION NUMBER: 1999-09-10

NUMBER OF SEQ ID NOS: 14

j SOFTWARE: Patentin Ver. 2.0

j SEQ ID NO 4

LENGTH: 1081

TYPE: PRT

CREATER PRT

CREATER PRT

CREATER PRT

TYPE: PRT

US-09-394-272-4
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                                                                                                                                        Query Match 66.7%; Score 36; DB 4; Length 1068; Best Local Similarity 66.7%; Pred. No. 81; Matches 6; Conservative 2; Mismatches 1; Indels
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83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ; OKGANISM: Arabidopsis thaliana US-09-394-272-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
-- Anna 6; Conservative
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 1068
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483 VIPPGMDFS 491
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435 VIPPGMDFS 443
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                                          ; LENGTH: 1068
; TYPE: PRT
; ORGANISM: Zea mays
US-09-394-272-8
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US-09-394-272-11
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PARTICONT: REJIECT THE CALL APPLICATION US/03394272

PARTICONT: REJIECT THE CALL APPLICATION OF STATES PRODUCING PLANTS WITH INCREASED TITLE OF INVESTION: REPRESSING OF SUCKORS PROGRAMIS SYPTIAGE

TITLE OF INVESTION: ALL OF SUCKORS PROGRAMIS SYPTIAGE

TITLE OF INVESTION: ALL OF SUCKORS PROGRAMIS SYPTIAGE

TITLE OF INVESTION: ALL OF SUCKORS PROGRAMIS SYPTIAGE

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Search completed: June 3, 2004, 12:03:08 Job time: 11.8 secs
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US-09-252-991A-31637

j Sequence 31637, Application US/09252991A

j Sequence 31637, Application US/09252991A

j Sequence 31637, Application US/09252991A

j Sequence 31637

general Information:
    APPLICATION:
    APPLICATION:
    APPLICATION:
    APPLICATION:
    AREX GLOVENCES RELATING TO PSEUDOMONAS

    TITLE OF INVENTION:
    AREX GLOVENCE ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

    TITLE OF INVENTION:
    AREX GLOVENCE:
    AREX GLOVE
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US-08-569-147-82
Sequence 82, Application US/08569147
PRECENT NO. 6180377
MUNICAL NO. 6180377
MUNICAL NO. 6180377
MUNICAL NO. 6180377
MUNICAL SEQUENCES: 95
NUMBER OF SEQUENCES: 95
MUNICALSER: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Compatible OPERATICATION LEW PC-DOS/MS-DOS OSCHWARE: Patentin Release #1.0, Version #1.25 (BPO) CURRENT APPLICATION DATA: S36
ATTORNEY/AGRY INFORMATION: S36
ATTORNEY/AGRY INFORMATION: MAGE: Trujillo, Doreen Yatko REGISTRATION NUMBER: CARP-0047
TELEPHONE: (215) 568-3439
INFORMATION POR SEQ ID NO: 82: SEQUENCE CHARACTERISTICA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cuery Match 63.0%; Score 34; DB 3; Length 140; Best Local Similarity 75.0%; Pred. No. 20; Matches 6; Conservative 0; Mismatches 2; Indels
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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-569-147-82
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                                                                          Query Match 63.0%; Score 34; DB 4; Length 10.65; Best Local Similarity 85.7%; Pred. No. 2e+02; Matches 6; Conservative 0; Mismatches 1; Indels
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31637
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RESULT 1
US-09-909-164-8
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                                                                                                                                      June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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Sequence 13,
Sequence 22,
Sequence 26,
Sequence 27,
Sequence 5,
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_MBW_PUB_pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NBW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NBW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NBW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NBW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-12
US-09-909-164-13
US-09-909-164-25
US-09-909-164-27
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US-09-909-164-5
US-09-909-164-9
US-09-909-164-10
US-09-909-164-10
US-09-909-164-32
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                                                                                          OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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Sequence 45, Appl Sequence 46, Appl Sequence 47, Appl Sequence 48, Appl Sequence 49, Appl	Sequence 50, Appl. Sequence 51, Appl. Sequence 7, Appl. Sequence 11, Appl. Sequence 11, Appl. Sequence 12, Appl. Sequence 23, Appl. Sequence 24, Appl. Sequence 24, Appl. Sequence 25, Appl. Sequence 25, Appl. Sequence 25, Appl. Sequence 26, Appl. Sequence 31, Appl. Sequence 33, Appl. Sequence 33, Appl. Sequence 34, Appl. Sequence 37, Appl. Sequence 37, Appl. Sequence 37, Appl. Sequence 38, Appl. Sequence 42, Appl.	
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## ALIGNMENTS

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Sequence 8, Application US/09909164
; Sequence 8, Application US/09909164
; Publication No. US20020068702A1
; GENERAL INFORMATION:
    APPLICANT: Lim-Wilby, Marguerita
    APPLICANT: MARGER: US/09/909,164
    CURRENT APPLICATION NUMBER: 60/220,101
    PRIOR PILING DATE: 2000-00-21
    NUMBER OF SEQ ID NOS: 62
    SOFTWARE: PatentIn version 3.1
    SEQ ID NO 8
    LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: 11-mer synthesized according to example 1 PEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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NAME/KEY: MISC FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
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LOCATION: (9). . (9)
OTHER INFORMATION: D-amino acid
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ORGANISM: artificial sequence
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NAME/KEY: MOD_RES
LOCATION: (11)..(11)
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Geo-90-90-164-22

| Sequence 22, Application US/09909164
| Publication No. US20200068702A1
| Sequence 22, Application S20200068702A1
| Publication No. US20200068702A1
| GENERAL INFORMATION:
| APPLICANT: Lim-Wilby, Marguerita
| FILE REFERENCE: IN01192-US
| CURRENT FILING DATE: 2003-03-25
| PRIOR PAPLICATION NUMBER: 2003-03-25
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 22
| LIM-THE APPLICATION NUMBER: LIM-WILD NO 22
| BANDAL LIM-WILD NO 22
| LIM-THE APPLICATION NUMBER: LIM-WILD NO 22
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CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTLY VERSION 3.1
SEQ ID NO 13
LENGTH: 11
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OTHER INFORMATION: ACETYLATION
FEATURE:
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OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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OTHER INFORMATION: AMIDATION
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
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NAME/KEY: MOD_RES
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| Sequence 1.2. Application US/09909164
| Publication No. US20020068702A1
| General Incomment of the periods of the p
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Sublication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corves International, Inc.

APPLICANT: Lim.Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Colle E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN01192-US
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                                                                                                                          Query Match 96.3%; Score 52; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.00097; Matches 11; Conservative 0; Mismatches 0; Indels
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LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (8)...(8)
CTHER INFORMATION: D-amino acid
US-09-909-164-12
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NAME/FEX: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
FEATURE:
                         ; OTHER INFORMATION: AMIDATION
US-09-909-164-8
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Sequence 5, Application US/09909164
; Bedication No. US20020068702A1
; Publication No. US20020068702A1
; Publication No. US20020068702A1
; RENERAL INFORMATION:
; APPLICANT: Lim-wilby, Marguerita
; APPLICANT: REFERENCE: IN01192-US
; FILE REFERENCE: IN01192-US
; CURRENT FILING DATE: 2000-07-21
; VUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5.
            APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INOING192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PAPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFWWARE: Patentin version 3.1
SEQ ID NO 27
LENGTH: 11
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Pred. No. 0.0097;
0; Mismatches 1; Indels
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OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KRY: MISC_FEATURE
1 LOCATION: (8)...(9)
2 OTHER INFORMATION: D-amino acids
US-09-909-164-27
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NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FRATURE:
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: artificial sequence
PEATURE:
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90.9%;
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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NAME/KEY: MISC_FEATURE
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NAME/KEY: MISC FEATURE
LOCATION: (6). . (6)
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Sequence 26, Application US/0909164

Publication No. US2020068702A1

Sequence 26, Application No. US2020068702A1

SEQUENCE 21 INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Brunck, Terence K

TITLE OF INVENTION NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS OF TREE REFERENCE: INOL192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-21
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Pred. No. 0.0097;
0; Mismatches
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
OTHER INFORMATION: norvaline-(CO)
                                     NAME/KEY: MISC_FEATURE

LOCATION: (9)...(9)

COTHER INFORMATION: D-amino acid
US-09-909-164-22
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NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11) ... (11)
OTHER INFORMATION: AMIDATION
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COTHER INFORMATION: D-amino acid
US-09-909-164-26
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90.9%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 11
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Best Local Similarity 90.5
Matches 10; Conservative
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US-09-909-164-27
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US-09-909-164-10

US-09-909-164-10

IS-09-909-164-10

Sequence 10. Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REPRENCE: INO192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: 60/220,101

PRIOR PRING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 10

LENTH: LIM
APPLICANT: Levy, odile E
APPLICANT: Levy, odile E
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
FILE REPERENCE: INO192-08
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: US/09/909,164
FRICH APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                      FRATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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1 LOCATION: (8) ...(8)
2 OTHER INFORMATION: D-amino acid
US-09-909-164-9
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LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
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OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Matches 10, Conservative
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEFATITIS C
FILE REFERENCE: INOI192-08
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2000-03-25
PRIOR PELING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Parentin version 3.1
SEQ ID NO 6
LENGTH: 11
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Pred. No. 0.015;
0; Mismatches 1; Indels
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Pred. No. 0.019
0; Mismatches
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Sequence 9, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
  OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (9)..(9)
OTHER INFORMATION: D-amino acid
FEATURE:
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: artificial sequence
                                                                                                                                                                   Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)..(11)
COTHER INFORMATION: AMIDATION
US-09-909-164-6
                         FEATURE:
NAMME/KEY: MOD RES
LOCATION: (11)..(11)
COTHER INFORMATION: AMIDATION
US-09-909-164-5
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Page 5

APPLICANT: Levy, Odile B

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TURBENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR PIPLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PACENTIN VERSION 3.1

SEQ ID NO 32

HENDY APPLICATION VERSION 3.1

SEQ ID NO 32
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| Sequence 35, Application US/0909164
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Lin-Wilby, Marguerita
| APPLICANT: Envy, Odile B
| APPLICANT: Brunck, Terence K
| TITLE OF INVENTION: NOVEE PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TITLE OF INVENTION: NOVEE: 109/09/909,164
| CURRENT FILING DATE: 2000-07-21
| VUMBER OF SEQ ID NOS: 62
| SOOFWARE: PatentIn version 3.1
| SEQ ID NO 35
| LENGTH: 11
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Pred. No. 0.015
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: NOD RES
LOCATION: (1) - (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: NOD RES
LOCATION: (11) . (11)
OTHER INFORMATION: AMIDATION
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US-09-909-164-32
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OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.5
Matches 10; Conservative
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Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Branck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INO192-US
CURRENT PILING DATE: 2003-03-25
RIOR APPLICATION NUMBER: 60/220,101
RIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
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Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.2%; Score 46; DB 12; Length 11; 90.9%; Pred. No. 0.015; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
                                                                                                                                                                                                NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (6). (6)
; OTHER INFORMATION: norvaline-(CO)
US-09-909-164-31
                                                                                                                                                                                                                                                                                NAME/KEY: MISC_FEATURE
1.OCATION: (8)...(9)
2.007HER INFORMATION: D-amino acids
35.09-909-164-10
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: artificial sequence
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                  OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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LENGTH: 11
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COCATION: (8)...(9); COTHER INFORMATION: D-amino acids US-09-909-164-41
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: artificial sequence
PEATURE:
Publication No. US20020068702A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAMES/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
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Publication No US20020069702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: NUMBER OF 101192-12

CURRENT FILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 40

LENGTH: 11
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PUTER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
NAME/KEY: MOD_RES
OTHER INFORMATION: ACETYLATION
FEATURE:
                                                                                                                                                                                                                         Score 46; DB 12; Length 11;
Pred. No. 0.015;
0; Mismatches 1; Indels
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Pred. No. 0.015;
0; Mismatches 1; Indels
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US-09-909-164-41
; Sequence 41, Application US/09909164
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                      FEATURE:
NAME/KEY:
NAME/KEY:
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                  FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
US-09-909-164-35
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US-09-909-164-40
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: artificial sequence
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
  OTHER INFORMATION: AMIDATION
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CREATE, INCOMPATION:
APPLICANT COTAG International, Inc.
APPLICANT Leav. Cortag International, Inc.
APPLICANT Leav. Coling Brinck Paraguerita
APPLICANT Leav. Coling Brinch Paraguerity
APPLICANT Leav. Coling Brinch Paraguerity
APPLICANT NOWERRE 10003-03-25
FILE REPRESENT APPLICATION NOWERS 60/220,101
PRIOR APPLICATION NOWERS 60/220,101
APPLICATION: APPLICATION NOWERS 60/220,101
APPLICATION: APPLICATION APP
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V1 protein - tobac
sucrose-phosphate
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unknown protein F2
sucrose-phosphate
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6-0-methylguanine-
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hypothetical prote
probable membrane
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                                                              June 3, 2004, 11:35:47; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                      283366
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                               283366 segs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
                                          - protein search, using sw model
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D69551
A42452
$72649
$72650
G96764
JC4783
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Maximum DB seq length: 200000000
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54
1 EEVVPXGMDYS 11
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Match Length DB
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1049
1068
1081
1083
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
Sequence:
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                                          OM protein
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                                                                Run on:
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Conserved hypothetical protein AF2411 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: 069551
B;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 344-370, 1997
Nature 390, 344-370, 1997
Nature 390, Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Vener, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Vener, J.C.
A;Atterence number: A69250; MUID:98049343; PMID:9389475
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

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Gaps

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Score 40; DB 2; Length 156; Pred. No. 1; 1; Mismatches 1; Indels

h Similarity 77.8%; 7; Conservative

Query Match Best Local Similarity

Best Loc Matches

||:| |||| EVMPLGMDY 58 2 EVVPXGMDY 10

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disease resistance (1908 2 T48899)	Ride Haan, M.; Maarse, A.C.; Grivell, L.A. submitted to the EMBL Data Library, May 1995 A; Accession: 854617 A; Accession: 854619 A; Accession: 854619 A; Accession: 854619 A; Accession: 854619 A; Cross-references: EMBL: 887331; NID: g1041652; PIDN: CAA60762.1; PID: g829123 A; Cross-references: EMBL: 887331; NID: g1041652; PIDN: CAA60762.1; PID: g829123 A; Cross-references: EMBL: 86877 A; Reference number: 866879 A; Reference number: 866879 A; Reference number: 866879 A; Reference number: 866879 A; Reference strain \$288C C; Generics:
148899 F8335 F8335 T30830 T31308 A99427 A99427 A99427 A96427 A96601 A9601 A11GNMENTS A11GNMENTS A11GNMENTS A11GNMENTS A11GNMENTS A11GNMENTS	Ride Haan, M.; Maarse, A.C.; Grivell, L.A. submitted to the EMBL Data Library, May 1995 Affecerace number: S54617 A.Accession: S54619 A.Accession: S54619 A.Residues: 1-156 ~ UER- A.Gross-references: EMBL:X87331; NID:g1041652; A.Gross-references: EMBL:X87331; NID:g1041652; A.Gross-references: EMBL:X87331; NID:g1041652; A.Gross-references: EMBL:X87331; NID:g1041652; A.Gross-references: EMBL:Z74920; NID:g1420109; A.Accession: S56877 A.Accession: S56879 A.Accession: S6879 A.Accession: S6879 A.Accession: S6879 A.Accession: S6879 A.Accession: S6879 A.Accession: S7880 C.Genetics: A.Accession: S7880 C.Genetics: A.Accession: S7880 C.Genetics: A.Accession: Access SGD:S005539 A.Accession: Access
	31; Maa Maa Maa Maa Maa Maa Maa Maa Maa Ma
1062 1062 3472 3472 1128 1128 1172 1172 1172 1172 1172 11	A.C.; (617 617 11.X873: 11.X873: 11.Z749; 81.Z749; 81.Z749; 81.Z749;
2 # # # # # # # # # # # # # # # # # # #	BEL I SS-4 SS-4 SS-4 SS-4 SS-4 SS-4 SS-4 SS
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34 34 34 34 33 33 33 33 33 33 33 33 33 3	w, m, m, m, m do the outbeck of the try ps s 1-15: s 1
30 34 63.0 908 2 T488 31 34 63.0 1062 2 T938 32 34 63.0 1062 2 T938 33 34 63.0 3472 2 T938 34 33 61.1 128 2 A994 35 33 61.1 122 2 S978 39 33 61.1 225 2 S978 40 33 61.1 267 2 S978 41 33 61.1 267 2 P992 42 33 61.1 267 2 G993 43 33 61.1 267 2 G993 44 33 61.1 267 2 G993 45 33 61.1 267 2 G993 46 33 61.1 267 2 G993 47 33 61.1 299 2 E904 C.Speches: Saccharomyces cerevisiae	R; de Haan, M.; Maarse, A.C.; Grivel: Submitted to the EMBL Data Library, A; Reference number: S54617 A; Accession: S54617 A; Residues: 1-156 CDEH- A; Recession: S6687 A; Reference number: S6687 A; Recession: S6687 A; Rocession: S6687 A; Residues: 1-156 CDEW- A; CCOSS-references: EMBL: 274920; NI: A; Experimental source: strain S288C C; Genetics: A; CCOSS-references: SGD: S0005539 A; Map position: 15R C; Superfamily: hypothetical protein

70.4%;

Query Match
Best Local Similarity 54.5
Matches 6; Conservative

| :|| |:| 120 ENIVPYGIDFS 130 1 EEVVPXGMDYS 11

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Cybecies: Arabidopsis thaliana (mouse-ear crees)
Cybecies: Arabidopsis thaliana (mouse-ear crees)
Cybecies: Arabidopsis thaliana (mouse-ear crees)
Cybecies: Ochar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
CyAccession: G96764
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Chung, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Ji, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.K.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Altle: Sequence and analysis of chromosome in of the plant Arabidopsis.
A;Accession: G96764
A;Status: preliminary
A;Molecule changers preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructos A; Pathway: sucrose biosynthesis
C; Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology C; Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis P;1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
sucrose-phosphate synthase (EC 2.4.1.14) isoform 3 - Citrus unshiu (fragment) c;Species: Citrus unshiu c;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000 C;Accession: 572650 F;Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T. Mol. Genet: 222, 346-351, 1996 A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate synth
                                                                                                                                                                                                                                                                                                                                                                                                              A)Residues: 1-348 «KOM»
A)Cross-references: EMBL:AB006660; NID:g2351059; PIDN:BAA22071.1; PID:g2351060
A)Experimental source: Efruit, CV. Miyagawa-Wase
A,Rybe: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-460 <STO>
A;Cross references: GB:AE005173; NID:g6692750; PIDN:AAF24856.1; GSPDB:GN00141
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 460;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sucrose-phosphate synthase (EC 2.4.1.14) - rice C, Species: Oryza sativa (rice)
                                                                                                                                                                                                                                                                                                 A,Accession: S72650
A,Status: nucleic acid sequence not shown
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 66.7 tes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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ses 7; Conserv
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Matches
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42452

V1 protein - tobacco yellow dwarf virus (strain Australia)

C; Species: tobacco yellow dwarf virus

C; Species: tobacco yellow dwarf virus

C; Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999

C; Accession: A42452

R; Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.

R; Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.

A; Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yelld A; Reference number: A42452; MUID:92188538; PMID:1546458
A;Molecule type: DNA
A;Residues: 1-363 <KLE>
A;Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Komatsu. A.; Takanokura, Y.; Omura, M.; Akihama, T. Mol. Gen. Genet. 222, 346-351, 1996
A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate syntha A;Reference number: S72648; MUID:96439842; PMID:8842155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Pathway: sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;1-341/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Yollonder type: mRNA
A.Kolecule type: mRNA
A.Kesidues: 1-341 <KOM>
A.Cross-references: EMBL:AB006319; NID:g258891; PIDN:BAA23215.1; PID:g2588892
A.Stxperimental source: fruit, cv. Miyagawa-Wase
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Citrus unshiu (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Citrus unshiu
C.Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C,Accession: S72649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                              Gaps
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A, Molacule type: DNA
A, Residues: 1-102 KNOR>
A, Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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Pred. No. 16;
2; Mismatches 1; Indels
                                                                                                                                       Length 363;
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                                                                                                                                       DB 2;
6.8;
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                                                                                                                                       Score 38; DB 2
Pred. No. 6.8;
3; Mismatches
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Pred. No. 4.3;
3; Mismatches
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60.08;

Query Match Best Local Similarity 60.0 Matches 6; Conservative

2 EVVPXGMDYS 11

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66.7%; ilarity 66.7%; Conservative

Query Match Best Local Similarity Matches 6; Conserv

228 VIPPGMDFS 236

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3 VVPXGMDYS 11

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C;Accession: T04103
R;Sakamcto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Pujimura, T.
Rjakamcto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Pujimura, T.
Bibat Sci. 112, 207-217, 1995
A;Title: Structure and FRLP mapping of a rice sucrose phosphate synthase (SPS) gene that A;Reference number: Z15212
A.Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc A.Pathway: sucrose biosynthesis (S.Superfamily: sucrose-phosphate synthase, sucrose-phosphate synthase homology C.Superfamily: sucrose-phosphate synthase homology C.Seywords: glycosyltransferase; haxosyltransferase; sucrose-biosynthesis P:176-674/Domain: sucrose-phosphate synthase homology <SSS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T04062
K;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 4
A;Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 60;
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Pred. No. 60;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-1083 <BEV>
A;Cross-references: EMBL:ALO49487
A;Cross-reference: EMBL:ALO49487
A;Experimental source: cultivar Columbia; BAC clone F28M11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: F28M11.40
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                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-1049 <VAL>
A;Cross-references: GB-U33175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
A)Ancte: UDPglucose-fructose-phosphate glucosyltransferase; Surrosephosphate-UDPglucosylt
C;Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-frud A; Pathway: sucrose biosynthesis
C; Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology C; Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;178-666/Domain: sucrose/sucrose-phosphate synthase homology <8SPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Zea mays (maize)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JQ1329; PQ0260
R;Worrell, A.C.; Brunneau, J.M.; Summerfelt, K.; Boersig, M.; Voelker, T.A.
Plant Cell 3, 1121-1130, 1991
A;Title: Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohyd
A;Reference number: JQ1329; MUID:92338937; PMID:1840396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 71-74;206-212;471-481;872-892 <WCRI>
C;Comment: This enzyme transfers the glucosyl group from UDPglucose to fructose-6-phosph
C;Comment: This enzyme is involved in the regulation of carbon partitioning in the leave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruct A, Pathway: sucrose biosynthesis
C, Superfamily: sucrose-phosphate synthase; sucrose-sucrose-phosphate synthase; sucrose-sucrose-sucrose biosynthesis
C, Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;180-663/Domain: sucrose/sucrose-phosphate synthase homology <8SPS>
                                             Accession: JC4783
Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: Sps1
A;Introns: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3;
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                                                                                                          Gene 170, 217-222, 1996
A/Title: Characterization of a rice sucrose-phosphate synthase-encoding gene.
A/Reference number: JC4783; WUID:96235138; PMID:8666248
                10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Molecule type: mENA
A;Residues: 1-1668 <WOR>
A;Cross-teferences: GB:M97550; NID:g168625; PIDN:AAA33513.1; PID:g168626
A;Accession: PQ0260
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66.7%; Score 36; DB 2; Length 1049;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 1; Indels
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Pred. No. 59;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sucrose-phosphate synthase (EC 2.4.1.14) - maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%;
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436 VIPPGMDFS 444
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Best Local Similarity
Matches 6; Conserv
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VIPPGMDFS
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A;Gene: CESP:C53A5.2
A;Map position: 5
A;Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2; 6
                                                                                                        probable alkaline proteinase APB0263 - Aeropyrum pernix (strain KI)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: H72784
H; A1284
H; Takamiya, M; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takamiya, M; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takamiya, M; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takamiya, DNA Res.
DNA Res. (33-101, 1999
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Residus: preliminary
A;Residus: 1-440 cxAm>
A;Residus: 1-440 cxAm>
A;Residus: 1-440 cxAm>
A;Cross-references: DDB0:AP000058; NID:g5103389; PIDN:BAA79178.1; PID:g5103657
A;Reperimental source: strain KI
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C;Gpecies: Caenorhabditis elegans
C;Accession: T20173; T23857
R;Mortimoze; B.
S;Mortimoze; B.
S;Mortimoze; B.
S;Mortimoze; B.
S;Mortimoze; B.
S;Mortimoze; Data Library, November 1996
A;Accession: T20173
A;Accession: T20173
A;Accession: T20173
A;Accession: Proliminary; translated from GB/EMBL/DDBJ
A;Molecule Lype: DNA
A;Residues: 1-1150 < WILD-
A;Accession: T23857
A;Accessio
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64.8%; Score 35; DB
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches
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C,Superfamily: subtilisin; subtilisin homology
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Best Local Similarity 66.7
Matches 6; Conservative
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562 VLPVGIDYS
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: H87660
E;Mierman, M.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
C;Genetics:
A;Genetics:
A;Gene: Spai
A;Map position: 1
A;Introns: 120/3; 200/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase; homology
C;Keywords: glycosyltransferase; hexosyltransferase
F;196-680/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: Z19842
A;Accession: T24111
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 <WIL>
A;Cross-references: EMBL;Z81109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
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A;Molecule type: DNA
A;Residues: 1-433 <STO>
A;Crost-references: GB:AE005673; NID:g13425020; PIDN:AAK25284.1; GSPDB:GN00148
C;Genetics:
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Pred. No. 60;
2; Mismatches 1; Indels
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64.8%; Score 35; DB 2; Length 425;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 2; Indels
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Pred. No. 35;
2; Mismatches 3; Indels
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A;Introns: 23/3; 56/3; 113/3; 257/2
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54.5%;
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66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
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453 VIPPGMDFS 461
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A;Gene: CESP:R10D12.10
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RESULT 13

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ALIGNMENTS
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HIS9_THEMA
GGD2_RAT
GGD2_HUMAN
GGD2_MOUSE
GGD1_BRARE
GGD1_XENLA
GGD2_CHICK
GGD2_XENLA
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Fusobacterium.
NCBI_TaxID=76856;
FUSIN
RESULT 1
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117.693 Million cell updates/sec
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Q8y6u8
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P15822
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                       Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                    141681 seqs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Y11K_TYDVA
SPS_ORYSA
SPS_MAIZE
SPS_CRAPL
FAF_DROME
KHLI_HUMAN
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Maximum Match 100%
Listing first 45 summaries
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                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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thermotoga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGURENCE FROW N.A.

SEQUENCE FROW N.A.

STRAIN=21886394; PubMed=11889109;

KEDLINE=21886394; PubMed=11889109;

KEDLINE=21886394; PubMed=11889109;

KEDLINE=21886394; PubMed=11889109;

REDLINE=21886394; PubMed=11889109;

REDLINE=21886394; PubMed=11889109;

REDLINE=21886394; PubMed N., Kardner W., Grechkin G., Zhu L.,

Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

Larsen N., Kyrpides N., Overbeek R.,

"Genome sequence and analysis of the oral bacterium Fusobacterium
nuclaarum strain ATCC 25868.";

"Genome sequence and analysis of the oral bacterium Fusobacterium
nuclaarum strain ATCC 2586.";

"Bacteriol. 184:2005-2018(2002).

-I CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +

phosphate + L-glutamate + carbamoyl phosphate;

-I CATALYTIC ACTIVITY: 2 ATP + L-glutamine (By similarity).

-I PATHWAY: Arginine biosynthesis, first step.

-I PATHWAY: Pyrimidine biosynthesis, first step.

-I PATHWAY: Pyrimidine biosynthesis, first step.

-I PATHWAY: Composed of two chains; the small (or glutamine) chain

promotes the hydrolysis of glutamine to ammonia, which is used by

the large (or ammonia) chains to synthesize carbamoyl phosphate (By similarity).
                                                                                    28-FBE-2003 (Rel. 41, Created)
28-FBE-2003 (Rel. 41, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (RC 6.3.5.5) (Carbamoyl-phosphate synthase large chain (RC 6.3.5.5) (Carbamoyl-phosphate synthase ammonia chain).
Pusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacteriase; Rusobacteriaceae;
PRT; 1058 AA
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7 QVVPSGINYS 16

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RESULT 3
SPS ORYSA
ID SPS ORYSA
AC Q43802;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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AR PFam; PF02142; MGS; 1.

DR PRINTS; PR00098; CPSASE.

DR PROSITE; PS00866; CPSASE.1 1.

DR PROSITE; PS00866; CPSASE.1; 2.

DR PROSITE; PS00867; CPSASE.2; 2.

KM Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KM Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KM Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KM Arginine biosynthesis; Complete proteome.

CARBOXPHOSPHATE SYNTHETIC DOMAIN.

402 546 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

**ARTERIC DOMAIN.**

**ARTERIC DOMAIN.**
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQUENCE FROM N.A. Med=1546458;
MORTINE=92188538; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
Morris B.A.M., Richardson E.A., Haley A., Zhan X., Thomas J.E.;
The mucleotide sequence of the infectious cloned DNA component of
The mucleotide warf virus reveals features of geminiviruses
infecting monocovyledonous plants.";
Virology 187:633-642(1992).
                                                                                                                                                                              ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 2.2; 1ve 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                              Score 38; DB Pred. No. 9.4; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A42452, A42452.
InterPror, IPRO02621, Gemini mov.
Pfam; PP01708, Gemini mov; I.
Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M81103; AAA47947.1; -.
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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190 EIVPNGLNYS 199
                                                                                                                                                  1058
1058
210
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                                                                                                                                                                                    153 21
302 35
284 28
300 30
820 820
832 83
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                                                                                                                                                                                                                                                                                                                                                                                                                      YIIK TYDVA
ID YIIK TYDVA
AC P31619;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way undified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         General 170:217-222(1996).

-I. FUNCTION: Involved in the regulation of carbon partitioning in the leaves of plants. May regulate the synthesis of sucrose and therefore play a major role as a limiting factor in the export of photoassimilates out of the leaf.

-I. CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14)
(UDP-glucose-fructose-phosphate glucosyltransferase).
Orya sativa (Rice).
Eukaryota, Viriglialntae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Lillopsida; Poales; Poaceae;
Enhartoideae, Oryzeae, Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sucrose 6-phosphate.
-!- ENZYME REGULATION: Activity regulated by phosphorylation and
moderated by concentration of metabolites and light.
                                                                                                                                                                                                                                                                                                                                                                                                                              Herrera-Estrella L.; "Characterization of a rice sucrose-phosphate synthase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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24;
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                                                                                                                                                                                                                                                                                                                                    STRAINE_cv. Indica-IR36; TISSUE=Leaf;
MEDLINE=96235138; PubMed=8666248;
Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gramens; TYSOUS,
Interpro; INTERPROS LYBOR LYBOR
Pfam; PF00534; Glycos Lransf_1; I.
Transferase; Glycosyltransferase; Phosphorylation.
22 29 POLY-GLY.
DOMAIN 695 698 POLY-GLU.
DOMAIN 775 779 POLY-ARG.
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Pred. No. 24;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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P31927;
01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U33175; AAC49379.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JC4783; JC4783.
Gramene; Q43802; -
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Best Local Similarity
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                                                                                                                                                                                                                                                            NCBI_TaxID=4530;
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SPS MAIZE
ID SPS MA
AC P3192'
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2 EVVPXGMDYS 11

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lamiids; Lamiales; Lamiales incertae sedis; Lindernieae;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                        Worrell A.C., Bruneau U.-M., Summerfelt K., Boersig M., Voelker T.A., "Expression of a maize sucrose phosphate synthase in tomato alters "Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohydrate partitioning.";
Plant Cell 3:1121-1130(1991).
-1- FUNCTION: Involved in the regulation of carbon partitioning in the leaves of plants. May regulate the synthesis of sucrose and therefore play a major role as a limiting factor in the export of photoassimilates out of the leaf.
-1- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +

BUCTOSE 6-phosphate.
-!- ENZYME REGULATION: Activity regulated by phosphorylation and moderated by concentration of metabolites and light.
-!- PATHWAY: Sucrose synthesis.
-!- SUBDWIT: Homodimer or homotetramer.
-!- DEVELOPMENTAL STAGE: Germinating seeds or mature leaves.
-!- PTM: Phosphorylated. However, phosphorylation is not essential for

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                     Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase 2 (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase 2).
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
                                                   (UDP-glucose-fructose-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enzyme function.
-!- SIMILARITY: Belongs to the glycosyltransferase family 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1; Length 1068; Pred. No. 25;
                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trache
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 1068 AA; 118575 MW; 074679B5E9A1D282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        naizezo; 1PRO), 29, Glyco trans 1.
Pfam; PF00534; Glycos transf 1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
DOMAIN 25
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1081 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                 STRAIN=CV. PIONEER 3184; TISSUE=Leaf;
MEDLINE=92338837; PubMed=1840396;
                                                                             phosphate glucosyltransferase)
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Eukaryota; Viridiplantae; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 66.7
les 6; Conservative
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                                                                                                                                                                                                                  NCBI_TaxID=4577;
                                                                                                                        Zea mays (Maize)
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1982_CRAPL
(C 004933,
T 15-DEC-1;
)T 15-DEC-1;
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                                                                                FAR DROME STANDARD, PRT; 2778 AA.
P55624; (097027;
01.NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 43, Last annotation update)
(Ubiquitin thiolesterase FAF) (Ubiquitin-specific processing protease FAF) (Deubiquiting enzyme FAF) (Rat facets:protein).
FAFOR BCDNA:LD22582 OR CG1945.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIR, T09837, T09837.
InterPro, IPR001296; Glyco_trans_1.
Pfam; PR00334; Glycos_transf=1; 1.
Transferase; Glycosyltransferase; Phosphorylation; Multigene family.
Transferase; 248
POLY-SER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 36; DB 1; Length 1081; 66.7%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               787 790 POLY-ARG.
1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fischer-Vize J.A., Rubin G.M., Lehmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Eye imaginal disk;
MEDLINE=93202020; PubMed=1295747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
Les 6; Conserv
Craterostigma.
NCBI_TaxID=4153;
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The fat facete gene is required for Drosophila eye and embryon development."

Consideration of the control of t
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60; 60:0007349; P:cellularization; IMP.
60; 60:0007456; P:cellularization; IMP.
60; 60:0007456; P:cellularization; Gensu Drosophila); IMP.
60; 60:00070456; P:cytoplasm; Cell fate differentiation (sensu Dr. .; IMP.
60; 60:0007097; P:nuclear migration; IMP.
60; 60:00016579; P:protein debbiquitionation; IDA.
60; 60:0006511; P:ubiquitin-dependent protein catabolism; IGI.
InterPro; IPR001394; Peptidase_C19.
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                                                                                                                                                                                                                                                                                                                 Isoid=P55824-3; Sequence=VSP_005269;
-1- TISGUE SPECIFTCITY: Bye disks and ovaties.
-1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-1- SIMILARITY: Belongs to peptidase family C19.
function.
CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0
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                                                                                                                                                                                                                                                                IsoId=P55824-2; Sequence=VSP_005270;
                                                                                                                                                                                                               IsoId=P55824-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, L04959, AAPO1345.1; -. SMBL, L04958, AAPO1346.1; -. SMBL, L04960; AAPO1347.1; -. SMBL, L04960; AAPO1348.1; -. SMBL, AE003779; AAPO139.1; -. SMBL, AE003779; AAPO139.1; -. SMBL, AF45677; AAD38652.1; -.
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PROSITE; PS00973; UCH 2 2; 1.
PROSITE; PS50235; UCH 2 3; 1.
Ubl conjugation pathway; Hydro
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54.5%;
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Best Local Similarity
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RESULT 7

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Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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58
94
139
142
147
154 AA;
                                                                                                                                                                                                                                                                                                             SECUENCE OF 58-154
                                                                                                                                                                                                                     NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transit peptide.
TRANSIT 1
CHAIN 58
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                                                                                                                                                                                                  TISSUB=Brain;
MEDINE=20277482; PubMed=10819331;
MEDINE=20277482; PubMed=10819331;
Magase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay M.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May play a role in organizing the actin cytoskeleton of the brain cells.
                                                                    Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                            MEDINE=20347694; PubMed=10888605; Koob M.D., Nemes J.P., Benzow K.A.; The SCAS transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHLI)."; Hum. Mol. Genet. 9:1543-1551(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C11C43D8282F9FF9 CRC64;
                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Cytoplasmic.
-! TISSUB SPECIFICITY: Highly expressed in brain.
-!- SIMILARITY: Contains 1 BTB/POZ domain.
-!- SIMILARITY: Contains 6 Kelch repeats.
KHLI HUMAN STANDARD; PRT; 748 AA. 09A64; 09M85; 09P238; 16-0CT-2001 [Rel. 40, Created) 16-0CT-2001 [Rel. 40, Last sequence update) 10-0CT-2003 [Rel. 42, Last annotation update) KK-1ch-1ike protein 1. KELCH-1ike protein 1.
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BTB.
KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
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EMBL; AF552279; AAF81716.1; -.
EMBL; AB040923; BAA96014.1; ALT_INIT.
EMBL; AL533738; CAC16128.1; -.
Genew; HGNC:6352; KLHL1.
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SEQUENCE OF 179-409 FROM N.A.
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                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                  MCBI_TaxID=9606;
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REPEAT
SEQUENCE
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MEDLINE=89386623; PubMed=2780537;
Yano H., Yano M., Tsugita A., Aso K., Nozu Y.;
Yano M., Tsugita A., Aso K., Nozu Y.;
Yano M., Suguence of plastocyanin from rice (Oryza sativa, subspecies japonica).";
Protein Seq. Data Anal. 2:385-389(1989).
Protein Seq. Data Anal. 2:385-389(1989).
-!- FUNCTION: Participates in electron transfer between P700 and the cytochrome bef complex in photosystem I.
-!- SUBCELLULAR LOCATION: Loosely bound to the inner thylakoid
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular cloning and characterization of plastocyanin precursor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzae, Oryza.
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DB 1; Length 748;
                                                                                                  0; Indels
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PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P20423; Q9SBB8;
01-FEB-1991 (Rel. 17, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Plastocyanin, chloroplast precursor.
Score 34.5; D
Pred. No. 35;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=cv. Ilpoom; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF093636; AAC78108.1; -. HSSP; P00289; 2PCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₩,
63.9%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                  127 EEVVP-GMDF 135
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1154
1139
142
                                                                                                                                                                                                          1 EEVVPXGMDY
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120 120 T -> N (IN CV. NK 1558). 155 AA; 15709 MW; DAA7EABESF6F4F91 CRC64;

VARIANT SEQUENCE

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à
                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I-SIMILARITY: Contains 1 plastocyanin-like domain.

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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=cv. NK 1558;
MEDLINE=9403081; PubMed=8223592;
Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                              pronuct terms. 277:97-104(1993).

-1. FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.

-1. SUBCELLULAR LOCATION: Loosely bound to the inner thylakoid membrane surface in chloroplasts.
                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBL_TAXID=4513;
                                                                                                                                                                                                                                                                       STRAIN=cv. Bomi;
Nielsen O.S., Gausing K.;
The precursor of barley plastocyanin: sequence of cDNA clones and
gene expression in different tissues.";
FEBS Lett. 225:159-162(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMEL; Y00704; CAA66666.1; -.

R PIR; S38255; S38255.

R HSSP; PO0289; 2PCF.

R InterPro; IPR001235; Capper_blue.

R InterPro; IPR008972; Cupredoxin.

R Ffam; PF00127; copper_blue.

R PRINTS; PR00156; COPPERBLUE.

R PROSTE; PS001255; Copper blue; 1.

R PROSTE; PS001255; COPPER_BLUE.

R PROSTE; PS001255; COPPER_BLUE; 1.

R PROSTE; PS00126; COPPER_BLUE; 1.

R CHLOROPLAST.

R CHLOROPLAST.
                         ö
Score 34; DB 1; Length 154;
Pred, No. 8.7;
                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLASTOCYANIN.
PLASTOCYANIN.LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
                                                                                                                                        01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plastocyanin, chloroplast precursor.
                                                                                                                     155 AA
                        2; Mismatches
  Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                    STANDARD;
                                                                  100 EDAVPSGVDVS 110
                                            1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155
155
155
140
143
143
                                                                                                                                                                                                                                                                                                                                                                                           promoter region.";
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                    PLAS HORVU
P08248,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
DOMAIN
METAL
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Dimitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
Complete amino acid sequence of poplar plastocyanin b.";
FEBS Lett. 226:17-22(1937).
I- STRAIN-CV. FEBS Lett. 226:17-22(1937).
Cytochrome b6-f complex in photosystem I.
Cytochrome b6-f complex in photosystem I.
SUBCELLULAR LOCATION: Loosely bound to the inner thylakoid membrane surface in chloroplasts.
SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYANINS A AND B.
SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Populus nigra (Lombardy poplar).
Makaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
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Pfam; PR0015; Copper blue; 1.

PRODITS; PR0015; Copper blue; 1.

Probom; PD001235; Copper blue; 1.

PR051FF; PS00196; Copper blue; 1.

Chloroplast; Electron transport; Copper; Thylakoid; Membrane;

Transit peptide; Multigene family.

Transit peptide; Multigene family.

TRANSIT 70 168 PLASTOCYANIN B.

DOMAIN 70 168 PLASTOCYANIN B.

CHAIN 70 168 PLASTOCYANIN LIKE.
Query Match
63.0%; Score 34; DB 1; Length 155;
Best Local Similarity 54.5%; Pred. No. 8.7;
Matches 6; Conservative 2; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=CV. Italical TISSUE=Leaf; STRAIN=CV. Italical TISSUE=Leaf; Reichert J. Genzelewski V., Haehnel W.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                          Filt.
01-0CT-1989 (Rel. 12, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                     PRT; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Last sequence upd
28-FEB-2003 (Rel. 41, Last annotation u
Plastocyanin B, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COPPER.
COPPER.
COPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z50186; CAA90565.1; -.
PIR; S00210; S00210.
PIR; S50206; S58208.
HSSP; P00299; IPLC.
InterPro; IPR000933; BlueCu 1.
InterPro; IPR000937; Copper blue.
InterPro; IPR008972; Cupredoxin.
                                                                                                                                                                               101 EDAVPSGVDVS 111
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                            1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 70-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3691;
                                                                                                                                                                                                                                                                                                                                                                        POPNI
              Query Match
                                                                                                                                                                                                                                                                                                                                     PLAT POPNI
ID PLAT P
AC P11970
                                                                                                                                                                                                                                                                                                             RESULT
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566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homologs;
                                                                                                                                                     R8L4 ARATH
Q9FJK8;
SQ SEQUENCE
                                                                                                                                          R8L4_ARATH
                                               Matches
                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL cutstation the European Bioinformatics Institute. There are no restrictions on its wee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                               ö
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
MEDLINE=98065943; PubMed=9403685;
MEDLINE=98065943; PubMed=9403685;
Lathigra R., Mite O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb U.F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
--- SUBCELLUTAR LOCATION: Cytoplasmic.
--- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain family. Subfamily 2.
                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine---
FRNA ligase beta chain) (PheRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
STRAIN=ATCC 35210 / B31;
STRAIN=ATCC 35210 / B31;
Strainebusch J.;
Strainebusch J.;
Strainebusch Tellinebusch J.;
Strainebusch Tellinebusch Strainebusch J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                     Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:586-586(1997).
-!- CARALYIIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP
diphosphare + L-phenylalanyl-tRNA(Phe).
-!- SUBUNIT: Tetramer of two alpha and two beta chains (By
                                              .
0
                     63.0%; Score 34; DB 1; Length 168; 54.5%; Pred. No. 9.5; tive 2; Mismatches 3; Indels
168 AA; 16981 MW; F20DA6EA2038AEEA CRC64;
                                                                                                                                                         566 AA.
                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U82978; AAB41019.1; -. EMBL; AE001153; AAC66870.1;
                                              Conservative
                                                                                   |: || |: |
112 EDAVPSGVDVS 122
                                                                                                                                                       STANDARD;
                                                                     1 EEVVPXGMDYS 11
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome
                                                                                                                                                                                                                                                                               NCBI_TaxID=139;
                                              6;
                                                                                                                                                       BORBU
SECUENCE
                                                                                                                                            SYFB_BORBU
                                              Matches
                                                                                                                                RESULT 11
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETATN=cv. Columbia;
SETAIN=cv. SETAI
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable disease resistance RPP8-like protein 4.
RPP8L4 OR ATSG48620 OR KISN18.9.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicocyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAINS-CV. COlumbia,
MEDLINE-99087489; PubMed-9872454;
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones.";

DNA Res. 5:297-336(1998).
                                                                                                                ö
Length 566;
                                                                                                           1; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding, Repeat, Leucine-rich repeat.
h Similarity 85.7%; Pred. No. 33; 6; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               908 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AB015468; BAB10695.1; -.
EMBL, AK117163; BAC41841.1; -.
InterPro; IPR000767; Disease_resist.
InterPro; IPR0011; LRR.
InterPro; IPR002182; NB-ARC.
Pfam; PF00560; LRR; 2.
Pfam; PF00531; NB-ARC; 1.
Pfam; PF00931; NB-ARC; 1.
Plant defense; ATP-binding; Repeat; Leu DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                           169 VPFGWDY 175
           Query Match
Best Local Similarity
                                                                                                                                                                                                                           4 VPXGMDY 10
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us-09-909-164-13.rsp

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MEDLINE=20271766; PubMed=10810142;
Cooley M.B., Pathirana S., Wu H.-J., Rachroo P., Klessig D.F.;
"Members of the Arabidopsis HRT/RPP8 family of resistance genes confer
"incompart of the Arabidopsis and comycete pathogens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2 AND RPP8-3, AND VARIANTS.
STRAIN-cv. Columbia, and cv. Landsberg erecta;
MEDINIS-99031019; PubMed-9811794;
MCDOWell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
Holub E.B., Dangl J.L.;
"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN=cv. Columbia,
MEDILINE=2254850; PubMed=14593172;
MEDILINE=2254850; PubMed=14593172;
MEDILINE=2254850; PubMed=14593172;
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
Arakawa T., Banh G., Banno F., Bowser L., Brooks S.Y., Carning P.,
Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen In F.,
Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
                                                                                                                                                                                                                                                                                                                                                                             ONTAGE OF SERVICES OF SERVICES
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein 8).

RPP8 OR HRT OR AT5G43470 OR MWF20.19.

Arabidopsis thaliana (Mouse-ear ores).

Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
MEDLINBE-20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                               ö
                                                                                                                                          DB 1; Length 908;
                                                                                                                                                                               2; Indels
                 559 LRR 1.
223 LRR 2.
367 LRR 3.
199 ATP (POTENTIAL).
104448 MW; 3111991B17239693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS.
                                                                                                                                                                                                                                                                                                                                                              908 AA
                                                                                                                                                         Pred. No. 54;
2; Mismatches
                                                                                                                                            Score 34;
  NB-ARC
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Cell 10:1861-1874(1998).
                                                                                                                                            63.0%;
                                                                                                                                                           60.08;
                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                              883 EKLVPGGEDY 892
                                                                                                                                                                                                                         1 EEVVPXGMDY 10
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                                                                               192 1
908 AA;
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NP BIND
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTERRACTION WITH TIP.

X MEDLINE-20196823; PubMed=11041886;

Ren T., Qu F., Morris T.J.;

Ren T., Qu F., Morris T.J.;

Ren T., Qu F., Morris T.J.;

THRT gene function requires interaction between a NAC protein and rival capsid protein to confer resistance to turning crinkle virus."; viral capsid protein to confer resistance proteins guard the FUNCTION: Disease resistance protein appropriate avirulence protein via an indirect interaction with this avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. The interaction with TIP (TCV-interacting protein) may be essential for the recognition of the avirulence proteins, and the triggering of the defense response.

C.-- SUBDIMIT: Interacts with the NAC protein TIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogen recognition.

-!- MISCELLAMEDUS: In cv. Columbia and cv. Landsberg erecta, RPPB specifically recognizes the Emco5 avirulence protein from Peronospora parasitica, while it is not the case in cv. Di-17, where it confers resistance to Turnip Crinkle Virus uppon recognition of the viral capsid protein.
-!- SIMILARITY: Belongs to the disease resistance NB-LRR family.
-!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
-!- SIMILARITY: Contains 1 NB-ARC domain.
-!- DATABASE: NAME-LRRS.
-!- DATABASE: NAME-LRRS.
-!- NOTE-Functional and comparative genomics of disease resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isold=Q8W4J9-2; Sequence=VSP_007171, VSP_007172; Note=Has been shown to exist_only in cv. Columbia so far; DOMAIN: The LRR repeats probably act as specificity determinant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogen recognition.

POLYMORPHISM: The strong polymorphisms present in cv. Di-17 and POLYMORPHISM: The strong pub to an unequal crossing-over between the highly related RPPS and RPHSA genes present in cv. Landsberg erecta. Such variations probably modify the specificity of
Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
Satou M., Tamee R., Vayeberg M., Wallender E.K., Wong C., Yamamura Y.,
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                               J.,
Kawai J.,
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2).
STRAINS-CV. COLUMDIA;
SERIA M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida .
Sati M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida .
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., I
Hayashizaki Y., Shinozaki K.,
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q8W4J9-1; Sequence=Displayed;
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WWW="http://niblrrs.ucdavis.edu".
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                                                                                                                                                                                                    genome.";
Science 302:842-846(2003)
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Query Match
Best Local Similarity 60..
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883 EKLVPGGEDY 892
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Matches 6; Conserv
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T -> I (in cv. Di-17).
S -> R (in cv. Di-17).
S -> R (in cv. Di-17).
H -> Q (in cv. Di-17).
I -> L (in cv. Di-17).
I -> L (in cv. Landsberg erecta).
K -> N (in cv. Landsberg erecta).
K -> N (in cv. Landsberg erecta).
R -> N (in cv. Landsberg erecta).
                                                                                                                        isoform 2).
/FTId=VSP 007171.
/FTId=VSP 007171.
/FIId=VSP 007172.
IDGQL -> VDEQI (in cv. Landsberg erecta).
G -> E (in cv. Di-17).
SGK -> RGE (in cv. Di-17).
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GKGV -> EKGI (in cv. Landaberg erecta).

GKGV -> EKGI (in cv. Landaberg erecta).

E -> D (in cv. Landaberg erecta).

F -> L (in cv. Di-17).

G -> Q (in cv. Di-17).

G -> U (in cv. Di-17).

G -> C (in cv. Di-17).

Y -> S (in cv. Di-17).

X -> T (in cv. Di-17).

X -> T (in cv. Di-17).

X -> T (in cv. Di-17).

Y -> K (in cv. Di-17).
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DSBISTYSELY -> YSKISAVDLFN (in cv. Landsberg erecta).

EISTYS -> KITTQE (in cv. Di-17).

A -> V (in cv. Landsberg erecta).

DNYLSWQ -> NKYLKVH (in cv. Di-17).

DN -> NR (in cv. Landsberg erecta).

WQ -> SH (in cv. Landsberg erecta).

WQ -> SH (in cv. Landsberg erecta).
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 C -> R (in cv. Di-17 and cv. Landsberg
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PRF -> SRFK (in cv. Di-17).

Y -> F (in cv. Di-17).

Y -> Y (in cv. Landsberg erecta).

C -> S (in cv. Di-17 and cv. Landsberg
                                                                                                         ATP (POTENTIAL).
WKMLLTSRNEGVGIH -> ELLWYIHEALFLLNS (in
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-> K (in cv. Di-17 and cv. Landsberg
      InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
Pfam; PF00560; LRR; 2.
Pfam; PF00561; NB-ARC; 1.
PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat; Alternative splicing; Polymorphism.
DOMAIN 146 459 NB-ARC.
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Arabloupsis.;

Plant Cell 10:1861-1874(1998).

-!- PUNCTION: Disease resistance protein. Resistance proteins guard
the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein.

That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. In contrast to RPB, it does not specifically recognize the Emcos avirulence protein from Peronospora parasitica.

This protein from Peronospora parasitica.

SPB, it does not specifically recognize the Emcos avirulence protein from Peronospora parasitica.

This protein is not present due to an unequal recossing over between the RPPB and RPBHA genes that creates a unique RPPB gene.

SIMILARITY: Belongs to the disease resistance NB-LRR family.

RPBB/HRT subfamily.

SIMILARITY: Contains 2 leucine-rich (LRR) repeats.

SIMILARITY: Contains 2 leucine-rich (LRR) repeats.

SIMILARITY: Contains 1 NB-ARC domain.

SIMILARITY: Contains 1 NB-ARC domain.

SIMILARITY: Contains 2 leucine-rich (LRR) repeats.

SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
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STRAIN=cv. Landsberg erecta;
MEDLINES9030193; PubMed=9811794;
MCDOWell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
Holub E.B., Dangl J.L.;
Intragenic recombination and diversifying selection contribute to the
evolution of downy mildew resistance at the RPP8 locus of
Arabidopsis.";
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Viridiplantae; Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Score 34; DB 1; Length 908;
Pred. No. 54;
2; Mismatches 2; Indels
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Print, PF0051, NB-ARC; 1.

Print, PF00531, NB-ARC; 1.

PRINTS, PR00314, NB-ARC; 1.

Plant defense, ATP-binding, Repeat, Leucine-rich repeat. DOMAIN 10 45 ENGINE-ZIPPER.

DOMAIN 16 459 NB-ARC.

REPEAT 602 625 LRR 1.

REPEAT 844 869 LRR 2.

REPEAT 844 869 LRR 2.

REPEAT 944 869 LRR 2.

REPEAT 944 869 LRR 1.

SEQUENCE 910 AA; 105263 MW; 581E9F65A19A12EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Disease resistance protein RPH8A (RPP8 homolog A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPH8A.
Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WWW="http://niblrrs.ucdavis.edu".
InterPro; IPR007057, Disease_resist.
InterPro; IPR001611; IRR.
InterPro; IPR0021182; NB-ARC.
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=96337999; PubMed=8688087;
MEDLINE=96337999; PubMed=8688087;
Sutton G.G.
Sutton G.G.
Sinke J.A., FlizGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Raich C.I.,
Overbeek R., Kirkness E.F., Weinfauch K.G., Mermann J.L., Nguyen D.,
Cott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.
Ulterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Fraser C.M., Smith H.O., Wosee C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1; Length 276;
Pred. No. 26;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGN: MAD939; TIROO163; SDRNP SM.
INTERPRO; IPRO05358; UPPO153.
Pfam. PRO3692; UPFO153.
Pfam. PRO3692; UPFO153.
Hypothetical protein; Complete proteome.
REQUENCE 276 AA; 33454 MW; 97BD69D392BC8FDF CRC64;
                                                                                                                                     Methanococcus jannaschii.
Archaea, Euryarchaeota, Methanococci, Methanococales,
Methanocaldococcaceae, Methanocaldococcus.
                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0939.
276 AA.
PRT;
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45.5%;
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PIR; C64417; C64417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 45.5
Matches 5; Conservative
  STANDARD;
                                                                                                                                                                                                 NCBI_TaxID=2190;
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Search completed: June 3, 2004, 11:49:53 Job time: 4.86667 secs

141 EEIIENGMEHS 151

1 EEVVPXGMDYS 11

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Q94.81 caulobacter Q94.81 aeropyrum p Q81.92 shigella fl O85.880 escherichia s Q81.92 shigella fl Q81.92 shigella fl Q95.84 carcinus ma Q94.67 rantocarabhi O82.673 escherichia O82.673 escherichia O82.673 escherichia O82.66 escherichia Q88.73 homo sapien Q88.15 chermoanaer Q86.15 treptococc Q86.16 ereptococc Q86.16 ereptococc Q86.16 ereptococc Q85.16 ereptococc Q8

027146 Q98K29

QBR9LS QBE5L9

Q8TBJ7

Q7V6Q4

**Q855K6** 

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SECUENCE FROM N.A.
STRAIN=FY1679;
MEDLINE=94019318; PubMed=8413243;
Dumont M.B., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).

Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "CYC2 encodes a factor involved in mitochondrial import of yeast cytochrome c.", Mol. Cell. Biol. 13:6442-6451(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FY1679;
De haan M., Maarse A.C., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=FY1679;
MEDLINE=94169519; PubMed=7764548;
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01-NOV-1996 (TrEMBLrel. 0
01-JUN-2003 (TrEMBLrel. 2:
ONF YOR013W.
PRELIMINARY;
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Submitted (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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 Sherman F.;
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  212479
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OSOGO archaecglob
OSOGO archaecglob
OSOSH citrus unsh
O22096 citrus unsh
O22096 citrus unsh
O27096 arabidopsis
O90547 arabidopsis
P93782 saccharum o
O95310 orvza sativ
O88064 orvza sativ
O88064 orvza sativ
O88064 eriotheir s
O88084 ciocheir s
O8858 clostridium
O88587 rhizobium t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q12479 saccharomyc
                                                               June 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                       1017041
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                      otal number of hits satisfying chosen parameters:
                                                                                                                                                                     1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                              M protein - protein search, using sw model
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Q301260
Q301260
Q822B1
O22081
O22081
Q9C9T7
P93782
Q9C9T7
Q93010
Q43010
Q85064
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sp_voints:*
sp_vertebrate:*
sp_vertebrate:*
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Gapop 10.0 , Gapext 0.5
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54
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Perfect score:
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Created) Last sequence update) Last annotation update)

156 AA

PRT;

ALIGNMENTS

Q815A7 Q8920 Q29920 Q29451

Q9YET8

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STRAIN=HTB831 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHS1, which complements a drug-
"Molecular cloning of a gene, DHS1, which complements a drug-
hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
EMBL, Z74920; CAA99201.1; -.
EMBL, X87331; CAA60762.1; -.
EMBL, X87331; CA4619.
SGD, S0005539; YOROJ3W.
SGD, S0005539; YOROJ3W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oceanobacillus iheyensis.
Bacteria; Firmicutes, Bacillales; Bacillaceae; Oceanobacillus.
NCBI_TaxID=182710;
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;
WEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.4%; Score 38; DB 16; Length 319; 60.0%; Pred. No. 18;
                                                                                                                                                                                                            74.1%; Score 40; DB 3; Length 156; 77.8%; Pred. No. 3; ive 1; Mismatches 1; Indels
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Nucleic Acids Res. 30:3927-3935(2002).
Nucleic Acids Res. 30:3927-3935(2002).
InterPro; IPR001279; Blactmase-like.
Pfam; PR00753; lactamase B; 1.
Hypothetical protein; Complete protecome.
BRQUENCE 319 AA; 35617 MW; 3BDAB4BF13E79E37 CRC64;
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Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical conserved protein.
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Last annotation update)
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                                                                                                                                                                                                                                     Local Similarity 77.8
ses 7; Conservative
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Matches 6; Conserv
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Q8ESV7
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Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., Morkenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., Morkeil L.K., Badger J.H., Glodek A., Zho, Coverbeek R., Gocayne J.D., Weidman J.F., MoDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Amson T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
PMBL; AB001109; AAB91255.1; -.
TIGR; AF2411; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
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Pred, No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 70.4%; Score 38; DB 17; Length 363; Local Similarity 54.5%; Pred. No. 20; see 6; Conservative 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfan; PP00296; bac luciferase; 1.
Hypothetical proteIn; Complete proteome.
SEQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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EMBL, AP005374; BAC09170.1; -
GO; GO: 0016021; C: integral to membrane; IEA.
GO; GO: 00160215; F: transporter activity; IEA.
GO; GO: 006810; P: transport; IEA.
InterPro; IPR001036; Acrflvin_res.
InterPro; IPR004764; HAB1.
PF00873; ACR_tran; III.
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PRINTS; PR00702; ACRIFLAVINRP.
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Best Local Similarity 63.0.
7; Conservative
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ENIVPYGIDFS 130
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843 EEVLPNGIGYS 853
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SEQUENCE 1044 A2
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01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25, At1g73750/F25P22_17.
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Best Local Similarity 66.77,
6; Conservative
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MEDLINE=2255087; PubMed=12663927;
Paulsen I.T., Baneriei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Foute D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
"Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                    Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NGEL_TaxID=1351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; Score 36; DB 16; Length 149; 70.0%; Pred. No. 20;
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                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JOCT-2003 (TrEMBLrel. 25, Last annotation update)
Large conductance mechanosensitive channel protein.
MSCL OR EF1152.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Sucrose-phosphate synthase (Fragment)
                                                                                                                                                                                                                                                                                                                                                GO; GO:0016620; C:membrane; IEA.
GO; GO:0016620; C:membrane; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001185; MS.channel.
Pfam; PF01741; MscL; 1.
PRINTS; PR01264; MSCH-HANNEL.
ProDom; PD007253; MS.channel; 1.
TIGRRPMs; TIGR00220; mscL; 1.
Complete proteome.
SEQUENCE 149 AA; 16127 WW; SS5799BF1E47D341
                                    149 AA.
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                                 PRT;
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Mol. Gen. Genet. 252:346-351(1996)
                                                                                                                                                                                                                                                                                                                           EMBL; AE016956; AA082828.1; -. TIGR; EF3152; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Citrus unshiu (Satsuma orange)
                                                                                                                                                                                                                                                                                                 Enterococcus faecalis.";
Science 299:2071-2074(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 70.0
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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SEQUENCE FROM N.A.
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STRAIN=cv. Miyagawa-Wase, TISSUE=Juice sacs and segment epidermis; Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.; "Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.)."; EMBL; AB006319; BAA23215.1; -. BMBL; AB0649; S72649; PAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Sapindales; Rutaceae; Citrus.
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MEDLINE-96439842; PubMed=8842155;
Komatsu A., Takanokura Y., Omura M., Akihama T.;
Takanokura Y., Omura M., Akihama T.;
"Cloning and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                          Score 36; DB 10; Length 341;
Pred. No. 50;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 36; DB 10; Length 348; 66.7%; Pred. No. 51; Live 2; Mismatches 1; Indels
                                                                                                                                                                                      341 341
341 AA; 38136 MW; 61417A69C4560777 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last anno
Sucrose-phosphate synthase (Fragment)
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66.7%;
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414 VIPPGMDFS 422
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ID P93782
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Kim C.J., Chen H., Cheuk R., Shinn P., Banh J., Bowser L.,
A Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
A lahida J., Jones T., Karlin, Heumann G., Kawal J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Southwick A.,
A Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Arabidopsis ORF clones.;
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Is Submitted (MAY-2002) to the EWBL/GenBank/DDBJ databases.
EMBL; AF419606; AA131938.1;
EMBL; AR419606; AA131938.1;
EMBL; AR419606; Piprodyl oligopeptidase activity; IEA.
CO; GO:0004287; F:prodyl oligopeptidase activity; IEA.
CO; GO:0006289; F:prodolysis and peptidolysis; IEA.
CO; GO:0004287; F:prodyl oligopeptidase activity; IEA.
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Bowes L., Carninci P., Dale C.M., Goldsmith A.D., Hayashizaki Y.,
Lahida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pred. No. 69;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
Arabidopsis thaliana (Mouse-ear cress)
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STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed=11130712;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                    NCBI_TaxID=3702;
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Matches
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Lissual Lear;
Sugilarto B., Sakakibara H., Sugiyama T.;
Sugilarto B., Sakakibara H., Sugiyama T.;
Differential Expression of Two Genes for Sucrose-Phosphate Synthase
in Sugarane: Molecular Cloning of the cDNAs and Comparative Analysis
of Gene Expression.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AB001337; BAA19241.1;
GO; GO:0046524; F:sucrose-phosphate synthase activity; IEA.
GO; GO:000658; P:biosyntheis; IEA.
InterPror, IRROUL296; Glyco_transf.
InterPror, IRROUL296; Glyco_transf.
Fam.; PF00534; Glycos transf. 1;
Glycosyltransferase; Transferase.
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Saccharum.
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Bai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southylok A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M. W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
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REMBL; AC012679; AAG52073.1; -.

PIR (99674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G9674; G96744; G9674; G96744; G96744
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Pred. No. 1.88+02;
1; Indels
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1047 AA.
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Matches 7; Conservative
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Les 6; Conservative
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PRT;
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                                                                                                                                               453 VIPPGMDFS 461
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                                                                                                                          3 VVPXGMDYS 11
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Best Local Similarity
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Q8S064
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                                                                                                                                                                                                                                                                   ED Arabidopsis sequencing project;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL04987; CAB39764.1; -.

EMBL; AL04987; CAB3135.1; -.

PIR; T04062; T04062.

FOO: 00.004651; F:sucrose-phosphate synthase activity; IEA.

GO; GO:0046757; F:transferase activity, transferring glycosyl. .; IEA.

GO; GO:00105757; F:transferase activity, transferring glycosyl. .; IEA.

GO; GO:0010296; P:biosynthesis; IEA.

InterPro; IPR001296; Glyco_trans 1.

Pfam; PF00534; Glycos_trans 1.

Flam; PF00534; Transferase.

Glycosyltransferase: Transferase.

SEQUENCE 1083 AA; 122688 MW; EFC126FCA2137BBI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Sucrose-phosphate synthase-like protein (EC 2.4.1.14).
PRABAIL 40 OR AT4G10120.
Arabidopsis thaliana (Mouse-ear cress).
Bridaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NGEL TAXID=3702;
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                                                                                                                                                     SEQUENCE FROM N.A.
Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnollophyta; Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
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01-NOV-1996 (TrEMBirel. 01, Last sequence update)
01-UDN-2003 (TrEMBirel. 24, Last annotation update)
Sucrose phosphate synthase.
SPSI.
             PRT; 1083 AA
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Best Local Similarity 66.70,
6; Conservative
          PRELIMINARY;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
10-JUN-2003 (TrEMBLRel. 21, Last annotation update)
10-JUN-2003 (TrEMBLel. 21, Last annotation update)
10-JUN-2003 (TrEMBLel. 21, Last anno
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A Sasaki T., Matsumoto T., Yamamoto K.;
A Sasaki T., Matsumoto T., Yamamoto K.;
A Sasaki T., Matsumoto T., Yamamoto K.;
Coros:Po678F11.";
L Gura:Po678F11.";
L Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases.
B KEMBL, AP003437; BAB86107.1; -.
R GO; GO:000459; F:L-lactate dehydrogenase activity; IEA.
R GO; GO:000459; P:L-lactate dehydrogenase activity; IEA.
R GO; GO:0006096; P:Losynthesis; IEA.
R GO; GO:0006096; P:Losynthesis; IEA.
R InterPro; IRR01597; L.DH:
R InterPro; IRR01597; L.DH:
R PROSITE; PRO01594; Glycos trans_1;
R PROSITE; PRO0164; L.DH: 1.
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01-MRA-2001 (TrEMBirel. 16, Last sequence update)
01-MRA-2001 (TrEMBirel. 16, Last sequence update)
01-MRA-2001 (TrEMBirel. 16, Last annotation update)
Na+/K+/2Cl-cotransporter (Fragment).
Briccheir sinensis (Chinese mitten crab).
Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Bumalacostraca; Bucarida; Decapoda; Plecypemata; Brachyura;
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR01296; Glyco_trans_1.
InterPro; IPR01557; L.IDH.
Pfam; PF00534; Glyco_transf_1; 1.
PROSITE; PS00064; L.IDH; 1.
SEQUENCE 1084 AA; 119417 MW; 4D0D79AFEDD2F92B CRC64;
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1100 AA; 121170 MW; 084F4604BA389CAD CRC64;
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X MEDLINE=21664373; PubMed=11792842;
X SIRAIN=13 (Type A)

SIRAIN=13 (Type A)

A Shimiau T., Obtani K., Hitakawa H., Obshima K., Yamashita A.,
Shiba T., Ogasawara N., Hatori M., Kuhara S., Hayashi H.;

"Complete genome sequence of Clostridium perfringens, an anaerobic T flesh-cater.",

"Complete genome sequence of Clostridium perfringens, an anaerobic F flesh-cater.",

"Complete genome sequence of Clostridium perfringens, an anaerobic machinal cater.",

"Food Not Natl. A. 99:996-1001 (2002).

"R EMBL; Ap003185; BAB79763.1; -...

"R GO; GO:00038424 F: cateralyric activity; IEA.

"R InterPro; IPR000505; MAD BS.

"InterPro; IPR000599; Thiff domain.

"R InterPro; IPR000599; Thiff domain.

"Pfan; PF00899; Thiff 1.

"Pfan; PF00899; Thiff 1.

"Pfan; PF00899; Thiff 1.

"Pfan; PF00899; Thiff 1.

"Pfan; PF00899; Thiff 1.
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Weihrauch D., Towle D.W.;

"Na+/H+-exchanger and Na+/K+/2Cl--cotransporter are expressed in gills of the euryhaline Chinese crab Eriocheir sinensis.";

Comp. Biochem. Physiol. 126:S158-S158(2000).

EMBL; AR301160; AAG39938.1; -.

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219 219

SEQÜENCE 219 AA; 24159 MW; 599442DA26F0D3F1 CRC64;
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Bacteridium, Pirmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBL_TaxID=1502;
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.8%; Score 35; DB 5; Length 219; Best Local Similarity 75.0%; Pred. No. 49; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                        219 219
219 Aa; 24159 MW; 599442DA26F0D3F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein CPE0057.
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108 BEIIPDDVDY 117 g

1 EEVVPXGMDY 10

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Search completed: June 3, 2004, 11:57:33 Job time: 29.8667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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June 3		

Run on:

52 1 EEVVPXGXHYS 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq 29Jan04:*

1: geneseq190s:*

2: geneseq1900s:*

4: geneseq22001s:*

5: geneseq22001s:*

6: geneseq2033s:*

7: geneseq2033s:*

8: geneseq20303ss:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMADTES

		de			SUMMAKIES		
Result No.	Score	ery	, T	DB	А	Description	ion
1	4.9	94.2	11	. 2	ABB80546	Abb80546	Hepatitis
ę S	49	94.2	11	ß	ABB80554	Abb80554	Hepatitis
0	49		11	Ŋ	ABB80550	ū	Hepatitis
Š 4	49	94.2	11	Ŋ	ABB80555	Abb80555	Hepatitis
S.	48		11	Ŋ	ABB80523	Abb80523	_
9	48		11	Ŋ	ABB80558	Abb80558	Hepati
7	48	٠	11	'n	ABB80537	Abb80537	Hepatitis
8	48	92.3	11	ហ	ABB80560	σ	
σ	48	92.3	11	w	ABB80527	Abb80527	Hepatit
10	48	92.3	11	Ŋ	ABB80541	Abb80541	Hepatitis
11	48	92.3	11	w	ABB80532	Abb80532	
12	48	92.3	11	Ŋ	ABB80531	Abb80531	Hepatitis
13	40	9	Н	ιΩ	ABB80548	Abb80548	겁
14	40	76.9	-	Ŋ	ABB80549	Abb80549	Hepatitis
15	40	76.9	-	w	ABB80547	Abb80547	
16	40	76.9	٦	'n	ABB80544	Abb80544	Į
17		76.9	11	Ŋ	ABB80556	Abb80556	-н
18			11	ហ	ABB80557	Abb80557	Hepatitis
91	40	76.9	11	'n	ABB80551	Abb80551	Hepatitis
20	40		11	ហ	ABB80553	Abb80553	Hepatiti
21			11	ß	ABB80552	Abb80552	Hepatit
22	40	76.9	11	w	ABB80545	Abb80545	Hepatitis
23			11	S	ABB80525	Abb80525	Hepat
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25		'n	11	2	ABB80561	Abb80561	Hepatitis

Hepatitis
Abb80521 Abb80522 Abb80522 Abb80524 Abb80563 Abb80563 Abb80563 Abb80563 Abb80563 Abb80563 Abb80563 Abb80564
ABB80521 ABB80522 ABB80536 ABB80536 ABB80564 ABB80564 ABB80565 ABB80553 ABB80529 ABB80529 ABB80529 ABB80529 ABB80529 ABB80528 ABB80528 ABB80528 ABB80528 ABB80528
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## ALIGNMENTS

RESULT 1	1 1.
ABBS0546 ID ABB	Jose ABB80546 standard; peptide; 11 AA.
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AC	ABB80546;
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Ы	08-OCT-2002 (first entry)
×	,
OE	Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #26.
ă	
₹	Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
3	virucide.
×	
SO	Synthetic.
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표	Key Location/Qualifiers
Ţ	Modified-site 1
ē	/actor "N-terminal acety"

		keto-amide linkage with			
Location/Qualifiers	_note= "N-terminal acetyl"	6 /note= "Norvaly1 carbonyl forming keto-amide linkage with	residue 7"	/note= "C-terminal amide"	
Key Modified eite	221	Modified-site	Modified-site		WO200208251-A2.
H	4 E4	FF	FI	F	X Z

31-JAN-2002. 

19-JUL-2001; 2001WO-US023169.

21-JUL-2000; 2000US-0220101P. (CORV-) CORVAS INT INC. Brunck TK; Lim-Wilby M, Levy OE,

WPI; 2002-361643/39.

Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.

Claim 17; Page 65; 69pp; English.

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of

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Gaps

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Indels

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Conservative
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 10;
                                                                                                                                                                                              Synthetic
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a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                               Gaps
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                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #34.
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                                                           Score 49; DB 5; Length 11; Pred. No. 0.0045; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                     'note= "N-terminal acetyl"
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                                                                                                                                                                      ABB80554 standard; peptide; 11 AA.
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                                                                                                                                                                                                            (first entry)
                                                    Query Match
Best Local Similarity 90.9.
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                                                                                                  1 EEVVPXGXHYS 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #30
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Pred. No. 0.004
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The sequence represents a peptide compound of the invention having hepetities C virus (HVV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HVC protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                           /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
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            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3.
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Pred. No. 0.0072;
0; Mismatches 1; Indels
                                                                                                                                                            note= "N-terminal acetyl"
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                               /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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Location/Qualifiers
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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/note= "C-terminal amide"
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ABB0560 standard; peptide; 11 AA.
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ABB0560;
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ABB0560;
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DT
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Hepatitis C virus NS3/NS4a serine proces
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Hepatitis C virus HCV; serine proces
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Synthetic.
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Modified-site | 10cation/Qualifiers
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Modified-site | 10ce "Norvalyl carl
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Modified-site | 10ce "Norvalyl carl
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Misc-difference | 8
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Modified-site | 11
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Modified-site | 11
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MODIFIED | 10ce "C-terminal and NOXX
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WO200208251-A2.
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Best Local Similarity 90.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                     (CORV-) CORVAS INT INC
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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV procease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                             ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C v protease.
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Pred. No. 0.0072;
0; Mismatches 1; Indels
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                Brunck TK;
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ilarity 90.9%;
Conservative
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residue 7"
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              Lim-Wilby M, Levy OE,
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Matches 10; Conserv
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activity usefu
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                                                                                                                                                                                                               ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
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                                           19-JUL-2001; 2001WO-US023169.
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                              Levy OE,
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                                                                                                              (CORV-) CORVAS INT INC
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                                                                                                                               Score 48; DB 5; Length 11;
Pred. No. 0.0072;
0; Mismatches 1; Indels
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        Claim 17; Page 65; 69pp; English
                                                                                                                                92.3%;
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                                                                                                                                         Local Similarity 90.5
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Modified-site
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pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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virucide.
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Pred. No. 0.0072;
0; Mismatches 1; Indels
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                            ABB80531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ਨੇ
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/note= "Norvalyl carbonyl forming keto-amide linkage with

residue 7"

Misc-difference

Modified-site

/note= "C-terminal amide" 'note= "D-form residue"

WO200208251-A2

31-JAN-2002

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.

Location/Qualifiers 'note= "N-terminal

Key Modified-site Modified-site

Synthetic

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #29

08-OCT-2002

ABB80549;

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note= "Norvaly1 carbony1 forming keto-amide linkage with
                                                                                                                                                                                                                    Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28
                                                                                                                                                                                                                                                                                                                                                                           'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                        standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-2000; 2000US-0220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2001; 2001WO-US023169
                                                                                                                                                                                                                                                                                                                                                                                                                                               residue 7"
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lim-Wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200208251-A2
                                                                                                                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                             08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2002
                                                                                                                                                                                                                                                                                    Synthetic
                  ABB80548
ID ABB80548
                                                                                  ABB80548;
                                                                                                                                                                                                                                           virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protease
RESULT 13
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ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus

ŢĶ;

Brunck

WPI; 2002-361643/39

Lim-Wilby M,

Novel peptide

protease.

activity

(CORV-) CORVAS INT INC

19-JUL-2001; 2001WO-US023169. 21-JUL-2000; 2000US-0220101P. The sequence represents a peptide compound of the invention having

Claim 17; Page 65; 69pp; English.

virus

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ò
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                            ical composition comprising the peptide as an active ingredient for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                         DB 5; Length 11
                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                 0.29;
                                                                                                                                                                                                                                                    Score 40; DB:
Pred. No. 0.29
0; Mismatches
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                       76.9%;
81.8%;
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
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RESULT 14
ABB80549
ID ABB80549 standard; peptide; 11 AA.
KX
1 EEVVPXGXHYS 11
                    검
                   EEVVEXGIDYS
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hepatifis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 5;
Pred. No. 0.29;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80547 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEVVPXGSSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80547;
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ABB80547
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
                                         'note= "N-terminal acetyl"
                                                                                /note= "C-terminal amide"
                         Location/Qualifiers
                                                                                                                                                                                  Brunck TK;
                                                                                                                                                                                                                                                   Claim 17; Page 65; 69pp; English.
                                                                                                                                 19-JUL-2001; 2001WO-US023169.
                                                                                                                                                 21-JUL-2000; 2000US-0220101P.
                                                                                                                                                                  (CORV-) CORVAS INT INC.
                                                                                                                                                                                  Lim-Wilby M, Levy OE,
                                                                                                                                                                                                  WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                      Sequence 11 AA;
                                                                                                WO200208251-A2
                         Key
Modified-site
                                               Modified-site
                                                                        Modified-site
                                                                                                                 31-JAN-2002.
        Synthetic.
```

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

0; Gaps Query Match 76.9%; Score 40; DB 5; Length 11; Best Local Similarity 81.8%; Pred. No. 0.29; Matches 9; Conservative 0; Mismatches 2; Indels

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1 EEVVPXGXHYS 11

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1 EEVVPXGTDYS 11

Search completed: June 3, 2004, 11:48:24 Job time: 45.9333 secs

us-09-909-164-42.rai

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Sequence 4794, Application US/09134001C

Sequence 4794, Application US/09134001C

Batent No. 6380370

GENERAL INCRAMITOR

TITLE OF INVERNION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVERNION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVERNION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF ILING DATE: 1998-108-13

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-10-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NOS: 5674

TYPE: PRI

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                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 73.1
Best Local Similarity 70.0
Matches 7; Conservative
1 EEVVPXGXHY 10
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US-09-252-991A-21444
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US-09-134-001C-4794
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Sequence 4794, Ap
Sequence 26615, A
Sequence 3, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6771, Ap
182, App
182, App
19, App
2, Appli
66, Appli
66, Appli
66, Appli
56, Appli
10, Appli
10, Appli
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7304, Ap
3, Appli
5, Appli
7, Appli
11, Appli
3, Appli
5, Appli
                                                                                                 June 3, 2004, 11:36:47; Search time 11.7333 Seconds (without alignments) 48.399 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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Sequence 3
Sequence 3
Sequence 6
Sequence 6
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1. /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4. /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-134-001C-4794
US-09-134-001C-4794
US-08-197-9528-3
US-08-107-5228-615
US-09-107-5328-6771
US-09-536-784-182
US-09-536-784-66
US-09-536-784-56
US-09-468-6568-4
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                                                                                                                                                                                                                                                                                                 otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-484-101B-3
US-08-484-101B-5
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-08-530-010-9
                                                                                                                                                                                                                                                                      389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                               finimum DB seq length: 0 faximum DB seq length: 2000000000
                                                                                                                                                            US-09-909-164-42
52
1 EEVVPXGXHYS 11
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Match Length DB
                                                                                                                                                                                                                         BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
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Sequence 21444, Application US/09252991A

Sequence 21444, Application US/09252991A

Parent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                          Sequence 11, Appl
Sequence 3, Appli
Sequence 7, Appli
Sequence 11, Appli
Sequence 32560, A
Sequence 3250, A
Sequence 15, Appl
Sequence 7284, Appl
Sequence 15, Appl
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
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US-08-484-101B-7

US-08-484-101B-9

US-08-484-101B-1

US-08-714-524D-3

US-08-714-524D-5

US-08-714-524D-9

US-08-714-524D-9

US-08-714-524D-1

US-08-714-524D-1

US-08-714-524D-1

US-09-134-001C-3950

US-09-134-001C-4185

US-09-134-001C-4185

US-09-348-035A-8065

US-09-348-459-165

US-09-342-647-4

US-08-459-065-2

US-08-459-065-2

US-08-342-647-4

US-08-459-065-2

US-09-342-647-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09215096
; Sequence 3, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION;
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
; TILE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE Pharmaceuticals, Inc.
STREBT: 3174 Porter Drive
CITY: Palo Alto
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
SOFTWARET APLICATION DATE:
APPLICATION NUMBER: US/09/215,096
FILING DATE:
FLING DATE:
PRIOR APPLICATION:
APPLICATION:
APPLICATION NUMBER: 08/879,995
PF-0326 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0;
TELECOMMUICATION INFORMATION:
TELEPHONE: 415-85-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DOS SOFTWARE: FABUSEQ for Win
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7.
Sansa 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 EQVVPGGGH 36
                                                                                                                                                                                                                                      ; TOPOLOGY: linear; iMMEDIATE SOURCE: ; LIBRARY: GenBank; ; CLONE: 163590 US-08-879-9958-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 163590
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGXH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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                                                                                                                                                                                                                                      RESULT 3
US-09-252-991A-26615
Sequence 26615, Application US/09252991A
Sequence 26615, Application US/09252991A
Sequence 26615, Application US/09252991A
Sequence 26615, Application US/09252991A
Setent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PEDILOGATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
IENGTH: 277
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                                                           69.2%; Score 36; DB 4; Length 1037; 63.6%; Pred. No. 56; tive 1; Mismatches 3; Indel8
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Pred. No. 21;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08879995A
Fatent No. 598566
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Freet
APPLICANT: Raser, Matthew R.
TILLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSENE: INCYTE Pharmaceuticals, Inc.
STREET: 3174 Forter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,995A
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
    ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                           Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                        199 KEVVSNGLHYS 209
                                                                                                                                            1 EEVVPXGXHYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
COUNTRY: US
ZIP: 94304
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US-08-879-995A-3
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Sequence 182, Application US/09536784

Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF EXCURNICS: 452
CORRESPONDENCE ADRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
            Patent No. 6159469
GENERAL INPORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 3; Length 447;
Pred. No. 89;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: DISACETC, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION DATA:
RILING DATE: 30-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.50 inch, 1.4Mb storage
                                                                                                                                                STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: Urs. ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MBDIUM TYPE: Diskette, 3.50 inch, 1.4M
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DAT
Sequence 182, Application US/08961083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 18;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear; MOLECULE TYPE: protein US-08-961-083-182
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|| | ||
178 IVPHGGHY 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6771, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette Stamm and David Bush
TITLE OF INVENTION: BUTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                ..
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                                                                            Score 34; DB 3; Length 126;
Pred. No. 14;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%; Score 33; DB 4; Length 63;
45.5%; Pred. No. 10;
tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: PC

COMPUTER: PC

COMPUTER: PC

COMPUTER: PC

COMPUTER: PC

COMPUTER: ACII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 05/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION NUMBER: 60/095,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: 1410 1998

ATTORNEY/AGENT INFORMATION:

NAME: ATINICAL DEMER: 40,489

REFERENCE/DOCKET NUMBER: 40,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...63
; SEQUENCE DESCRIPTION: SEQ ID NO: 6771:
US-09-107-532A-6771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Waltham
STATE: Massachusetts
                                                                                Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.5
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGXHYS 11
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                                                                                                                                                                                                                                             1 EEVVPXGXH 9
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US-09-107-532A-6771
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US-08-961-083-182
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    JS-09-215-096-3
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskerte
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTERO; for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Blias J
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTHWARE: FESELSEQ for Windows Version 2.0
SOCHWARE: FESELSEQ for Windows Version 2.0
CURSTENTION NUMBER: US/08/821,119
FILING DATE: 19-MAR-1997
CLASSIFFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107.204-US
TELLECHMUNICATION INFORMATION:
TELLECHMUNICATION INFORMATION:
TELLECHMUNICATION INFORMATION:
TELLECHMUNICATION INFORMATION:
TELLECHMUNICATION INFORMATION:
TELLECHMUNICATION 109-9655
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Pred. No. 1.2e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 600 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein FRAGMENT TYPE: internal
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 VPKGWHYS 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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Sequence 6, Application US/09468656A

Patent No. 6582706

GENERAL INPORMATION:

APPLICANT: Johnson, John E.

TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus

TITLE OF INVENTION: Monifs

TITLE OF INVENTION: Monifs

FILE REFERENCE: 469201-444

CURRENT APPLICATION NUMBER: US/09/468,656A

CURRENT FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: 60/113,048

PRIOR PILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
63.5%; Score 33; DB 4; Length 447;
Best Local Similarity 62.5%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 2; Indels
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Patent No. 5821104
GENERAL INFORMATION:
APPLICANT: Holm, Kaj Andre
APPLICANT: Halkier, Grethe
APPLICANT: Lehmbeck, Grethe
APPLICANT: Lehmbeck, Jan
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
NUMBER OF SEQUENCES: 23
              PRIOR APPLICATION COLLIGATION
PRIOR APPLICATION NUMBER: 08/961,083
FILING DATE: 0CT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
RECTSTRATION NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 182:
  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                          LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.5%;
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Best Local Similarity 62.5
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US-09-468-656A-6
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ADDRESSEE: No. 58211040 No. 5821104disk of No. 5821104th America, Inc. STREBT: 405 Lexington Avenue
STREBT: 405 Lexington Avenue
STREBT: Now York
STRTE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: No. 59898890 No. 5989889disk of No. 5989889th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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; Sequence 2, Application US/08821118
; Patent No. 598989
; GENERAL INFORMATION:
    APPLICANT: Rey, Michael
    APPLICANT: Rey, Michael
    APPLICANT: Rey, Michael
    TITLE OF INVENTION: HAVING TRIPEPTIDE AMINOPEPTIDES
    TITLE OF INVENTION: ACTIVITY
    NUMBER OF SEQUENCES: 7
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: NO. 5989889 NO. 5989899th ACTIVITY
    ADDRESSEE: NO. 5989899th ACTIVITY
    ADDRESSEE: NO. 5989899th ACTIVITY
    ADDRESSEE: NO. 5989890th ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 600;
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4107.400-US

us-09-909-164-42.rai

184 IVPHGDHY 191

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Sequence (65 Application US/09536784

Sequence Application US/09536784

Setent No. 6573082

GENERAL INFORMATION:

APPLICANT: Choi et. al.

TILE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF EXQUENCES: 452

CORRESPONDENCE ADDRESS:

ADDRESSER: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 56, Application US/08961083;
Patent No. 6159469
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
STREET: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
COPPRATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-0ct-1997
CLASSIFICATION NUMBER: 08/961,083
FILING DATE: OCT-1997
ATTORNEY/AGBNT INFORMATION:
NAME: MACHINES MACKS
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
TTELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
TTELEPHONE: AS A mainto acids
TTELEF = minto acids
TTELEF = minto acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.5%; Score 33; DB 4; ; Best Local Similarity 62.5%; Pred. No. 1.6e+02; Matches 5; Conservative 1; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-536-784-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|| | ||
184 IVPHGDHY 191
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US-08-961-083-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Choi et. al.

APPLICANTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF INCUENCES:

ADDRESSE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

STRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 2; Length 600;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
REFERENCE/DOCKET NUMBER: 4107
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
TELEX: 107-878-9655
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 600 amino acids TYPE: amino acid STRANDEDNESS: 81ngle TOPOLOGY: linear MOLECULE TYPE: protein FRACHENT TYPE: internal 15-08-821-118-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 763 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VPXGXHYS 11
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Gaps

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Length 763; 2; Indels

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STRANDEDNESS: single

TOPCOGY: linear

NOLECULE Protein

SEQUENCY Protein

SEQUENCE DESCRIPTION: SEQ ID NO: 56:

US-09-536-784-56

Query Match

Best Local Similarity 62.5%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps

Qy 3 VVPXGXHY 10

Db 185 IVFHGDHY 192

Search completed: June 3, 2004, 12:03:08

Job time: 11.8 8ecs
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RESULT 1
US-09-909-164-30
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                                                                                                                                                                                               June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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1. /cgn2 6/ptodata/1/jubpaa/USO7 PUBCOMB.pep:*
2. cgn2 6/ptodata/1/jubpaa/PCT NEW PUB.pep:*
3. /cgn2 6/ptodata/1/jubpaa/USO6 NEW PUB.pep:*
4. /cgn2 6/ptodata/1/jubpaa/USO6 NEW PUB.pep:*
5. cgn2 6/ptodata/1/jubpaa/USO6 NEW PUB.pep:*
6. /cgn2 6/ptodata/1/jubpaa/PCTUS PUBCOMB.pep:*
7. /cgn2 6/ptodata/1/jubpaa/PCTUS PUBCOMB.pep:*
7. /cgn2 6/ptodata/1/jubpaa/USO8 PUBCOMB.pep:*
9. /cgn2 6/ptodata/1/jubpaa/USO8 PUBCOMB.pep:*
10. /cgn2 6/ptodata/1/jubpaa/USO9 PUBCOMB.pep:*
11. /cgn2 6/ptodata/1/jubpaa/USO9 NEW PUB.pep:*
12. /cgn2 6/ptodata/1/jubpaa/USO9 NEW PUB.pep:*
13. /cgn2 6/ptodata/1/jubpaa/USOO NEW PUB.pep:*
4. /cgn2 6/ptodata/1/jubpaa/USOO NEW PUB.pep:*
5. /cgn2 6/ptodata/1/jubpaa/USOO NEW PUB.pep:*
7. /cgn2 6/ptodata/1/jubpaa/USOO NEW PUB
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/cgn2_6/ptodata/1/pubpaa/US10_RW PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-34
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     M protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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52
1 EEVVPXGXHYS 11
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32	33	S S	36	37	40	41	'n	equence 6,	Seguence 8, Appli	equence 9,	equence 10	equence 12	13	14	Sequence 17, Appl	58	13	equence 20	22	23	equence 24	equence 26	2	equence 43	45	46	47	equence 48	4
-09-909-164-	-09-909-164-3	-09-909-164-3	.09-909-1	-09-909-164-3	-09-909-164-4	-09-909-164-	-09-909-164	-09-909-164-	-09-909-164-	-09-909-164-	-09-909-164-1	-09-909-164-	-09-909-164-1	-09-909-164-1	4-1	-09-909-164	-09-909-164-1	-09-909-164-2	-00-909-16	-09-909-164-2	-09-909-164-2	-09-909-164-	-09-909-164-2	-09-909-164-4	-09-909-164-4	-09-909-164-4	-09-909-164-4	-09-909-164-4	-09-909-16
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## ALIGNMENTS

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Sequence 30, 3pplication US/09909164

Publication No. U520020068702A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile B.
ITILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEBATITIS C.
ITILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEBATITIS C.
FILE REPRENCE: ILON NUMBER: U50/9999,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1

LENGTH: 11

LENGTH: 11

LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANTS: artificial sequence PRATURE: ORGANTS: STRATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
CTHER INFORMATION: norvaline-(CO)
US-09-909-164-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1). (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
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Length 11;

DB 12;

Score 49;

94.28;

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APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Marguerita
APPLICANT: Lavy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT PELLOR DATE: 2003-03-25
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENT OF NOVEL PROTECT OF NOTICE OF SEQ ID NOS: 62
LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.2%; Score 49; DB 12; Length 11; 90.9%; Pred. No. 0.0038; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LUCATION: (6)...(6)

OTHER INFORMATION: norvaline-(CO)
US-09-909-164-38
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                      NAME/KEY: MOD_RES
LOCATION: (1)...(1)
CTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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LOCATION: (8). (8)
OTHER INFORMATION: D-amino acid
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LOCATION: (1) . (1)
OTHER INFORMATION: ACETYLATION
                       SOFTWARE: PatentIn version 3.1 SEQ ID NO 38 LENGTH: 11 TYPE: PRT
                                                                                                                                             ORGANISM: artificial sequence PEATURE:
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NAME/KRS: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.5-
Best Local 10; Conservative
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NUMBER OF SEQ ID NOS: 62
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Sequence 38, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: IN NOVE PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
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ORGANISM: artificial sequence
PRATURE:
OFFER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB 12; Length 11;
Pred. No. 0.0038;
0; Mismatches 1; Indels
                                 1; Indels
   Pred. No. 0.0038;
                                 0; Mismatches
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (9)...(9)

OTHER INFORMATION: D-amino acid

MS-09-909-164-34
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.9%;
Matches 10; Conservative
Best Local Similarity 90.9%;
Matches 10; Conservative
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NAME/KEY:
NOD RES
LOCATION: (11)...(11)
FEATURE:
INFORMATION: AMIDATION
                                                                                                                               1 EEVVPXGXHYS 11
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US-09-909-164-34
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Sequence 15. Application US/09909164
; Sequence 15. Application US/09909164
; Publication No. US20020068702A1
; Dublication No. US20020068702A1
; Dublication No. US20020068702A1
; APPLICANT: Corvas International, Inc.
; APPLICANT: Lim-Wilby, Marguerita
FILE OF INVENTION: NOVED PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 62
; SEQ ID NO 15
; ENGTH: 11
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Pred. No. 0.006
0; Mismatches
       CURRENT APPLICATION NUMBER: US/09/909,164
                        CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION WHMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
PEATURE:
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US-09-909-164-11
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
PEATURE:
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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                                                                                                                                                                                           TYPE: PRT ORGANISM: artificial sequence
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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NAME/KEY: MISC_FEATURE
LOCATION: (6).7(6)
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Euro, Odile E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: 209/909,164
CURRENT FILING DATE: 2000-07-21
NUMBER: CONTROL OF 101
PRIOR FILING DATE: 2000-07-21
NUMBER: OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOW-PETIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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                                                                        Score 49; DB 12; Length 11;
Pred. No. 0.0038;
0; Mismatches 1; Indels
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LOCATION: (1)...(1)
CTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
; OTHER INFORMATION: D-amino acids US-09-909-164-39
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OTHER INFORMATION: D-amino acid
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Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: artificial sequence
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Best Local Similarity 90.9
Matches 10; Conservative
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sequence 25, Application US/09909164

publication No. US20020068702A1

GENERAL INFORMATION

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENCE: INJUINJ2-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

LENGTH: 11
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CURRENT APPLICATION NUMBER: US/09/909,1
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOPTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC FEATURE
1 LOCATION: (9). 7(9)
2 OTHER INFORMATION: D-amino acid
US-09-909-164-21
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NAME/KRY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
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                                                                                                                                                                                          TYPE: PRT ORGANISM: artificial sequence
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC_FEATURE
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                                                                                                                                                                                                                                                                                                             Sequence 116, Application US/09909164

Publication No. US2020068702A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INO1192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 16

LENTH: 11
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
                                                                      Score 48; DB 12; Length 11;
Pred. No. 0.006;
0; Mismatches 1; Indels
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     ; OTHER INFORMATION; norvaline-(CO) US-09-909-164-15
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LOCATION: (6).7(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: NOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: D-amino acid
US-09-909-164-16
                                                                      Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserva
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US-09-909-164-21
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Page 5

APPLICANT: Levy, Odile E

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFREENCE: IN0192-US

CURRENT PILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 44

LENGTH: 11
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| Sequence 28 Application US/09909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc.
| APPLICANT: Lim-Wilby, Marguerita
| FILE REFERENCE: IN01192-US
| CURRENT FILING DATE: 2000-07-21
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| LangTH: 11
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100.0%; Pred. No. 0.006;
tive 0; Mismatches 0
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OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: NOD RES
LOCATION: (1) (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11) (11)
OTHER INFORMATION: AMIDATION
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LOCATION: (8). (9)
OTHER INFORMATION: D-amino acids
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ORGANISM: artificial sequence
FEATURE:
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Best Local Similarity 100.
Matches 11; Conservative
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OTHER INFORMATION: Met(0)
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NAME/KEY: MISC_FEATURE
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Sequence 42

Sequence 42

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REPERENCE: IN NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILICATION NUMBER: 60/220,101

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

LENGTH: 11
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Pred. No. 0.006;
0; Mismatches 1; Indels
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Pred. No. 0.006;
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; Sequence 44, Application US/09909164
; Publication No. US20020068702A1
; GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.; APPLICANT: Lim-Wilby, Marguerita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                     OTHER INFORMATION: norvaline-(CO)
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; LOCATION: (8)..(8)
OTHER INFORMATION: D-amino acid
3S-09-909-164-25
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: artificial sequence
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OTHER INFORMATION: AMIDATION
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NAME/EXE:
NAME/E
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Best Local Similarity 100.
Matches 11, Conservative
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Matches 9; Conserval
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Sequence 29, Application US/09909164

Sequence 29, Sequence 29, Sequence 29, Sequence 29, Sequence 20, Septicant Informational, Inc.

APPLICANT: Lin-Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Erunck, Terence K

TITLE OF INVENTION: NOVEL EPPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFRENCE: INOI192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: 60/220,101

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

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NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 12; Length 11; Pred. No. 0.24; 0; Mismatches 2; Indels
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76.9%; Score 40; DB 12; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 2; Indels
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NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
US-09-909-164-28
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
FEATURE:
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Best Local Similarity 81.8%;
Matches 9; Conservative
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
                                      FEATURE:
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NOTHER INFORMATION: AMIDATION
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RESULT 15 US-09-909-164-31 ; Sequence 31, Application US/09909164

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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30         32         61.5         225         257810         hypothetical proce           31         32         61.5         226         26169         prohibitin 2 [impo           32         61.5         312         2 AF3211         probablit 2 [impo           33         32         61.5         364         2 AF3211         probable approte           35         32         61.5         364         2 IT7267         probable approte           36         32         61.5         374         2 Gebble approte           36         32         61.5         454         2 Gebble approte           37         32         61.5         454         2 Gebble approte           38         32         61.5         454         2 Gebble approte           40         32         61.5         454         2 Gebble approte           41         32         61.5         454         2 Gebble approte           41         32         61.5         516         2 A6963         photochetical prote           41         32         61.5         627         2 A6963         photochetical prote           41         32         61.5         627         2 A696	RESULT 1 T02590 DNA binding protein EREBP-2 - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Abceses: Nicotiana tabacum (common tobacco) R;Obme-Takagi, N.; Shinshi, H. R;Obme-Takagi, N.; Shinshi, H. A;Attle: Ethylene-inducible DNA binding proteins that interact with an ethylene respons A;Reference number: Z14671; MUID:95276459; PMID:7756828 A;Reference number: Z14671; MUID:95276459; PMID:7756828 A;Retus: preliminary; translated from GB/EMBL/DDBJ A;Actus: preliminary; translated from GB/EMBL/DDBJ A;Actus: preliminary; translated from GB/EMBL/DDBJ A;Actus: preliminary; translated from GB/EMBL/DDBJ A;Experimental source: strain BY4; tissue-type leaf Query Match Best Local Similarity 60.0%; Pred: No. 9.8; Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	1 EEVVPXGXHY 10 
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RESULT 2
A72207

free proteinase activity modulator HflK - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Nitle: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Residues: Transfer preliminary
A;Residues: 1-308 cARN>
A;Residues: 1-308 cARN>
A;Residues: 1-308 cARN>
A;Residues: 1-308 cARN>
A;Residues: Tannary
A;Residues:

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41 WPSGIHY 48

WPXGXHY

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V1 protein - tobacco yellow dwarf virus (strain Australia)
() Species: tobacco yellow dwarf virus
() Species: tobacco;
() Species: tobacco;
() Accession: A42452
() Arcession: A42452
() Archite: The nucleotide sequence of the infectious cloned DNA component of tobacco yell
() Archite: The nucleotide sequence of the infectious cloned DNA component of tobacco yell
() Archite: The nucleotide sequence of the infectious cloned DNA component of tobacco yell
() Archite: The nucleotide sequence of the infectious cloned DNA component of tobacco yell
() Archite: A2452; MUD: 92188538; PMID: 1546458
() Archite: A2452
               PEBS Lett. 366, 46-48, 1995
A; Title: The nuclectide sequence of the bacteriophage T5 ltf gene.
A;Reference number: $65934; MUID: 95309401; PMID: 7789514
A;Reference number: $65934; MUID: 95309401; PMID: 7789514
A;Reference number: $65934; MUID: 95309401; PMID: 7789514
A;Residues: 1-1396 «KAL»
A;Residues: 1-1396 «KAL»
A;Residues: 1-1396 «KAL»
A;Residues: 1-1396 «KAL»
A;Reliman, A.V.; Kryukov, V.M.; Bayev, A.A.
Nucleic Acids Res. 16, 6230, 1988
A;Raliman, A.V.; Kryukov, V.M.; Bayev, A.A.
A;Reference number: $01984
A;Reference number: $01984
A;Retence number: $01984
A;Residues: 294-985; MUID: $8289370; PMID: 3267228
A;Residues: 934-985; A.V.; 987-1396 «KA2»
A;Residues: 934-985; A.V.; 870-1396 «KA2»
A;Conseins: EMBL: X07559
R;Kaliman, A.V.; Kulshin, V.E.; Shlyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M.
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N;Alternate names: neuromedin K
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: A25905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kocani, H.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 83, 7074-7078, 1986
A;Title: Structure and gene organization of bovine neuromedin K precursor.
A;Reference number: A25905; MUID:86313713; PMID:3462746
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A,Residues: 1-126 <KOT>
A,Residues: 1-126 <KOT>
A,Cross-references: GB:M14351, NID:g163587; PIDN:AAA30723.1; PID:g163590
C,Superfamily: neurokinin B precursor
F;1-26/Domain: signal sequence #status predicted <SIG>
F;1-26/Product: protachykinin B #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: ltf
C,Keywords: late protein; tail fiber
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1360 KTIPAGDHYS 1369
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nes 5; Conserv
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C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AF3286
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Accession: AF3282
                                                                                                                                                                                                                                                                                                                                                       C,Accession: E69086
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Olu, D.). Spadafora, R.; Vicaine, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Ciu, D.; Spadafora, R.; Vicaine, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary, nucleic acid sequence not shown, translation not shown
A;Molecule type: DNA
A;Residues: 1-360 «MT»
A;Cross-references: GB:AE000923; GB:AE000666; NID:g2622766; PIDN:AAB86115.1; PID:g262277
A;Experimental source: strain Delta H
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A;Cross-references: GB:AE008917; PIDN:AAL51457.1; PID:g17982167; GSPDB:GN00190
                                                                                                                                                                                                                                                               cell division protein - Methanobacterium thermoautotrophicum (strain Delta H) C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L-shaped tail fiber protein - phage TS
N;Alternate names: ltf protein
C;Species: phage TS
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 17-Nov-2000
C;Accession: 865934; 801984; §36851
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Pred. No. 49;
2; Mismatches 3, Indels
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4; Mismatches

5; Conservative

Best Local Similarity Matches 5; Conser

|::|| | |:: 98 EDLVPMGSHHT 108

1 EEVVPXGXHYS 11

A; Experimental source: strain 16M

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1028 <KU A; Accession: AF3286

67.3%; 54.5%;

Query Match
Best Local Similarity 54.00.

|::|| | || EKIVPPGARYS 86

EEVVPXGXHYS 11

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C;Superfamily: cell division protein MJ0174

C, Genetics: A, Gene: MTH1642

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coenzyme F420-quinone oxidoreductase (EC 1.6.5.-) 56K chain - Archaeoglobus fulgidus N;Alternate names: sarcosine oxidase alpha chain soxA homolog C;Speciess Archaeoglobus fulgidus C;Speciess Archaeoglobus fulgidus C;Speciess Archaeoglobus fulgidus C;Accession: A69284; Beequence_revision 05-Dec-1997 #text_change 19-May-2000 C;Accession: A69284; A5665 Tomb, U.F.; White, O.; Neelson, K.E.; Ketchum, K.A.; Dodson: R;Klenk, H.P.; Clayton, R.A.; Tomb, U.F.; White, O.; Neelson, G.G.; Gill, S.; Kirkness, E.F. Glodek, A. Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Avaute 390, 364-370, 1997
A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S Smith, H.O.; Woese, C.R.; Venter, J.C.
A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S A.Authors: Accession: A69284
A.Fitle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaek A;Reference number: A69250; MUID:98049343; PMID:9389475
A.Accession: A69284
A.Accession: A69284
A.Accession: A69284
A.Accession: A69284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Modecule type: DNA
A; Residues: 1-534 «KLE»
A; Residues: 1-534 «KLE»
A; Crossing and Carlotter, Co.; Thauer, R.K.
Bur. J. Biochem. 223, 503-511, 1994
A; Title: F(420) H(2): quinone oxidoreductase from Archaeoglobus fulgidus. Characterizati:
A; Reference number: 845665; MUID:94333340; PMID:8055920
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Infect. Immun. 67, 871-878, 1999
A;Title: Lmb, a protein with similarities to the LraI adhesin family, mediates attachmer
A;Reference number: Z24091; MUID:99115568; PMID:9916102
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A; Residues: 2, 'X', 4, 'X', 6-7, 'X', 9-10,'XX',13-14 <KUN>
A; Roe: the authors could not distinguish between glutamate and cysteine for residues
C; Superfamily: glutamate synthase small chain
C; Keywords: oxidoreductase
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A;Experimental source: strain R268
C;Superfamily: Streptococcus agalactiae hypothetical 92.4K protein
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C.Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
C.Accession: T46758
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65.4%; Score 34; DB 2; Length 822;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 2; Indels
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A;Molecule type: DNA
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Best Local Similarity 45.5
Matches 5; Conservative
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119 DKVFPHGSHYT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein - Deinococcus radiodurans (strain R1)
()Species: Deinococcus radiodurans
()Species: Deinococcus radiodurans
()Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
()Accession: C7558 # A.; Heidelberg, U.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
Kymhite, O; Eisen, J.A.; Heidelberg, U.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
K.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75550; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <WHI>
A;Crosa-references: GB:AE001889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795
A;Experimental source: strain R1
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-95 <GRA
A;Residues: 1-95 <GRA
A;Cross-references; EMBL.AF022972; PIDN:AAC48234.1; GSPDB:GN00023; CESP:FlOD2.3
A;Experimental source: strain Bristol N2; clone FlOD2
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28717
R;Graves, T.; Wohldmann, P.; Gillam, B.
aubmitted to the EWBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F10D2.
A;Reference number: Z20515
A;Accession: T28717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 65.4%; Score 34; DB 2; Length 279; Best Local Similarity 75.0%; Pred. No. 19; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.4%; Score 34; DB 2; Length 495; illarity 50.0%; Pred. No. 36; Conservative 2; Mismatches 3; Indels
                          DB 2; Length 126;
                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: CESP:F10D2.3
A;Map position: 5
A;Introns: 37/2; 90/1; 113/1; 183/3; 356/3; 380/3; 428/2
                       Score 34; DB 2
Pred. No. 8.2;
1; Mismatches
                       Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 ENIVPTGKHH 227
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                                                                                                                                                                                                                                      28 EQVVPGGGH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 VPLGRHYS 107
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Best Local Similarity
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                                                                                                                                                                 1 EEVVPXGXH
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A, Map position: 1

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RESULT 10 A69284

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C;Superfamily: AIDS trans-regulatory splicing protein
C;Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation
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Job time: 9 secs
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55.6%;
                                                                                  63.5%;
                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                           107 ETVPAGGNYS 116
                                                                                                                                                                                                       2 EVVPXGXHYS 11
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EEILPQGVH 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary A; Molecule type: DNA
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NyAlternate names: anti-repression trans-activator; art protein; rev protein; trs protein
C;Species: simian immunodeficiency virus SIVCpz
A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: 809988
R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Axture 345, 356-3199
A;Tile: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: 809983; MUD:90259077; PMID:2188136
                                                                                                                                                                                                                                                                                                                     A,Gene: pyrAB
C,Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cidecession: E97985
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; R;Hoskins, J.A.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; P. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Ballido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MID:21429245; PMID:11544234
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C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1255-1240, 2001
Trille: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUD:21311952; PMID:11418146
A;Accession: R89892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-167 **KUX>
A;Cross-references: GB:BA000018; PID:g13701002; PIDN:BAB42298.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-46 «KUR»
A;Cross-references: GB:AE007317; PIDN:AAK99713.1; PID:g15458516; GSPDB:GN00174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein spr0909 [imported] - Streptococcus pneumoniae (strain R6) C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 82;
1; Mismatches 3; Indels
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Pred. No. 4.5;
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62.5%;
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Best Local Similarity 60.0%;
Matches 6; Conservative
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190 EIVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EVVPXGXHYS 11
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21 IVPHGGHY 28
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Best Local Similarity
Matches 5; Conser
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A; Introns: 27/1
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Alexportmental source: strain 95c.

Risimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Simpson, A.J.G.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neco, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Fereira, A.G.S.

submitted to GenBank, June 2000

A.Authors: Ferralara, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajiam, J.P.; Krieger, J.E.; Kuramee, E.B.; Laigendado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, N.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, J.P.; Krieger, J.E.; Kuramee, E.B.; Laigendado, M.A.; Mischins, A.W.; Marsukuma, J.P.; V.E.; de Sa, R.G.; Santelli, R.V.; Sawase A.Authors: da Silva, A.C.R.; da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Verjovski-Almeida, S.; Vettore, A.L.; A.Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: 182618
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seque Nature 406, 151-157, 2000
A;Title: The ganome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The ganome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: D$2618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 11156 <SIM>
A;Cross-references: GB:AE004014; GB:AE003849; NID:g9107044; PIDN:AAF84752.1; GSPDB:GNOC
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Pred. No. 17;
2; Mismatches 2; Indels
1; Length 124;
                                                                                       Indels
Score 33; DB
Pred. No. 13;
                                                                                            1; Mismatches
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R HAMAP; MF_01210; -; 1.

R InterPro; IPR005483; Cara_L_glu.

R InterPro; IPR005483; Carae_L_D2.

R InterPro; IPR005481; CPase_L_D2.

R InterPro; IPR005481; CPase_L_D2.

R InterPro; IPR004861; CPase_L_D3.

R InterPro; IPR004861; CPase_L_D3.

R InterPro; IPR004862; MGS_llke.

R InterPro; IPR004862; CPase_L_D2; 2.

R Ffam; PP02289; CPSase_L_D2; 2.

R Ffam; PP02189; PP02886_L_D3; 1.

R Ffam; PP02189; PP02886_L_D3; 1.

R Ffam; PP02189; PP02886_L_D3; 1.

R Ffam; PP02182; PS08866; CPSASE_L; 2.

R RRINTS; PR00866; CPSASE_L; 2.

R RRINTS; PR00866; CPSASE_L; 2.

R PROSITE; PS00866; CPSASE_L; 2.

R PROMAIN 402 546 CARABANOYL PHOSPHATE SYNTHETIC DOMAIN.

FT DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

FT REPEAT 547 1057 ALLOSTERIC DOMAIN.

FT REPEAT 547 1057 ALLOSTERIC DOMAIN.

FT REPEAT 547 1057 ALLOSTERILAL!

FT REPEAT 548 ALLO
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CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN
ALLOSTERIC DOMAIN.
                                                                                               15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR SE0879.
                                                                                                                                                                                                                                             Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the carB family.
                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
PubMed=12950922;
                                                 CARB STAEP
Q8CPJ4;
RESULT 2
CARB_STAEP
                                                   THE FILLET IN THE PRESENCE OF COURSE OF THE PROPERTY OF THE PR
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STRAIN=ATCC 2586;

MEDINE=21886394; PubMed=11889109;

Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Rapatral V., Anderson I., Ivanova N., Grechkin G., Zhu L.,

Rapatral V., Batran A., Gardner W., Grechkin G., Zhu L.,

Asieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

Laren N., Wyrpides N., Walunas T., Pusch G., Haselkorn R.,

Fonstein M., Kyrpides N., Voverbeek R.;

"Genome sequence and analysis of the oral bacterium Fusobacterium

nucleatum serain ATCC 25586.";

"Genome sequence and analysis of the oral bacterium Fusobacterium

nucleatum serain ATCC 25586.";

"Genome sequence and analysis of the oral bacterium Fusobacterium

"Growphate + L-glutamate + carbamoyl phosphate."

"Dorante A. L-glutamate + carbamoyl phosphate.

"Dorante Binds amanganese ions per subunit (By similarity).

"COPACTOR: Binds amanganese ions per subunit (By similarity).

"COPACTOR: Binds amanganese ions per subunit (By similarity).

"SUBUNIT: Composed of two chains; the small (or glutamine) chain

promotes the hydrolysis of glutamine to ammonia, which is used by

the large (or ammonia) chain to synthesize carbamoyl phosphate (By

similarity).

"SUMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                               Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain)
                                                                                                                                                                                                                               ö
                                                                                                                                                             Score 36; DB 1; Length 1057;
Pred. No. 14;
1; Mismatches 3; Indels
MANGANESE 2 (BY SIMILARITY).
20 MANGANESE 3 (BY SIMILARITY).
32 MANGANESE 3 (BY SIMILARITY).
117391 MW, 894407080B1CAE59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAR; MP_01210; 1.

HAMAR; MP_01210; 1.

INTERPRO; IPRO06215; Cara L. glu.

INTERPRO; IPRO05403; CPASE_L. D2.

INTERPRO; IPRO05404; CPASE_L. D3.

INTERPRO; IPRO05404; CPASE_L. D3.

INTERPRO; IPRO04362; MGS_IIKE.

Pfan; PPO0289; CPSASE_L. Chain; 2.

Pfan; PP02189; CPSASE_L. D3; 1.

Pfan; PP02187; CPSASE_L. D3; 1.

Pfan; PP02187; MGS; I.

PRINTS; PR00189; CPSASE.

TIGRFAMS; TIGR01369; CPSASE.
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                                                                                                                                                                       69.2%;
                                                                                                                                                                                                       63.68;
                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                189 KEVVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                 1 EEVVPXGXHYS 11
      300
820
832
   300 30
820 82
832 83
1057 AA;
                                                                                                                                                                                                Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARB OR FN0422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARB FUSNN
QBRG86;
                                                                     METAL
SEQUENCE
                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
CARB FUSNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=92188518; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.B.;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.B.;
The nucleotide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
infecting monocotyledonous plants.";
Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                Score 35; DB 1; Length 1396;
Pred. No. 31;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 1; Length 102;
Pred. No. 3.4;
2; Mismatches 2; Indels
                                              -> A (IN REF. 2).
18CD2192F65FFFC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l protein. -
102 Aa; 11178 MW; A40ECF1E0AF55867 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurokinin B precursor (NKB) (Neuromedin K).
                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-CT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 AA.
                                                                                                                                                                                                                                                                                                                        102 AA
                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                              986 v -:
; 147989 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A42452; A42452.
InterPro; IPROD5621; Gemini mov.
Pfam; PF01708; Gemini mov; I.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.4%;
60.0%;
                                                                                                    67.3%;
                                                                                                                                            5; Conservative
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1360 KTIPAGDHYS 1369
                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                  2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S65934; S36851.
Late protein.
CONFLICT 986 96
SEQUENCE 1396 AA;
                                              986 9
1396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                   Y11K TYDVA
P31619;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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TKNK BOVIN
                                                                                                                         Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
PROSITE; PS00866; CPGASE 1; 2.
PROSITE; PS00867; CPSASE 2; 2.
Aginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
ATP-binding; Manganese; Complete proteome.
DOMAIN 402 546 OLIGOMERIZATION DOMAIN.
DOMAIN 547 929 CARRENOIS PROSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                              ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE I (BY SIMILARITY).

MANGANESE I AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage T5.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
T5-like viruses.
VCBI_TaxID=10726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY PARTIAL SEQUENCE FROM N.A.
MEDLINE-88289770; PubMed-3267228;
Kaliman A.V., Kryukov V.M., Bayev A.A.;
"The nucleotide sequence of batteriophage T5 DNA at the region between early and late genes.";
Nucleic Acids Res. 16:6230-6230(1988).
-!- FUNCTION: Noneseential protein that mediates binding to the polymannose O antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-95308401; PubMed=7789514;
MRDLINE-95308401; PubMed=7789514;
Kaliman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.
KTYNKOV V.M.;
"The nucleotide sequence of the bacteriophage T5 ltf gene.";
FEBS Lett. 366:46-48(1995).
                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 1; Length 1058; Pred. No. 23; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaliman A.V.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleotide sequence of the bacteriophage T5 ltf
Lett. 366:46-48(1995).
                                                                                                                                            ALLOSTERIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLTF_BPT5 STANDARD; PRT; 1396 AA. P13300; 048502; 01-JAN-1990 (Rel. 13, Created) 01-FB-1996 (Rel. 33, Last sequence update) 01-RB-2000 (Rel. 39, Last annotation update) L-shaped tail fiber protein (LTF protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X69460; CAA49220.1; -.
EMBL; AJ001191; CAA04591.1; -.
PIR; S01982; S01982.
                                                                                                                                                                                                                                                                                                                                            117451
                                                                                                                                                                                                                                                                                                                                                                                  67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                     60.0%;
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|| | :||
EIVPNGLNYS 199
                                                                                                    546
929
1058
1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                            832 83
1058 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                          DOMAIN
REPEAT
REPEAT
NP_BIND
NP_BIND
METAL
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VLTF BPTS ID VLTF RESULT 4

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                                                                                                                                                                                        Lancet 357:1225-1240(2001).

-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + prosphate + L-glutamate + carbamoyl phosphate.

-!- COFACTOR: Binds a manganese ions per subunit (By similarity).
-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis, first step.
-!- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
-!- SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REMEL; AP003361; BAB57365.1.

REMEL; AP003132; BAB42298.1; -.

REMEL; AP003132; Cara_L glu.

REMEL; PR00649; Carae_L D2.

REMEL; PR00549; CPASSE_L D3.

REMETPRO; IPR00549; CPASSE_L D3.

REMETPRO; IPR00549; CPASSE_L D3.

REMETPRO; IPR00589; CPASSE_L D3.

REMETPRO; REMETPRO; REMETRY CPASSE_L D3.

REMETPRO; REMETPRO; REMETRY CPASSE_L D3.

REMETPRO; REMETRY CPASSE_L D3.

REMETPRO; REMETRY CPASSE_L D3.

REMETPRO; REMETRY CPASSE_L D3.

REMETRY PR00142; MGS. 11.

REMETRY PR00142; MGS. 
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 ATP (POTENTIAL).
52 ATP (POTENTIAL).
64 MANGANESE 1 (BY SIMILARITY).
68 MANGANESE 1 AND 2 (BY SIMILARITY).
60 MANGANESE 2 (BY SIMILARITY).
52 MANGANESE 3 (BY SIMILARITY).
63 MANGANESE 3 (BY SIMILARITY).
64 MANGANESE 3 (BY SIMILARITY).
65 MANGANESE 3 (BY SIMILARITY).
66 MANGANESE 3 (BY SIMILARITY).
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Pred. No. 38;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.48;
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CARB STAAW
ID CARB STAAW
AC P58940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                    SEQUENCE FROM N.A. DubMed=3462746; MEDLINE=86313713; PubMed=3462746; MEDLINE=86313713; PubMed=3462746; Medline=1 B., Hoshimaru M., Nawa H., Nakanishi S.; Kotani H., Hoshimaru M., Nawa H., Nawa H., Acad. Sci. U.S.A. 83:7074-7078(1986).

Proc. Natl. Acad. Sci. U.S.A. 83:7074-7078(1986).

-I- FUNCTION: Tachykinina are active peptides which excite neurons, evoke behavioral responses, are potent vascdilators and secretagogues, and contract (directly or indirectly) many smooth secretagogues, and contract (directly or indirectly) many smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21311952. PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Ruroda M., Ohta T., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q99UE5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last annotation update)
phosphate synthetase ammonia chain.
CARB OR PYRAB OR SATU203 OR SA1046.
Staphylococcus aureus (strain Muso / Arcc 700699), and
Staphylococcus aureus (strain N315).
Bacteria, Firmicutes Bacillales; Staphylococcus.
NCBI_TAXID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION (G-96 PROVIDE AMIDE GROUP) 446EF433498EC059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R EMBL; M14351; AAA30723.1; --
R EMBL; M14349; AAA30723.1; --
R EMBL; M14349; AAA30723.1; JOINED.
R EMBL; M14349; AAA30723.1; JOINED.
R EMBL; M14349; AAA30723.1; JOINED.
R EMBL; M14350; AAA30723.1; JOINED.
R InterPro; IPR003635; Neurokinin.
R InterPro; IPR002640; Tachy Neurokinin.
R Pfam; PF03823; Neurokinin.
R ProDom; PD020370; Neurokinin.
R ProDom; PS020370; Neurokinin.
R ProDom; PS020370; Neurokinin.
R ProDom; PS020370; Neurokinin.
R ProDom; S190310; Neuropeptide; Cleavage on pair of basic residues;
M Amidation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEUROKININ B.
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86 95 NE
99 126 99 126
95 95 4M
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Best Local Similarity
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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBD outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lancet 359:1819-1827 (2002).

-!- CATALYTIC ACTYVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.

-!- CATALYTIC ACTYVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.

-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis; first step.
-!- PATHWAY: Pyrimidine biosynthesis; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
-!- SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-22040717; PubMed=12044378;
MEDLINE-22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 ATP (POTENTIAL).
352 ATP (POTENTIAL).
294 MANGANESE 1 (BY SIMILARITY).
296 MANGANESE 2 (BY SIMILARITY).
310 MANGANESE 2 (BY SIMILARITY).
820 MANGANESE 3 (BY SIMILARITY).
821 MANGANESE 3 (BY SIMILARITY).
312 MANGANESE 3 (BY SIMILARITY).
313 MANGANESE 3 (BY SIMILARITY).
31 17185 MW; D8E3B09F9BC6F152 CRC64;
                                                                                      6.3.5.5) (Carbamoyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFIDITY PP02142; NOC. 1 PRINTS; PR00098; CPSASE.
TIGRFAMS; TIGR01369; CPSASE.1; 1. 2.
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; Arginine biosynthese; Complete protecome.
Argining; Manganese; Complete protecome.
ATP-binding; Manganese; Complete protecome.
CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 1; Length 1057;
Pred. No. 38;
1; Mismatches 3; Indels
                                                                                                                                                          Staphylococcus aureus (strain MW2),
Bacteria; Firmicutes; Bacillales; Staphylococcus,
NCBI_TaxID=196620;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, inst sequence update)
28-FEB-2003 (Rel. 41, inst annotation update)
Carbamoyl-phosphate synthase large chain (EC opposphate syntheteae ammonia chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF 01210; -; 1.
InterPro; IPR006275; CarA L glu.
InterPro; IPR005481; CPase L
Pfam; PF00289; CPsase L
Pfam; PF00289; CPsase L
Pfam; PF02786; CPsase L
Pfam; PF02787; CPsase L
Pfam; PF02186; CPsase L
Pfam; PF02187; MGS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP004825; BAB94951.1; -.
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832 83
1057 AA;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    acquired MRSA.";
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SEQUENCE
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NP BIND
NP BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 345:356-359(1990).
-!- FUNCTION. REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
-!- SUBCELLUTAR LOCATION: Nuclear; accumulates in the nucleoli.
-!- PTM: Phosphoprotein whose state of phosphorylation is mediated by a specific serine kinase activity present in the nucleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=90259077; PubMed=2188136;
Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
Huet R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-359(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation, AIDS, Phosphorylation, Nuclear protein.
SEQUENCE 124 AA, 13701 MW, FS877DIBDF65A7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28.FEB-2003 (Rel. 41, Last annotation update)
REV protein (Anti-repression transactivator protein) (ART/TRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 6.8;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMEI YEAST STANDARD; FKI; 400 AA. 003010; P87330; Cleated)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Molosis negative regulator UMEI.
UMEI OR WIM3 OR YPL139C OR LP17C.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                   124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, X52154; CAA36405.1; -.
PIR; S0998; VKLJSI.
HIV, X52154; REVXCPZ.
InterPro; IPR000625; REV_protein.
Pfam; PP00424; REV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%;
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                                                                                                                                                                                   STANDARD;
                                                 190 EIVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 ETVPAGGNYS 116
2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EVVPXGXHYS 11
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                                                                                                                                                                              REV SIVCZ
P17280;
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                                                                                                                                                              MEDLINE=22426901; PubMed=12522265;
WEDLINE=22426901; PubMed=12522265;
Van Ham R.C.H.U., Ramerbeek J., Palacios C., Rausell C., Abascal F.,
Van Ham R.C.H.U., Farnandez J., Jümenez L., Postigo M., Silva P.J.,
Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
Reductive genome evolution in Buchnera aphidicola...;
Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003)...
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.
                               Buchnera aphidicola (subsp. Baizongia pistaciae).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
MCBI_TaxID=135842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      van Vliet-Reedijk J.C., Planta R.J.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBL011W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NUV-1997 (Rel. 35, Last amouation update)
Hypothetical 83.6 kDa protein in CCP1-MET1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AR014017; AA027114.1; -.
InterPro; IPR001140; ABC_TM_transpt.
InterPro; IPR003439, ABC_transporter.
Pfam; PF00066; ABC membrane; 1.
Pfam; PF00065; ABC_tran; 1.
PROSITE; PS50929; ABC_TYIF; 1.
PROSITE; PS00201; ABC_TRANSPORTER 1; FALSE_NEG.
PROSITE; PS003033; ABC_TRANSPORTER 2; 1.
ATP-binding; Transport; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
AGC TRANSPORTER.
ATP (POTENTIAL).
Multidrug resistance-like ATP-binding protein mdlB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%; Score 33; DB 1; 50.0%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 743 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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Best Local Similarity 50.0.
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SEQUENCE FROM N.A.
STRAIN=S288c;
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NP_BIND
SEQUENCE
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TRANSMEM
TRANSMEM
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     CCERRROCCOSTE
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            SEQUENCE FROM N.A.

STRAIN=S2886 ( AB972;

MEDLINE=97313271; PubMed=9169875;

Bussey H., Storme R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Araujo R., Barrell B.G., Badcock K., Davis R.W., Chung E., Churcher C.M., Coster F., Davis R.W., Chung E., Churcher C.M., Diraclor F., Davis R.W., Diraclor B., S., Delius H., Diraclor B.K., Davis R.W., Duncan M., Friesen J.D., Frizz C., Goffeau A., Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W., Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W., Annicke-Smith S., Mamarh R., Johnston M., Kalman S., Kleine K., A. Komp C., Kurdi O., Leshkari D., Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D., Marathe R., Namarh A., Nentwich U., Oeffner P., Pearson D., Petel F.X., Pohl T.W., Purnelle D., Schafer M., Schafe M., Schafer M., Schafe M., Scharen S., Schroeder M., Sdicu A.M., Tettelin H., Urnestarazu L.A., Ushinsky S., Vienerdeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H., Hani J.; Wedler H., Winnett E., Fructions I. Schrams S., Schroeder S., Wedler H., Winnett E., Fructions I. Struks Silvachoromyces cerevisiae chromosome XVI."; I. Nature 387:103-105(1997).

-I - FUNCTION: TRANSCRIPTIONAL MODULATOR WITH ROLES IN MEIOTIC REGULATION AND SILEMING NEGARIYE REGULATIOR OF MEIOSIS.

-I - SIMILARITY: STRONG, TO YEAST WIMI AND WIM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license afterment (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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GGO; GO:0005634; C:nucleus; IDA.
GO; GO:0003714; F:transcription co-repressor activity; IDA.
GO; GO:0040020; P:regulation of meiosis; IGI.
InterPro; IPR001680; WD40.
InterPro; IPR001680; WD40.
SMART; SM00320; WD40; 3.
PROSITE; PS00678; WD REPEATS 1; FALSE NEG.
PROSITE; PS00678; WD REPEATS 1; FALSE NEG.
PROSITE; PS00694; WD REPEATS REGION; PALSE NEG.
Transcription regulation; Melosis; Repeat; WD repeat.
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
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GermOnline; 144121; -.
TRANSFAC; T04309; -.
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85 IVPLGLHY 92
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5; Conserv
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10-OCT-2003
10-OCT-2003
10-OCT-2003
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Best Local S
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Gaps

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RESULT 11
MDLB BUCBP

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or send an email to license@isb-sib.ch)
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GAAB METTH
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Matches
     S74444468
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                                                                                                                                                                                                                                                                                                                                            GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0004366; F:glycerol-3-phosphate O-acyltransferase acti. . .; IDA.
GO; GO:0008664; P:phospholipid blosynthesis; IDA.
InterPro; IPR002123; Acyltransferase.
Ffam; PF01553; Acyltransferase; 1.
SMART; SM00563; PlsC; 1.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Peptide methionine sulfoxide reductase msrA (BC 1.8.4.6) (Protein-mathonine-S-oxide reductase) (Peptide Met(O) reductase).
Wibrio parahaemolyticus.
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Vibrionaceae, Vibrio.
NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.5%; Score 33; DB 1; Length 743; Best Local Similarity 75.0%; Pred. No. 43; Antches 6; Conservative 0; Mismatches 2; Indels
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TRANSMEM 31 55 POTENTI
TRANSMEM 69 85 POTENTI
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GermOnline; 140046; -.
SGD; S0001775; GPT2.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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-!- CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine H(2)0 = AWP + diphosphate + GWP + L-glutamate.

-!- PATHWAY: GWP biosynthesis.

-!- SUBUNIT: Heterodimer composed of a glutamine amidotransferase subunit (A) and a GWP synthase subunit (B) (Pocential).

-!- SIMILARITY: Belongs to the GWP synthase family.
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16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (BC 6.3.5.2) (GMP synthetase).
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Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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InterPro; IPR001674; GMP_synth_C.
Pfam; PF00958; GMP_synt_C;
TICRFAMS; TICR0884; guad, Crerm; 1.
Ligase; GMP_biosynthesis; Purine_biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                61.5%; Score 32; DB 1; Length 212; llarity 55.6%; Pred. No. 19; Conservative 2; Mismatches 2; Indels
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29 35 ATP (BY SIMILARITY).
308 AA; 34403 MW; F2DCF6ED202CAECI CRC64;
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HSSP; P04079; 1GPM.
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nes 5; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and characterization of a full-length cDNA coding for ovine aldolase B from fetal mesonephros.";
Biochin. Biophys. Acta 1219:223-227 [1934].
-!- CATALYTIC ACTIVITY. D fructose 1,6-bisphosphate = glycerone phosphate + D-glycertaldehyde 3-phosphate.
-!- PATHWAY: Glycolysis; sixth step.
-!- FATHWAY: Glycolysis; sixth step.
-!- SUBUNIT: Homocretramer [8p similarity].
-!- SUBUNIT: Homocretramer [8p similarity].
-!- Glycolytic enzyme are found, aldolase A in muscle, aldolase B in liver and aldolase C in brain.
-!- SIMILARITY: Belongs to class I fructose-bisphosphate aldolase family.
                              Gaps
                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Pructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase).
                                                                                                                                                                                                                                                                                                                                     TISSUE=Mesonephros;
MEDLINE=94368863; PubMed=8086469;
Gianquinio L., Pailhoux E.A., Bezard J., Servel N., Kirszenbaum M.,
                                                                                                                                                                                                                                          Ovis aries (Sheep).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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Score 32; DB 1; Length 308;
Pred. No. 29;
0; Mismatches 4; Indels
                                                                                                                                                363 AA
                                                                                                                                                PRT;
  61.5%;
Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                STANDARD;
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Search completed: June 3, 2004, 11:49:54
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Q911h8 thermoplesm 016912 caenorhabdi 029966 archaeoglob Q8772 streptococc Q8281 streptococc Q84281 streptococc Q84281 streptococc Q84591 streptococc Q859xv4 streptococc Q950x5 sulfolobus Q950x5 streptococc Q950x7 streptococcc Q950x

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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence A1987856.
TADA31 OR 1110004B19RIK.
Buks musculus (Mouse).
Bukaryots, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Straubberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
BMD; BC0321935; AH32195.1; -.
MD; MOI:1915724; Tada31.
GO; GO:0030374; F:ligand-dependent nuclear receptor transcrip.
GO; GO:0005515; F:protein binding; IPT.
SROUENCE 413 AA; 46621 MM; A9BBAIDC70CDA0D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 11; Length 413; Pred. No. 2.7; 1; Mismatches 3; Indels
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                    Q9XST4
Q57489
Q9PC35
Q87D36
                                                                                     Q8E4U1
Q8DZ81
Q8NZ82
Q8K5Q1
Q99XV4
                                                                                                                                                                         Q96YHS
Q8CYU7
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Q8YWP1
Q867A5
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(TrEMBLrel. 01, I
(TrEMBLrel. 25, I
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Best Local Similarity 63.6%;
Matches 7; Conservative
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SEQUENCE FROM N.A.
01-NOV-1996
01-NOV-1996
01-OCT-2003
   046486;
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ID 04
AC 04
DT 01
DT 01
   28K289
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Q80214 stephylococ
Q80419 nicotiana t
Q91w50 nicotiana t
Q98muc rhizobium 1
Q9x262 thermotoga
Q38317 lactobacill
Q27679 methanobact
Q7xcg3 oryza sativ
Q81mc drosophila
Q87j11 brucella
Q87j11 brucella me
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                                                                                                    June 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                    1017041 segs, 315518202 residues
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                                                                         protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                        summaries
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1: SP_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
5: Sp_numan:*
5: Sp_numan:*
6: Sp_numan:
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Q46486
Q8CPJ4
Q8CPJ4
Q9LW50
Q9RHU6
Q9X2E2
Q9X317
Q28317
Q27679
Q277679
Q281KE6
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Q8DIH0
Q7WNB7
Q7W0Z3
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 su
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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52
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Match
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Perfect score:
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Gaps

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InterPro; IPR005481; CPase L. N.

InterPro; IPR004563; MGS like.

InterPro; IPR004563; MGS like.

DR Pfam; PF00289; CPSase L. Chain; 2.

DR Pfam; PF00786; CPSase L. D2; 2.

DR Pfam; PF00786; CPSase L. D2; 2.

DR Pfam; PF001842; MGS; 1.

DR Pfam; PF00184; CPSASE L. D3; 1.

PROSTIE; PS00866; CPSASE 1; 2.

PROSTIE; PS00866; CPSASE 1; 2.

R PROSTIE; PS00866; CPSASE 2; 2.

R COMplete Proteome.

SEQUENCE 1057 AA: 11777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 63.6%;
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 KEVVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGXHYS 11
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Q40479;
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A Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z., Chen Z., Wen Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z., Chen Z., Wen Y., Wen Y., Chen Z., Wen Y., Ren S., Li H., Fu G., Guben Z., Re Zhang Y., Ren S., C:cytoplasm; IEA.

R MBL; AEO16746; AA004476.1; ---

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004109; F:Carbamoyl-phosphate synthase activity; IEA.

GO; GO:004109; F:Carbamoyl-phosphidase activity; IEA.

GO; GO:004109; F:Carbamoyl-phosphidase activity; IEA.

GO; GO:004109; F:Carbamoyl-phosphidase activity; IEA.

GO; GO:006526; P:arginine biosynthesis; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

RO; GO:001886; P:pyrimidine base biosynthesis; IEA.

RINTERPRO; IRRO05493; CarA L. Glu.

RINTERPRO; IRRO05494; CPASE-L. LD.

RINTERPRO; IRRO05490; CPASE-L. LD.

RINTERPRO; IRRO05490; CPASE-L. LD.
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                                                                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES—C.xerosis; STRAIN=M82B;
MEDLINE=96117603; PubMed=855900;
Tauch A.v. Kassing F., Kalinowski J., Puhler A.;
"The Corynebacterium xerosis composite transposon Tn5432 consists of the identical insertion sequences, designated IS1249, flanking the erythromycin resistance gene ermCX.";
Plasmid 34;119-131(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                             Corynebacterium xerosis, and Corynebacterium striatum.
Corynebacterium striatum.
Bacteria; Actinobacteria; Actinobacteridae; Corynebacterineae; Co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBCPU4;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carbamoyl-phosphate synthase large chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
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                                   Hypothetical protein (GcrA).
GCRA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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130 DVIPEGXHYA 139
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Q8CPJ4
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STEALN=BY4, TISSUE=Leaf;
STEALN=BY4, TISSUE=Leaf;
MEDLINE=95276459; PubMed=7756928;
Cheme-Takaqi M., Shinshi H.;
Cheme-Takaqi M., Shinshi H.;
The ethylene responsive element.";
The thylene responsive element.";
The thylene responsive element.";
The thylene responsive resp
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                                                                                                       69.2%; Score 36; DB 16; Length 1057; 63.6%; Pred. No. 88; 21; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
67.3%; Score 35; DB 10; Length 233;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 3; Indels
1057 AA; 117391 MW; 8944D7D8DB1CAES9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
EREBP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 AA.
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317 AA
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                                                    67.3%;
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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                                                Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                 194 VIPEGTHYN 202
                                                                                                                                                                                                                      3 VVPXGXHYS 11
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-20399450; Pubmed=10945353;

Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;

Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;

Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;

Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;

Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;

Falant T., Sato F., Falantia S., Sato F.;

Falantia Call Physiol. 41:817-824(2000).

HSSP, O80337; 2GCC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000375; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPRO1471; TE ERF.
Pfam; PF00847; AP2-domain; 1.
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DNA Res. 7:31-38 (2000).
BNB Age. 7:31-38 (2000).
GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
GO; GO:0005189; F:electron transporter activity; IEA.
InterPro; IPR000345; CytC heme BS.
InterPro; IPR003245; CytC heme BS.
PEam; PF00167; Cytcchrome C1; 1.
PRINTS; PR00603; CYTCCHROMEC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.3%; Score 35; DB 10; Length 237; 60.0%; Pred. No. 29;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Ethylene-responsive element binding factor.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=21082930; PubMed=11214968;
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Complete proteome.
SEQUENCE 285 AA; 30961 MW; 31D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; IF ERF; 1.
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Best Local Similarity
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MEDINE-S2873146; PubMed=10360571;
Melson K.B., Clayton R.J., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Elsen J.A., White O.,
Salzberg J.L., Smith H.O., Venter J.C., Frassr C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
Mature 199:132-329 (1999).
BMBL, AR2001819; AAD56885.1; -.
PIR, A72207.
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBI_TaxID=2336;
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=12417;
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Score 35; DB 16; Length 285;
Pred. No. 35;
                                                            Indels
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Altermann E.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
FTSH protease activity modulator HFLK.
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Last sequence update)
Last annotation update)
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"Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
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(TrEMBLrel. 16, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 45.5 hes 5, Conservative
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01-MAR-2001 (
01-MAR-2001 (
01-OCT-2003 (
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Best Local S
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Q7XTG3
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Q9E1X6
ID Q9E1X
AC Q9E1X
DT 01-MA
DT 01-OC
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=3231538; Pubmed=8472861;
Fremaux C., De Antoni G., Raya R., Klaenhammer T.;
"Genetic organization and sequence of the region encoding integrative functions from Lactobacillus gasseri temperate bacteriophage phi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDGUENCE FROM N.A.

Engel G., Altermann E., Klein J., Henrich B.;

"Structure of a genome region of the Lactobacillus gasseri temperate phia edh covering a repressor gene and cognate promoters.";

Gene 210:67-70 (1998).
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                                        MEDLINE=99384014; PubMed=10452953; Altermann E., Klein J., Henrich B.; Primary Etructure and features of the genome of the Lactobacillus gasseri temperate bacteriophage phi-adh."; Gene 236:333-346(1999).
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MEDLINE-98037514; PubMed-5371463;

Smith D.R., Doucette-Stam L.A., DeLoughery C., Lee H.-M., Dubois J.

Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Aldredge T., Bashirzadeh R., Hakely D., Cook R., Gilbert K.,

Fapdaforn R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruco A., Bush D., Safer H., Patwell D., Prabhakar S.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
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                                                                                                                                                                                               MEDLINE=95138034; PubMed=7836307;
Henrich B., Binishofer B., Blaesi U.;
"Primary structure and functional analysis of the lysis genes Lactobacillus gasseri bacteriophage phi-adh.";
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Methanobacteriaceae; Methanothermobacter.
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Last sequence update)
Last annotation update)
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GO; GO:0003796; F.198cayme activity; IEA.
GO; GO:0016999; P:cell wall catabolism; IEA.
GO; GO:0009253; P:cell wall catabolism; IEA.
InterPro; IPR002053; Glyco hydro_25.
InterPro; IPR003646; SH3 bac.
Pfam; PF01183; Glyco hydro_25; 1.
ProDom; PF0016420; Glyco hydro_25; 1.
SWART; SM00641; Glyco hydro_25; 1.
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Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.O., Zhu G.F., Tu Y.F., Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao Y., Hu Y., Hu O.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhang W.H., Han B., Feng O., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.C., Mu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu X., Li T., Zhang Y.J., Hu H., Jia P.X., Qian Y.M., Xing K., Zhou B., Chen Z.H., Hao P., Zhang L., Ru M., Zhang R.Q., Guan J.P., Hong G.F.;
Zhang R.Q., Guan J.P., Hong G.F.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

SHORL, ALGOG433, CARGO1515.1, EVER SHORL, ALGOG433,
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Sukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Enrhartoideae, Oryzeae, Oryza.
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| Compared genome analysis and comparative genomics...;
| J. Bacteriol. 179:7135-7155 (1997).
| R MREL; ARON0923; AAB66115.1; ---
| P. R. E69086; B69086.
| R GO; GO:00005634; C:nucleus; IEA.
| GO; GO:0000510; P:cytokinabiosynthesis; IEA.
| GO; GO:0000510; P:cytokinabiosynthesis; IEA.
| R InterPro; IPR005140; eRF1 1.
| R InterPro; IPR005140; eRF1 1.
| R InterPro; IPR005140; eRF1 2.
| R InterPro; IPR005140; eRF1 1.
| R Pfam; PF03464; eRF1 2; I.
| R Pfam; PF03465; eRF1 2; I.
| R Pfam; PF03465; eRF1 3; I.
| R Pfam; PF03465; eRF1 3; I.
| R Pfam; Complete protecome.
| Cell division; Complete protecome.
| Cell division; Complete protecome.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
03991214_12.4 protein.
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SEQUENCE
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Q8YJ11;
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Matches
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RN SEQUENCE FROM N.A.

RAGEN M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RAGEN M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandrews P., Stang O., Champe M., Pfeiffer B.D.,

RA Baradon R.C., Baxerdal G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Ffannkoch C., Baldwin D.,

RA Besson K.Y., Berman B.P., Bharler B.D.,

RA Besson K.Y., Berman B.P., Buller H., Cadleu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davises P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davises P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davises P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davises P.,

RA Cherry J.M., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Goson K.J., Hentwan T.J., Hermandez J.R., Houck J.,

RA Harris N.L., Harvey D., Helman T.J., Hermandez J.R., Houck J.,

RA Harris N.L., Harvey D., Helman T.J., Hermandez J.R., Houck J.,

RA Lasko P., Lei Y., Leviteky A., Li J., Li Z., Liang Y., Lin X.,

Alali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A.,

Markulov G., Maltei B., McIntosh T.C., McLeod M.P., McPherson D.,

Liu X., Mattei B., McIntosh T.C., Murphy D., Murphy D., Murphy D., Murphy D., Wallen H.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,

Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Shen H.
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                                                                                                                                                                                                                                                                                          Gaps
                                                                                           Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R., "Complete Sequence of the Simian Varicella Virus Genome.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBU databases.

EMBL, AF275348; AAG27217.1; --
GO, GO:0019012; C:virion; IEA.

GO, GO:0019012; C:virion; IEA.

InterPro, IPRO07640; Herpes UL17.

Hypothetical protein.

Flypothetical protein.

SEQUENCE 678 AA; 75850 MW; A17B09E30512PE3C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG30437-PC.
CG30437-PC.
CG30437 OR CG10398 OR CG10408.
CG3040437 OR CG10398 OR CG10408.
Enkaryota; Metacoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachygera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                           67.3%; Score 35; DB 12; Length 678; 50.0%; Pred. No. 90;
                                                                                                                                                                                                                                                                                         Indele
                                                                                                                                                                                                                11 protein. –
678 AA; 75850 MW; A17B09E30512FE3C CRC64;
          Cercopithecinė herpesvirus 7.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                         2; Mismatches
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                     1 EEVVPXGXHY 10
 Hypothetical protein.
                                                                                   SEQUENCE FROM N.A.
                                                      NCBI_TaxID=35245;
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Celuiker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.A.
Branzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Adacal and J.W., Contert V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibeyam C., Jalali M., Kruse D., Lip., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Racide J., Paragas V., Park S., Patel S., Petelffer B.,
Phouanenavong S., Pittman G.S., Patel S., Pitchards S., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zavari J.S., Smith H.O., Venter J.C., Rubin G.M.;
"Sequencing of Drosophila melanogaster genome.",
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong K.M., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Mistra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Mistra S., Crosby M.A., Matthews B.B., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Krommiller B., Marshall B., Millburn G., Richter J., Ruseo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Galbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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BMBL; AE003786; AAN16124.1; -.
FlyBase; FBGN005043; CG30437;
GO, GO:0005507; F:copper ion binding; IEA.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR00295; Cupredoxin.
InterPro; IPR00295; Cuox copper BS.
Pfam; PF00394; Cuox copper BS.
PROSTTE; PS000099; MULTICOPPER OXIDASE1; 1.
PROSTTE; PS000080; MULTICOPPER_OXIDASE2; 1.
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Last sequence update)
Last annotation update)
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TIGRFAMS; TIGR00915; 2A0602; 1.
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                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=16M / ARTCC 23456 / Biotype 1;
MEDLINB=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Selkov B., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Rizer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;
The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
Droc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
PRES. AR5286; AF3286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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I. DNA Res. 9:123-130(2002).

E. REMBI, APPON5374; BAC0910.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005215; Firansporter activity; IEA.
GO; GO:0006810; P:transporter activity; IEA.
R GO; GO:0006810; P:transport; IEA.
R InterPro; IPR004764; HAEI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 16; Length 1028;
Pred. No. 1.4e+02;
2; Mismatches 3; Indels 0
                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Multidrug efflux transporter.
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MEDLINE=22225144; PubMed=12240834;
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PRINTS; PR00702; ACRIFLAVINRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.3%;
llarity 54.5%;
Conservative
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                         Brucella melitensis.
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Best Local Similarity
Matches 6; Conserv
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                                                                                      NCBI_TaxID=29459
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SEQUENCE FROM N.A.

RATAILSESSO / ArCC BAA-588;

RATISE D.B., Holden M., Preston A., Murphy L.D., Thomson N.,

RATISE D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

Rethenol T., Golling M., Cronin A., Davis P., Doggett J.,

RA Leather S., Morberzak H., O'Neil S., Ormond D., Price C.,

RA Leather S., Morberzak H., O'Neil S., Ormond D., Price C.,

RADDIOWIESCH B., Rutter S., Sanders B., Seuger K.,

RADDIOWIESCH B., Rutter S., Sanders B., Squares S., Stevens K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

And D., Mitchead S., Barrell B.G., Maskell D.J.;

ROCMPATALIVE analysis of the genome sequences of Bordetella pertussis,

RESTORMED PARADICTURES and Bordetella bronchiseptica.";

RMEL, EXEGUENCE S., SML.
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                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales;
Alcaligenaceae, Bordetella.
NCBI_TaxID=518;
                                                                     67.3%; Score 35; DB 16; Length 1044; 63.6%; Pred. No. 1.4e+02; ive 1; Mismatches 3; Indels (
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Complete proteome. SEQUENCE 1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         262 AA.
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Job time: 29.8667 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative enoyl-CoA hydratase. BB1123.
                                                                                                            63.6%;
                                                Query Match
Best Local Similarity 63...
Restrict 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 66.7
Les 6, Conservative
                                                                                                                                                                                                                                                 843 EEVLPNGIGYS 853
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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SEQUENCE 262 AA
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
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ALIGNMENTS

note= "Norvalyl carbonyl forming keto-amide linkage with Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide. Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C $^\circ$ Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #29 'note= "N-terminal acetyl" /note= "C-terminal amide" note= "D-form residue" Location/Qualifiers ABB80549 standard; peptide; 11 AA. Brunck TK;

virus

Gaps

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Indels

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Mismatches

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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protesse. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.014;
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90.9%;
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Best Local Similarity
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DB 5; 0.014;

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93.8%; 90.9%;

Query Match Best Local Similarity

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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Ity useful for treating disorders associated with hepatitis C virus
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                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORV-) CORVAS INT INC
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200208251-A2
                                                                                                                                                                                                                                                                    Key
Modified-site
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                                                                                                                 08-OCT-2002
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                                                                                                                                                                                                                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protease.
                                                                                 ABB80552;
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Gaps

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1; Indels

RESULT 5
ABB80545
ID ABB8
XX
AC ABB8
XX
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21-JUL-2000; 2000US-0220101P.
                                                                                                                  WPI; 2002-361643/39.
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                                                                                                                                                                                                                                                                    Sequence 11 AA;
        WO200208251-A2
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                                                                                                                                   Novel peptide activity usefu
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Modified-site
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                          31-JAN-2002
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                                                                                                                                                       protease
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                                                                                                                                                                                                                                                                                   The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha **Etoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Norvalyl carbonyl forming keto-amide linkage with
                           /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus, HCV; serine protease, inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
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                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 5; Length 11;
Pred. No. 0.023;
0; Mismatches 1; Indels
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                'note= "N-terminal acetyl"
                                                                               /note= "C-terminal amide"
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/note= "C-terminal amide"
                                                              note= "D-form residue"
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Location/Qualifiers
                                                                                                                                                                                           Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB80521 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                    Claim 17; Page 64; 69pp; English
                                                                                                                                     19-JUL-2001; 2001WO-US023169.
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90.9%;
                                                                                                                                                        21-JUL-2000; 2000US-0220101P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGXSYS 11
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                                                                                                                                                                                           Lim-Wilby M, Levy OE,
                                                                                                                                                                          (CORV-) CORVAS INT INC
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                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                               Sequence 11 AA;
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Modified-site
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                                                                                                                                                                                                                                          activity | protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virucide.
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                 otide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB
Pred. No. 0.02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal amide"
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                                                                                                                                                             Brunck TK;
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19-JUL-2001; 2001WO-US023169
                                                  21-JUL-2000; 2000US-0220101P.
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                             Lim-Wilby M, Levy OE,
                                                                                                          (CORV-) CORVAS INT INC
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Brunck TK;

Levy OE,

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The sequence represents a peptide compound of the invention having hepatitis of virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB80536 standard; peptide; 11 AA.
                                                                                                                                                                                                                   Claim 17; Page 64; 69pp; English.
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Best Local Similarity 90.9
Matches 10; Conservative
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                     CORV-) CORVAS INT INC
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                                                                                                 WPI; 2002-361643/39
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11 AA;
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                                                         Lim-Wilby M,
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Modified-site
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                                                                                                                                                                                 protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virucide.
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ABB80536
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(first entry)

carbonyl forming keto-amide linkage with

note= "N-terminal acetyl"

note= "Norvalyl

residue 7"

Location/Qualifiers

/note= "C-terminal amide"

Brunck TK;

note= "D-form residue"

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                                                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "2-aminoisobutyryl carbonyl residue forming a keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoemide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide compound having hepatitis C virus protesse inhibitory activity useful for treating disorders associated with hepatitis C ^\circ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serine protease inhibitor peptide #46
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                                                                                                                                                                                                                               Score 44; DB 5; Length 11;
Pred. No. 0.023;
0; Mismatches 1; Indels
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                                            Claim 17; Page 64; 69pp; English
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                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                            1 EEVVPXGXSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-361643/39
                                                                                                                                                                                                     Sequence 11 AA;
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                  protease
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Gaps

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1; Indels

Mismatches

DB 5;

Score 44; Pred. No.

91.7%; 90.9%;

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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha **Letoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with RVO protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                carbonyl forming keto-amide linkage
                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #45.
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Pred. No. 0.023;
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                                                                                                                                                                                                                                                                                                                                               'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "C-terminal amide"
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                                                                                                  ABB80565 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORV-) CORVAS INT INC
   WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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Modified-site
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                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                   ABB80565;
                                                                                                                                                                                                                                                  virucide.
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                                                                  RESULT 12
ABB80565
ID ABB8
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pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus
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                                                                             Score 44; DB 5; Length 11;
Pred. No. 0.023;
0; Mismatches 1; Indels
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Pred. No. 0.023;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                              ABB80563 standard; peptide; 11 AA
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                                                                               91.78;
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                                                                               Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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Matches 10; Conserv
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Matches
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Gaps

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Length 11; 1; Indels 7

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carbonyl residue forming a keto
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Pred. No. 0.023;
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                                         /note= "(s,s)allothreonyl ca
-amide linkage with residue
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/note= "C-terminal amide"
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90.9%;
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Best Local Similarity 90.5
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                                                                                                                                                                       note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47.
                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #15
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                                                                                                                                           'note= "N-terminal acetyl"
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                                                                                                                                                                                     residue 7"
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
/note= "C-terminal amide"
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                                                              31-JAN-2002.
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Brunck TK;

Gaps .; 0 Query Match

91.7%; Score 44; DB 5; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 1; Indels

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Search completed: June 3, 2004, 11:48:24 Job time: 45.9333 secs

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COMPUTER: IBM PC compatible
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/cgm2_6/ptcdata/2/iaa/5B_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-637-759B-236
US-08-817-3558-236
US-09-201-945-236
US-09-201-945-236
US-09-134-006-4848
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US-09-134-006-4848
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PCT-US91-02714-26
US-08-459-16-2
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US-09-136-060-3738
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Listing first 45 summaries
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No.
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28 30 62.5 626 3 US-08-961-083-220 Sequence 220, App 29 30 62.5 626 4 US-09-536-784-220 Sequence 220, App 30 62.5 1308 4 US-09-536-784-220 Sequence 6588, App 31 30 62.5 3079 3 US-09-413-814-93 Sequence 93, Appl 33 29 60.4 10 2 US-09-413-814-80 Sequence 80, Appl 34 29 60.4 10 2 US-09-61-51 Sequence 19, Appl 35 29 60.4 20 1 US-08-410-81-51 Sequence 19, Appl 37 29 60.4 20 1 US-08-140-81-53 Sequence 53, Appl 37 29 60.4 28 1 US-08-140-81-53 Sequence 53, Appl 39 29 60.4 100 2 US-09-041-155-09-8 Sequence 57, Appl 40 29 60.4 145 3 US-08-144-84 Sequence 4, Appl 41 29 60.4 145 3 US-08-413-974 Sequence 4, Appl 41 29 60.4 145 3 US-08-413-944 Sequence 4, Appl 41 29 60.4 145 3 US-08-413-288-4 Sequence 4, Appl 41 29 60.4 145 3 US-08-413-284-4 Sequence 4, Appl 41 29 60.4 145 3 US-08-143-284-4 Sequence 4, Appl 41 29 60.4 145 4 US-08-13-284-4 Sequence 4, Appl 41 29 60.4 145 4 US-08-13-284-4 Sequence 4, Appl 41 29 60.4 145 4 US-08-13-26-4 Sequence 4, Appl 41 29 60.4 US-08-13-26-4 Sequence 4, Appl 41 29 60.4 US-08-13-26-26 4 Sequence 4, Appl	RESULT 1 US-09-408-020-4 i Sequence 4, Application US/09408020 i GENERAL INFORMATION: APPLICANT: Schleper, Christa TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REFERENCE: DCORP.002-0 CURRENT APPLICANT: 00/102,29-0 FILE REFERENCE: 1999-09-29 PRIOR APPLICANT: 00/102,29-0 PRIOR APPLICANT: 00/102,29-0 NUMBER OF SEQ ID NOS: 123 SOFTWARE: PRESCO FOR Windows Version 3.0 SEQ ID NO 4 LENGTH: 3472 TYPE: PRI CORANISM: Cenarchaeum symbiosum US-09-408-020-4 Query Match GLES OF STATES	Db 2294 EDVIPRGISFS 2304 Db 2294 EDVIPRGISFS 2304 US-08-637-759B-236 Sequence 236, Application US/08637759B Sequence 236, Application US/08637759B Sequence 236, Application US/08637759B Sequence 236, Application US/08637759B PAPLICANT: David William Holden APPLICANT: David William Holden TITLE OF INVENTION: Identification of Genes NUMBER OF SEQUENCES: 501 CORRESPONDENCE ADDRESS: 801 ADDRESSEE: Pattea L. Pabst STREET: 2800 One Atlantic Center STREET: 1201 West Peachtree Street CITY: Atlanta CITY: Atlanta COUNTRY: USA STREET: 330309-3450 CONNTRY: USA
И И И И И И И И И И И И И И И И И И И В О О Н И И А И О С В В О С Н И И А И	RESULT 1 US-09-40 US-09-40 Sequent GENERAL APPLII APPLII TITLE TITLE TITLE TOURRE PRIOR PRIOR SSOTW SSOTW SSOTW SSOTW US-09-40 US-09-40 ORGA US-09-40	DD' RESULT 2 Sequent Patentine Paten

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66.7%; Score 32; DB 4; Length 45; 60.0%; Pred. No. 9.9; tive 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4

US-09-201-945-236

US-09-201-945-236

Sequence 236, Application US/09201945

Patent No. 642215

Patent No. 642215

GENERAL INFORMATION:

APPLICANT: David William Holden

TITLE OF INVENTION:

CORRESSED ADDRESS:

STREET: 2800 One Atlantic Center

STREET: 1201 West Peachtree Street

CITY: Atlanta

COMPUTR: 1204

COMPUTR: Georgia

COMPUTR: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTR: 180 PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CUBSSIFICATION:

APPLICATION NUMBER: US/09/201,945

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION:

PRIOR APPLICATION:

ATTOMER'AGENT INFORMATION:

ATTOMER'AGENT INFORMATIO
                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
                                       SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 amino acids
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-236
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Best Local Similarity
Matches 6; Conserva'
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STRANDEDNESS: si
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Pred. No. 9.9;
1; Mismatches 3; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSITCATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PADST, PALTEA L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1201 WEST PERCELLED COUNTRY: USA
COUNTRY: USA
ZIP: 3309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
OPERATING SYSTEM: PC-DCS/NS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRICK APPLICATION NUMBER: US/08/871,355A
FILING DATE: 10-DEC-1995
CLASSIFICATION: 435
PRILING DATE: 11-DEC-1995
CLASSIFICATION: A35
APPLICATION NUMBER: RSWS 101 CON
TELESCAMMUNICATION INFORMATION:
NAME: Pabst, Patrea L
RESTRATION NUMBER: RSWS 101 CON
TELESCAMMUNICATION INFORMATION:
TELESCAMMUNICATION INFORMATION:
TELESCAMMUNICATION INFORMATION:
TELESCAMMUNICATION INFORMATION:
TELESCAMMUNICATION INFORMATION:
TELESCAMMUNICATION INFORMATION:
TELESCAMMUNICATION OF 873-8795
INFORMATION FOR SEQ ID NO: 236:
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APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGXSY 10
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Sequence 4848, Application US/09134000C

Batent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERBOCOCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.6%; Score 31; DB 3; Length 159; 66.7%; Pred. No. 63;
64.6%; Score 31; DB 2; Length 159;
66.7%; Pred. No. 63;
ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTEY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSER for Windows Version 2.0
SOFTWARE: FastSER for Windows Version 2.0
SOFTWARE: PAPICATION DATA:
APPLICATION NUMBER: US/09/018,211
FILING DATE:
APPLICATION NUMBER: US/09/018,211
FILING DATE: 18-APR-1997
APPLICATION NUMBER: 9067993.4
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimm., Edward R
RESISTRATION NUMBER: 38 891
                                                                                                                                                                                                                                                                 US-09-018-211-4

Sequence 4, Application US/09018211

Sequence 4, Application US/09018211

Sequence 4, Application US/09018211

SETECT INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSE: SmithKine Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acida
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 66.7
Matches 6, Conservative
                                                      6; Conservative
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123 EEVLPDGTS 131
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Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                셤
                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REPERENCE: 11000/J020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 3.0
SOFTWARE: FastSEQ for Mindows Version 3.0
SEQ ID NO 73
LENGTH: 947
TYPE: PRT
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APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMDITY: USA

ZIP: 19406-0939

COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,086
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: 9607993.4
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: GIMM: Edward R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
RECISTRATION NUMBER: 38,891
RELEPONE: 610-270-4418
TELEFONE: 610-270-4418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 4;
Pred. No. 2.8e+02;
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                                                   Sequence 73, Application US/09228986 Patent No. 6359198
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Patent No. 5866390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66./
6, Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein JS-08-844-086-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pinus radiata
IS-09-228-986-73
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ESULT 5
S-09-228-986-73
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Sequence 26, Application PC/TUS9102714

GENERAL INFORMATION:
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE Bicknell
STREET: Street
STREET: Street
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Sequence 34, Application US/09424978B

Sequence 34, Application US/09424978B

Setent No. 6664445

APPLICANT: Falco. Saverio Carl
APPLICANT: Rafalski, U. Antoni
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Thoree, Catherine J.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
FILE REFERENCE: BB-108.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
FILE REPERENCE: B1-109.
FILE OF INVENTION NUMBER: US 60/048,771
PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin version 3.1

SEQ ID NO 34

LENTH: 507
                                                                                                                                                                                                                                                                        Score 31; DB 4; Length 181; Pred. No. 73; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 507;
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Pred. No. 2.3e+02;
1; Mismatches 3
CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTWARE: Patentin version 3.1 SEQ ID NO 4848 LENGTH: 181
                                                                                                                                                                                TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Burkholderia capacia
US-09-424-978B-34
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             145 EEVVPTSEDY 154
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                                                                                                                                                                                                                                                                                                                                                                  1 EBVVPXGXSY 10
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STATE: Illino
                                                                                                                                                                                                                               US-09-134-000C-4848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-424-978B-34
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TELEMONY STATE: PLOSA CONTINUES READABLE FORM:

MEDIUM TYPE: RIPRY CONTINUES PORM:

CONTINUES READABLE FORM:

MEDIUM TYPE: RIPRY CONTINUES PORM:

CONTINUES READABLE FALCHING NETWER: PLOSANGE #1.0, Version #1.25

CHASTITION NUMBER: PROPERTY OF #1.0, Version #1.25

APPLICANTON NUMBER: PROPERTY OF #1.0, VERSION THE PROPERTY OF TH
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85.7%; Pred. No. 2.8e+02; :ive 0; Mismatches 1; Indels

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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                            31 EEVVPAG 37
                                                                                   1 ERVVPXG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-474-379C-28
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Factont No. 5882642

GENERAL INFORMATION:
APPLICANT: Choi, Gil Ho
APPLICANT: Choi, Gil Ho
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION: Hypovirulence
NUMBER OF SEQUENCES: 3
CORRESPONDENCES: 3
CORRESPONDENCES: 3
CORRESPONDENCES: 3
CORRESPONDENCES: 3
STREET: 340 Kingeland Street
CITT. Nutley
CITT. Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.6%; Score 31; DB 2; Length 622;
                                                                                                                                                                                                                                                                                                                         Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: U/ILD
COMPUTER: ELADRY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSNIT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,065
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/832,117
APPLICATION NUMBER: US 07/832,117
APPLICATION NUMBER: 34,240
RIGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8589
TELECOMMUTATION INFORMATION:
TELECOMMUTATION INFORMATION:
TELECOMMUTATION INFORMATION:
TELECOMMUTATION INFORMATION:
TELECOMMUTER: (201) 235-3500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARRATIERISTICS:
LENGTH 652 milto acids
                  TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TOPLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

CRIGANISM: Endothia parasitica (Cryphonectria

CRGANISM: parasitica)

STRAIN: EP713

US-08-459-146-2
                                                                                                                                                                                                                                                                                                                    Query Match 64.6%; Score 31; DB 2; 18est Local Similarity 85.7%; Pred. No. 2.8e+02; Matches 6; Conservative 0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Endothia parasitica (Cryphonectria
ORGANISM: parasitica)
STRAIN: EP713
INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 622 ami-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 622 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 EEVVPAG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXG 7
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                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Golicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ATTATE: Illinois
COMPUTER: Illinois
COMPUTER: Illinois
COMPUTER: Illinois
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATA:
APPLICATION NUMBER: US/07/688,352C
FILING DATE: 19910419
CLASSIFICATION NUMBER: US/07/511,715
FILING DATE: 20-ARR-1990
ATTORNEY/AGENT INPORMATION:
NUMBER: 27400
FILIERPAN: (312) 346-5750
TELERPAN: (312) 346-5750
TELERPAN: (312) 346-5750
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APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLOUING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: PROCESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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US-07-688-352C-28
; Sequence 28, Application US/07688352C
; Patent No. 5527896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 28, Application US/08474379C; Patent No. 5977305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
TOPOLOGY: 1:--
OLECIT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75.0
Section 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-07-688-352C-28
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us-09-909-164-43.rai

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APPLICATION NUMBER: US/09/146,249A
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UNE-09-146-249A-28

Sequence 28, Application US/09146249A

Patent No. 60692410N:

Patent No. 60692410N:

APPLICANT: Wigher, Michael H.

APPLICANT: Colicelli John J.

TITLE OF INVENTION: Cloning by Complementation and Related

TITLE OF INVENTION: Processes

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS: 85

CORPET: Chicago

STREET: Chicago

STREET: Illnois

CONTY: United States of America

CONTY: United States of America

CONTYR: INPOSE COMPATION: PROPER PROPERTY PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
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Pred. No. 3.2e+02;
                                                                                      3: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & B.
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
CUNTRY: United States of America
ZIP: 6606-6402
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 07-UNM-1995
CLASSIFICATION: 435
PRICK APPLICATION NUMBER: US 07/511,715
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Clough, David W.
REGISTRATION NUMBER: 35,107
REFERENCE/DOCKET NUMBER: 2786(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.6%;
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amino acid
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Best Local Similarity 75.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 WPAGGSY 208
         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVPXGXSY 10
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Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2;
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECHOME: 312/44-6300
TELEFRAX: 312-474-6300
TELEFRAX: 19-886
SEQUENCE CHARACTERISTICS:
LENGRAYION FOR SEQ.
INFORMATION OR SEQ.
SEQUENCE CHARACTERISTICS:
LENGRAYION AND ADDRESSED OF TARRESTICS:
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THE TARRESTICS TOR TARREST
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Job time: 11.8 secs
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 WPAGGSY 208
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US-09-909-164-28
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                                                                                                                                                            (without alignments)
91.741 Million cell updates/sec
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Sequence 9, A
Sequence 10,
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Sequence 36,
Sequence 37,
Sequence 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28,
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Sequence 19,
Sequence 20,
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Sequence
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                                                                                                                                   June 3, 2004, 11:57:42 ; Search time 33.7333 Seconds
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1: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/USO_NEW PUB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                              1155919
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-29
US-09-909-164-35
US-09-909-164-37
US-09-909-164-37
US-09-909-164-5
US-09-909-164-6
US-09-909-164-9
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US-09-909-164-23
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US-09-909-164-23
US-09-909-164-23
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                                                                                                                                                                                                                                                                                                                                                                                             1155919 seqs, 281338677 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 20000000000
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48
1 EEVVPXGXSYS 11
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Match Length
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                                                                                                                                                                                                                                     Fitle:
Perfect score:
                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                        Run on:
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ALIGNMENTS

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Sequence 28 Application US/09909164

| Sequence 28 Application US/09909164
| Publication No. US2020068702A1
| CENERAL INFORMATION:
| APPLICANT: Corves International, Inc.
| APPLICANT: Lim-Wilby, Marguerita
| APPLICANT: Levy, Odile B
| APPLICANT: Lim-Wilby, NoveL PETIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| FILE REFERENCE: IN01192-US
| CURRENT FILING DATE: 2003-03-25
| PRIOR APPLICATION NUMBER: 60/220,101
| PRIOR PLING DATE: 2000-00-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 28
| LENGTH: 11
| TYPE: PRI
| PRABTICE PRIOR PRESENCE: PRESENCE |
| PRIOR PRESENCE: PRESENCE |
| PROGRAMISM: ARTIFICIAL SEQUENCE |
| PRESENCE: PRESENCE |
| PROGRAMISM: ARTIFICIAL SEQUENCE |
| PRESENCE |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: 11-mer synthesized according to example 1 PEATURE:
NAME/KEY: MOD_RES
LOCATION: (1) - (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
NAME/KEY: MOD_RES
OCHER INFORMATION: (11)
OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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Sequence 36, Application US/09909164
; Sequence 36, Application US/09909164
; Publican No. US20020068702A1
; GENERAL INFORMATION:
    APPLICANT: Lim-Wilby, Marguerita
    CURRENT APPLICATION NUMBER: US/09/909,164
    CURRENT FILING DATE: 2000-07-21
    NUMBER OF SEQ ID NOS: 62
    SOFTWARE: PatentIn version 3.1
    SEQ ID NO 36
    LUMCTH: 11
    LUMCTH: 11
    APPLICANT: Lim-Wilby, Marguerita
    APPLICANT: Lim-Wi
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                                                                                                   TYPE: PRT
ORGANISM: artificial seguence
FRATURE:
OCHER INFORMATION: 11-mer synthesized according to example 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%; Score 45; DB 12; Length 11; 90.9%; Pred. No. 0.0077; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11]... (11)
OTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)... (6)
COTHER INFORMATION: norvaline-(CO)
FEATURE:
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THER INFORMATION: norvaline-(CO)
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LOCATION: (1)...(1)
CTHER INFORMATION: ACETYLATION
FRATURE:
NAME/KEY: MOD_RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
CTHER INFORMATION: D-amino acid
US-09-909-164-33
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NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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NAME/KEY: MISC FEATURE
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                                                                                                                                                                                                                                                                         Sequence 33, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Oddie E
APPLICANT: Levy, Oddie E
APPLICANT: Levy, Oddie E
APPLICANT: NOVEL PERTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERBNCE: 1N01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
PRICK APPLICATION NUMBER: 60/220,101
PRICK FILING DATE: 2000-07-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.8%; Score 45; DB 12; Length 11; 90.9%; Pred. No. 0.0077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
      Best Local Similarity 90.9%; Pred. No. 0.0077; Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (9)...(9)

COTHER INFORMATION: D-amino acid

MS-09-909-164-29
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LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
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NAME/KEY: MOD RES
LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
FEATURE:
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Best Local Similarity 90.9
Matches 10; Conservative
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Sequence 6, Application US/09909164

| Sequence 6, Application US/09909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Lim-Wilby, Marguerita
| TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TITLE OF INVENTION NUMBER: 60/220,101
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SEQ ID NO 6
| LENGTH: 11
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/URE:
NAME/URE:
OCCUPATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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Pred. No. 0.013;
0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VEXBION 3.1
SEQ ID NO 5
LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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                                                                                                                                                                                                      TYPE: PRT ORGANISM: artificial sequence
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Best Local Similarity 90.9%;
Matches 10; Conservative
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NAMENKEY:
DOCATION: (11)
LOCATION: (11)
CTHER INFORMATION: AMIDATION
US-09-909-164-5
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Sequence 37, Application US/09909164

Publication No. US20020068702A1

Publication No. US20020068702A1

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: NUMBER: US/09/909,164

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 37

LENGTH: 11
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APPLICANT: Corvas international, inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: BRUNCA, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS
FILE REFERENCE: IN01192-US
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                                                                                      Score 45; DB 12; Length 11;
Pred. No. 0.0077;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09909164
Publication No. US20020068702A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (8)...(9)
COTHER INFORMATION: D-amino acids US-09-909-164-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
          OTHER INFORMATION: D-amino acid JS-09-909-164-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: artificial sequence
                                                                                      Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.9
Marches 10; Conservative
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Sequence 14, Application US/09909164

| Sequence 14, Application US/09909164
| Publication US20020068702A1
| Publication No. US20020068702A1
| GRNERAL INPORMATION:
| APPLICANT: Lim-wilby, Marguerita
| APPLICANT: NUMBER: US/09/909,164
| CURRENT FILING DATE: 2000-07-21
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOOTHARE: Patentin version 3.1
| SEQ ID NO 14
| LINGTH: 11
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: 11-mer synthesized according to example 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%; Score 44; DB 12; Length 11; 90.9%; Pred. No. 0.013; tive 0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD RES
LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
FRATURE: MANGE FRATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (8).7(9)
CITHER INFORMATION: D-amino acids
US-09-909-164-10
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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NAME/KEY:
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
PEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: MOD RES
LOCATION: (1) \(\tilde{\text{.}}\)(1)
OCTHER INFORMATION:
FEATURE:
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ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: artificial sequence
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Best Local Similarity
Matches 10; Conserva
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Sequence 9, Application US/09909164

Bublication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Corvae International, Inc.
APPLICANT: Lim'wilby, Marguerita
APPLICANT: Larw, odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT PILLNG DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Version 3.1
SEQ ID NO 9
LENGTH: 11
TYPE: PRI
TYPE: 
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: IN01192-US
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                                                                                                        Score 44; DB 12; Length 11;
Pred. No. 0.013;
0; Mismatches 1; Indels
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1 Similarity 90.9%; Pred. No. 0.013;
10; Conservative 0; Mismatches
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Publication No. US20020068702A1
GENERAL INFORMATION:
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OTHER INFORMATION: norvaline-(CO)
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| NAME/KEY: MISC_FEATURE
| LOCATION: (8) ...(8)
| OTHER INFORMATION: D-amino acid
| US-09-909-164-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                   Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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OTHER INFORMATION: AMIDATION
                  ; OTHER INFORMATION: AMIDATION US-09-909-164-6
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
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Best Local
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US-09-909-164-23

i Sequence 23, Application US/09909164

i Sequence 23, Application US/09909164

i Publication No. USZ0020068702A1

i GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Oddile B

APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

ITILE REFERENCE: IN01192-US

CURRENT FILING DATE: 2000-03-03

PRIOR PELING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 23

LENGTH: 11

'TYPE: PRT

ORGANISM: artificial sequence

PERIOR PRIOR PRITORS

ORGANISM: artificial sequence
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                                                                                                                                              TYPE: PRT
ORGANISM: artificial sequence
FRATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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THER INFORMATION: norvaline-(CO)
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| LOCATION: (9)...(9)
| OTHER INFORMATION: D-amino acid
US-09-909-164-20
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NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC. FEATURE
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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NAME/KRSY MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Matches 10; Conservative
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Sequence 19, Application US/0990164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: IN01192-US

CURRENT FILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PELING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PRECENT IN VERSION 3.1

TYPE: PRI

TYPE: PRI

TYPE: PRI

TYPE: PRI

TYPE: PRI

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Publication No. U520020068702A1
Publication No. U520020068702A1
Publication No. U520020068702A1
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Lievy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Levy, Odile B
APPLICANT: Levy, NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TILE REPERBNCE: IN01122-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILIAG DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
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OTHER INFORMATION: 11-mer synthesized according to example 1
PEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
PEATURE:
NAME/KEY: NO RES
NAME/KEY: NO RES
NAME/KEY: (1)...(11)
OTHER INFORMATION: AMIDIATION
                                                                                                         Score 44; DB 12; Length 11;
Pred. No. 0.013;
0; Mismatches 1; Indels
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LOCATION: (6). (6)
CTHER INFORMATION: norvaline-(CO)
US-09-909-164-19
; OTHER INFORMATION: norvaline-(CO) US-09-909-164-14
                                                                                                             Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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FRATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
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CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VETBION 3.1
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: June 3, 2004, 12:57:16 Job time: 33.7333 secs
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NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)..(8)
OTHER INFORMATION: D-amino acid
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                                                                                                                                                                                                         TYPE: PRT ORGANISM: artificial sequence
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/09909164

Publication No. US20020068702A1

General Information No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

FILE REFERENCE: 1001192-105

CURRENT APPLICATION NUMBER: 105/09/909,164

CURRENT FILING DATE: 2003-03-25

FRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin Version 3.1

SEQ ID NO 24

LENTH: 11

LENTH: 11
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Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corves International, Inc.
APPLICANT: Lim.Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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91.7%; Score 44; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 1; Indels
                                                                              Score 44; DB 12; Length 11; Pred. No. 0.013;
                                                                                                                                1; Indels
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NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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NAME/KSY: NOD RES
LOCATION: (1)...(1)
OTHER INFORMATION:
ACETURE:
NAME/KEY: NOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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LOCATION: (8)..(9)

COTHER INFORMATION: D-amino acids

US-09-909-164-24
          ; OTHER INFORMATION: D-amino acid US-09-909-164-23
                                                                           Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                           1 EEVVPXGQSYS 11
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GenCore version 5.1.6
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M protein - protein search, using sw model

tun on:

June 3, 2004, 11:35:47; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec

US-09-909-164-43 48 Perfect score: itle:

1 EEVVPXGXSYS 11

lequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

dinimum DB seq length: 0 daximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Jatabase

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description			V1 protein - tobac	hypothetical prote	_	ATP-dependent DNA	trans-regulatory s	tolB protein - Hae	hypothetical prote	hypothetical prote	3-phosphoshikimate	zinc finger protei		DNA-binding protei	5	hypothetical prote	hypothetical prote	dTDPglucose 4,6-de	dTDP-glucose 4,6-d	hypothetical prote	periplasmic sorbit	ATP-dependent DNA	probable ABC subst	type II secretion	3	hypothetical prote		ag-	
SUMMARIES	σī	T31308	S57810	A42452	D69493	T34536	AF3286	VKLJSI	F64064	E75619	T24111	D82163	S22293	A30481	A34203	E69342	S75817	803833	815299	AF0767	AG2945	C98337	AH2679	C82900	2	746	T05331	500	597	235
	DB	;		(1																										
	Length	3472	225	102	165	259	1028	124	427	227	425	426	670	890	2717	123	284	319	361	361	437	450	541	544	561	573	612	622	646	653
d	Query Match	75.0	72.9	70.8	70.8	70.8	70.8	68.8	68.8	66.7		66.7	66.7	66.7	66.7	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6
	Score	36	35	34	34	34	34	33	33	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
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hypothetical prote	leucine-tRNA ligas	leucyl-tRNA synthe	leucine-tRNA ligas	probable sulfate p	sulfate permease -	hypothetical prote	hypothetical prote	isoleucine-tRNA li	K-Cl cotransport p	K-Cl cotransport p	K-Cl cotransport p	probable chitinase	K-Cl cotransport p	conserved hypothet	hypothetical prote
\$61239	H86726	H95029	C97901	T39116	T40413	AG1860	T17275	A42399	T18369	T31429	T14114	D82246	T31432	D87046	T04456
C)	N	N	~	N	N	N	N	н	~	N	C)	N	N	N	77
701	829	833	833	840	877	926	1014	1081	1085	1085	1086	1088	1116	1152	1548
64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6
31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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hypothetical 367K protein - Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Accession: T31308
R;Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
A;Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
A;Fitle: Genomic analysis reveals chromosomal variation in natural populations of the ur
A;Accession: T31308

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2294 EDVIPRGISFS 2304
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RESULT 2

hypothetical protein precursor (clone TPP11) - tomato C;Species: Lycopersicon esculentum (tomato) C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000

C,Accession: S57810
R,Milligan, S.B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
A;Title: Nature and regulation of pistil-expressed genes in tomato.
A;Reference number: S57808; MUID:95375233; PMID:7647301
A;Accession: S57810
A;Accession: S57810
A;Molecule type: m2NA
A;Molecule type: m2NA
A;Residues: 1-225 < MIL.
A;Cross-references: EMBL:U20592; NID:9924625; PIDN:AAA80497.1; PID:9924626
C;Superfamily: plant Kunitz-type proteinase inhibitor

Query Match
72.9%; Score 35; DB 2; Length 225;
Best Local Similarity 54.5%; Pred. No. 7;
Matches 6; Conservative 3; Mismatches 2; Indels 1 EEVVPXGXSYS 11 :|||| | :|: 32 DEVVPNGKTYA 42 ò 심

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Gaps

us-09-909-164-43.rpr

Fri Jun

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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
R;Datession: AF386
R;Dalvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
J; Mazur, M.; Goltsman, E.; Selkov, E.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten
A;Reference number: AD3252; PMID:1175668
                                                                                                                                                                                                                                                                                                                                                                                   ATP-dependent DNA helicase BME10275 [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis
C;Species: Drucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:AAL51457.1; PID:g17982167; GSPDB:GN00190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: AIDS trans-regulatory splicing protein Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 59;
2; Mismatches 3; Indels
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                                         Indels
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Pred. No. 13;
1; Mismatches
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A;Molecule type; DNA
A;Residues: 1-1028 <KUR>
A;Cross-references: GB;AE008917; P
A;Experimental source: strain 16M
Best Local Similarity 60.0%;
Matches 6; Conservative
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54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                2 EVVPXGXSYS 11
                                                                                                                                                                                           22 EVAPAGASYN 31
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                                                                                                                                                                  C;Accession: A42462

C;Accession: A42462

R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.

Virology 187, 633-642, 1992

A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yellogy A;Reference number: A42452; MUID:92188538; PMID:1546458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE000968; GB:AE000782; NID:g2689291; PIDN:AAB89307.1; PID:g264859
C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF1949
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                                                                  VI protein - tobacco yellow dwarf virus (strain Australia)
C,Species: tobacco yellow dwarf virus
C,Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, October 1999
A;Reference number: Z21540
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                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA
A,Residues: 1-102 <MOR>
A,Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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Pred. No. 8.3;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein DXFZp434C031.1 - human (fragment)
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Pred. No. 4.9;
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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Query Match

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R.Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Asture 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301
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c;Species: Rattus norvegicus (Norway rat)

C;Species: P3-dan-1998 #sequence_revision 06-Peb-1998 #text_change 20-Sep-1999

C;Accession: S22293; 178656

R;Mitchelmore, C.; Traboni, C.; Cortese, R.

R;Mitchelmore, C.; Traboni, C.; Tortese, R.

R;Mitchelmore, C.; Traboni, C.; Traboni, C.; Asids Rese 19, 1991

A;Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-A;Reference number: I58280; MUID:91187610; PMID:1901405
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A;Molecule type: DNA
A;Molecule type: DNA
A;Mosicules: 1-426 <HELP.
A;Residues: 1-426 <HELP.
A;Cross-references: GB:AE004251, GB:AE003852; NID:g9656248; PIDN:AAF94882.1; GSFDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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C;Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carbox
                                                                                                                                                                                                                                                                                   Ribercy, C. submitted to the EMBL Data Library, October 1996
A;Reference number: Z19842
A;Reference number: Z19842
A;Accession: T24111
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rodecule type: DNA
A;Rosidues: 1-425 <WIL>
A;Cross-references: EMBL: 281109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:RIOD12.10
A;Experimental source: clone R10D12
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                                                                                                                                            Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
Accession: T24111
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; Species: Vibrio cholerae
; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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Pred. No. 62;
1; Mismatches 3; Indels
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                                                                                                                      hypothetical protein R10D12.10 - Caenorhabditis elegans
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Pred. No. 62;
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Best Local Similarity 50.0°
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Best Local Similarity 60.0
Matches 6; Conservative
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Gene: CESP:R10D12.10
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D82163
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[White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
[White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
[M.; Shan, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
[S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
[Science 286, 1571-1577, 1999
[Viltle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
[Virtle: Genome rumber: A75250; MUID:20036896; PMID:10567266
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4;Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12657.1; PID:g6460953; TIGR:DRB0d
4;Experimental source: strain R1
                 "Spaces 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
"Accession: F64064; JC5213
"F2161schmann, R.D.; Addms, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, F. Godsapho, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; File, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Puhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
"Yathors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, Y.Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
"Yathors: Incleic acid sequence not shown; translation not shown
"Nobecule type: DNA
"Status mucleic acid sequence not shown; translation not shown
"Homelenger of the status of the stat
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4,Cross-references: GB:U32470, NID:g1685076; PIDN:AAC44597.1; PID:g1685080
4;Experimental source: strain 1479
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Sene 178, 75-81, 1996

*/Title: Isolabrion and characterization of the Haemophilus influenzae tolQ, tolR, tolA
*/Reference number: JC5212; MUID:97080550; PMID:8921895
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2;Superfamily: Deinococcus radiodurans megaplasmid hypothetical protein DRB0013
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Species: Deinococcus radiodurans
Date: 03-Dec.1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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Pred. No. 32;
2; Mismatches 3; Indels
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Species: Haemophilus influenzae
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Best Local Similarity 54.5%;
Matches 6; Conservative
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A,Cross-references: GB:AE001054; GB:AE000782; NID:g2689377; PIDN:AAB90501.1; PID:g26498
C;Superfamily: uncharacterized conserved protein
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                            Length 2717;
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                       Score 32; DB 2; Length 271
Pred. No. 4.5e+02;
l; Mismatches 2; Indels
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ne : 10 secs
                          Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 50.0%;
Matches 5; Conservative
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Job time
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;Baldwin Jr., A.S.; LeClair, K.P.; Singh, H.; Sharp, P.A.
ol. call. sbil. 10, 1406-1414, 1990
reference number: A34779; MUID:90205817; PMID:2108316
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C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
C;Accession: A,4203; A34779
K;Fan, C.M.; Maniatish T.
Genes Dev. 4, 29-42, 1990
A;Title: A DNA-binding protein containing two widely separated zinc finger motifs that A;Reference number: A34203; MUID:90169514; PMID:2106471
                                                                                                                                                                                                                                                                                                                                                                                                                    Dacteriocin BCN5 - Clostridium perfringens plasmid pIP404
C;Species: Clostridium perfringens
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Nov-1999
C;Dacession: A30481; S03779
T;Bacteriol: 168, 1189. 1196, 1986
T;Bacteriol: 168, 1189-1196, 1986
T;Title: Characterization of a bacteriocinogenic plasmid from Clostridium perfringens
Accession: A30481
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;Residues: 1-890 <GAR>
;Cross-references: GB:M32882; GB:J03309; NID:g150738; PIDN:AAA98249.1; PID:g150739
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A;Status: nucleic acid sequence not shown
A;Molecule type: mRNT
A;Molecule type: mRNT
A;Residues: 1.670 <MIT>
A;Cross-references: EMBL:X54250; NID:g57519; PIDN:CAA38151.1; PID:g57520
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Keywords: DNA binding; transcription regulation; zinc finger
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C;Superfamily: Clostridium perfringens plasmid pIP404 bacteriocin BCN5
C;Keywords: bacteriocin
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Pred. No. 1.4e+02;
1; Mismatches 2; Indels
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Best Local Similarity 66.7%;
Matches 6; Conservative 1
                                                                                                                                                                                                                                                                                                                              376 VVPAGLTYS 384
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                                                                                                                                                                                                                                                                                              3 VVPXGXSYS 11
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Residues: 1-2717 <FAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: A34203
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Gaps

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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M protein - protein search, using sw model

June 3, 2004, 11:32:06 ; Search time 4.86667 Seconds

tun on:

(without alignments)
117.693 Million cell updates/sec

US-09-909-164-43 48 1 EEVVPXGXSYS 11 Perfect score:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

141681 segs, 52070155 residues searched: otal number of hits satisfying chosen parameters:

finimum DB seq length: 0 faximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Jatabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STAMMIN

	ption	homo sapien	fusobacteri	tobacco yel	archaeoglob	homo sapien	chimpanzee	haemophilus	vibrio chol	clostridium	homo sapien	cryphonectr	salmonella		lactococcus	streptococc						streptococc	schizosacch	tetrahymena	homo sapien	III BTIII		-	oryctolagus	rattus norv				homo sapien
	Description	060312	Q8rg86	P31619	028330	Q9nzm5	P17280	P44677	Q9krb0	P08696	P15822	P10941	P26391	P53607	09chb6	Q8e2v2	Q8d885	Q8k8s1	Q8p2t2	097880	09a1p0	08drb6	074377	P36422	09 y666	Q9wv13	09up95	09 j i 88	028677	Q63632	Q91v14	09h2x9	063633	6Aupo
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SUMMARIES	Д	A10A HUMAN	CARB FUSIN	Y11K_TYDVA	YJ49 ARCFU	GSR2_HUMAN	REV SIVCZ	TOLE HAEIN	AROA VIBCH	BCNS_CLOPE	ZEP1 HUMAN	YHA1 CRYPA	RFBB_SALTY	THD1 BURCE	SYL LACLA	SYL_STRA3	SYL_STRMU	SYL_STRP3	SYL_STRP8	SYL_STRPN	SYL_STRPY	SYL_STRR6	SULH SCHPO	SYI_TETTH	S127 HUMAN	S127_MOUSE	S124 HUMAN	S124 MOUSE	S124 RABIT	S124_RAT	S125 MOUSE		S125_RAT	S126_HUMAN
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

numan and mouse cDNA sequences.

SEQUENCE OF 337-1499 FROM N.A. TISSUE-Brain;

Q924n4 mus musculu Q90hf homo sapien Q8ndf homo sapien Q8nd 92 pyrococcus Q5d 19 pyrococcus Q9hnu2 halobacteri P71841 mycobacteri Q9rbx corynabacte Q8tpf methanosarc Q8ptb methanosarc Q8ptb methanosarc Q9zle3 helicobacte
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ALIGNMENTS

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bata N.K.,
Hopkins R.F., Jordan H., Moore T., Maxs S.I., Wang J., Heich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Poshiyuki S., Carninci P., Prange C.,
Raha S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunsarane P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Batkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Renergian A., Schein J.E., Jones S.J.M., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1] SECURICE FROM N.A. SECURICE FROM N.A. SECURINE-21225279; PubMed=11326269; MEDLINE-21225279; PubMed=11326269; Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S., Oshimura M.; Arpressed gene, ATP10C, encodes a putative syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome."; Nat. Genet. 28:19-20(2001).
                                                                       060312; 096914;
30-MAY-2000 (Rel. 39, Created)
28-FB22003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Potential phospholipid-transporting ATPase VA (EC 3.6.3.1) (ATPVA)
ATP10A OR ATP10C OR ATPVC OR KIAA0566.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
MEDLINE=21313119, PubMed=11353404;
Herzing L.B.K., Kim S.-J., Cook B.H. Jr., Ledbetter D.H.;
Herzing L.B.K., Kim S.-J., Cook B.H. Jr., Ledbetter D.H.;
"The human aminophospholipid-transporting ATPase gene ATP10C ma
adjacent to UBB3A and exhibits similar imprinted expression.";
Am. J. Hum. Genet. 68:1501-1505(2001).
                                              PRT; 1499 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Skin;
MEDLINE-22388257; PubMed-12477932;
                                              STANDARD;
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SEQUENCE FROM N.A.
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HUMAN
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EXTRACELLULAR (POTENTIAL).

POTENTIAL

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EXTRACELLULAR (POTENTIAL)

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POTENTIAL. EXTRACELLULAR (POTENTIAL)

1229 1250 1268 1293

427 1031 1035

CYTOPLASMIC (POTENTIAL).

POTENTIAL.

1193 1223

N

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R MIN; 105830; -.
R GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004012; F:phospholipid-translocating ATPase activity; NAS.
R GO; GO:0008360; P:regulation of cell shape; NAS.
R InterPro; IPR001757; ATPase_E1-E2.
R InterPro; IPR005839; Plippase.
R InterPro; IPR005839; Plippase.
R Pfam; PF00702; Hydrolase; 1.
R PRINTS; PR00119; CATATPASE.
R TIGRRAMS; TIGR01494; ATPASE-Plipid; 1.
R PROSITE; PS001054; ATPASE_E1_E2; 1.
R Hydrolase; Transmembrane; Phosphylation; Magnesium; ATP-binding; M Multigene family.
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EXTRACELLULAR (POTENTIAL)
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106
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107
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TRANSMEM
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Query Match
Best Local Similarity 72.7
Matches 8; Conservative 469 EEVVPRGGSVS 479 1 EEVVPXGXSYS 11 DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN DOMAIN MOD RES METAL SEQUENCE RANSMEM TRANSMEM OBRGB6; CARB_ FUSIN ठे 셤 Nograe T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,

Nograe T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,

Nomura N., Ohara O.;

RT Prediction of the coding sequences of unidentified human genes. IX.

RT The complete sequences of 100 new CDNA clones from brain which can

RT Code for large proteins in vitro.";

RD NA Res. 5:31-39 (1998).

RC -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.

C. -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -!- TISSUS EPECIFICITY: Widely expressed, with highest levels in kidney, followed by lung, brain, prostate, testls, ovary and compact to the strine.

CC -!- DISEASE: Defects in ATP10A are a cause of Angelman syndrome (AS)

(MIN:105830]; also known as 'happy puppet syndrome'. As is characterized by features of severe motor and intellectual catardation, microcephaly, ataxia, frequent jerky limb movements and flapping of the arms and hands, hypotonia, hyperactivity, hypotylementation, seizures, absence of speech, frequent smiling characterized by macroscomia, a large mandible and open-mouthed characterized by macroscomia, a large mandible and open-mou This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

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Gaps

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Score 36; DB 1; Length 1499; Pred. No. 13; 0; Mismatches 3; Indels

Q -> R (IN REF. 4). MW; D4996A4D0635A68D CRC64;

167687

POLY-GLU

POTENTIAL. CYTOPLASMIC (POTENTIAL). PHOSPHORYLATION (BY SIMILARITY). MAGNESIUM (BY SIMILARITY). MAGNESIUM (BY SIMILARITY).

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                                                                                                                                                                                                                                                                                                                    A TRAINMATCC 2586;

XR MEDLINE-21866394;

XR MEDLINE-21866394;

A MEDLINE-21866394;

A MEDLINE-21866394;

A MEDLINE-21866394;

A MAGRADA A., Bathen A., Gardner W., Grechkin G., Zhu L.,

RA Dattacharyya A., Bathen A., Gardner W., Grechkin G., Zhu L.,

RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

A Larsen N., D'Souzaa M., Walunas T., Pusch G., Haselkorn R.,

RA Donstein M., Kyrpides N., Overbeek R.,

"Genome sequence and analysis of the oral bacterium Fusobacterium

RT U. Deacteriol. 184:2005-2018(2002).

C. -! - CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +

Dhosphate + L-glutamate + carbamoyl phosphate.

C. -! - CATALYTIC ACTIVITY: 2 ATP + L-glutamine to constant (By similarity).

C. -! - PATHWAY: Arginine biosynthesis.

C. -! - PATHWAY: Arginine biosynthesis.

C. -! - CATALYTIC Composed of two chains; the small (or glutamine) chain

C. -! SUBUNIT: Composed of two chains; the small (or glutamine) chain

C. -! SUBUNIT: Composed of two chains; the small which is used by

C. -! - All arge (or ammonia) chain to synthesize carbamoyl phosphate (By
                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB ON ENVALS.
Pusobacterium nucleatum (subsp. nucleatum).
Bacteria, Pusobacteria; Fusobacteriaceee;
PRT; 1058 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fhe large (or ammonia) chain to synthes:
similarity).
-!- SIMILARITY: Belongs to the carB family.
STANDARD;
                                                                                                                                                                                                                                                      NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                   R HAMAP; MF 01210; -; 1.

R HAMAP; MF 01210; -; 1.

R INTEPIRO; 1PR00549; Caral Lglu.

R INTEPIRO; 1PR00549; CPase L D2.

R INTEPIRO; 1PR00549; CPase L D2.

R INTEPIRO; 1PR00549; CPase L D2.

R INTEPIRO; 1PR00549; CPase L D3.

R Pfam; PF02186; CPase L D3; 1.

R Pfam; PF02187; CPase L D3; 1.

R Pfam; PF02187; CPase L D3; 1.

R PRINTS; PR0099; CPSASE L D3; 1.

R PROSITE; PS00866; CPSASE 1; 2.

R PROSITE; PS00866; CPSASE 1; 2.

R Ardinine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; Ardinine biosynthesis; Pyrimidine Diosynthesis; Dyrimidine Diosynthesis; Dowain.

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ATP (POTENTIAL).

MANGARESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

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MEDILIPE-92188538; PubMed=1546458;

MEDILIPE-92188538; PubMed=1546458;

Morits B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

Morits B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

"The nucleotide sequence of the infectious cloned DNA component tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants.";

Virology 187:633-642(1992).
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Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBL_TaxID=31599;
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01-UUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
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or send an email to license@isb-sib.ch).
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STRAIN-VC-16/ DSW 4304 / ATCC 49558;
STRAIN-VC-16/ DSW 4304 / ATCC 49558;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Doddson R.J., Gwinn M., Hickey B.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkess E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Kirkess E.S., Reich C.I., Moheil L.K., Badger J.H., Glodek A., Zhou L.
Coverbeek R., Gocayne J.D., Weidman J.F., Mononald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
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                                                                                                                                                     BNDS, A42452; A42452.
InterPro; IPR002621; Gemini_mov.
Pfam; PF01708; Gemini_mov; I.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A40ECFIE0AF55B67 CRC64;
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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165 AA; 17588 MW; BBC17054810ADBF8 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein AF1949.
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                                                                                                                                EMBL; M81103; AAA47947.1; -.
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Best Local Similarity 60.0
Matches 6; Conservative
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028330;
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60 EESIPDGASY 69

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Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCHLULAR LOCATION: Nuclear.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Expressed at high levels in heart and pancreas, moderate levels in placenta, liver, skeletal muscle, and kidney, and low levels in brain and lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=99214318; PubMed=10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
Anovel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins ICP22 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after infection.";
J. Virol. 73:3810-3817(1999).
                                                                                                                                                         SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Schatthauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
GSRZ HUMAN STANDARD; PRT; 478 AA.
QSNZMS; QSBTC6; QSHAX6; QSNPP1; QSNPR4; QSUFI2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE OF 12-478 FROM N.A.
Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                            MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 218-477 FROM N.A.
                                                                                                                                                                                                                                                          Genomics 64:44-50(2000).
                                                                                             (Human)
                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
                                                                                                                                    NCBI_TaxID=9606
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                                                                                              Homo sapiens
                                                                                 GLTSCR2.
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A -> S (IN REF. 2; AAH04229).

A -> S (IN REF. 2; AAH04229).

D -> H (IN REF. 3).

PEGNILRDERKSFORRNMIEPRERAKFKRYKVKLVEKRAF

REIQ -> VLTVSCRGAPCPVMTPSLLPVPPRGYGRHHGCP

WAGPYGPMER (IN REF. 5).

EGNILRDERKSFORRNMIEPRERAKFKKYKVKLVEKRAFR

EIQL -> REQHSFETGSRAFRGGI (IN REF. 3).

7718923E348CB52B CRC64;
                                                                                                                                                                                                                                                                                                                                                                       /FIIGWAR 011486.
628 -> HEG (IN REF. 2; AAH04229).
G -> R HEG (IN REF. 3).
RRKEQIWEKLAKQGELPREVRRAQARLINPSATRAKPGPOD
RYERP -> SGRSEYGRSWPERASSPGGAQGPSPVAQPFCN
KGPNAPGHRIAA (IN REF. 3).
SDNPLIDRPLYGQDEFFIE -> INNPDKPVWPGCLPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-90259077; PubMed=2188136; MedinEs G., Wain-Hobson S.; MedinEs-9059077; MedinEs-90607; MedinEs R., Meyerhans A., Roelants G., Wain-Hobson S.; "Genetic organization of a chimpanzee lentivirus related to HIV-1."; Nature 345;136-139(1990).

-I- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
-I- STUGELLIARA LOCATION: Nuclear; accumulates in the nucleoli.
-I- PTM: Phosphoprotein whose state of phosphorylation is mediated by a specific serine kinase activity present in the nucleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 41, Last annotation update)
(Anti-repression transactivator protein) (ART/TRS).
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Viruses; Rētroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11723;
-!- SIMILARITY: Belongs to the GLTSCR2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AA
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GO; GO:0005622; C:intracellular; NAS.
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                                                                                                                                                     EMBL, AF182076, AAF62873.1, --
EMBL, BC004229, AAH04229.1; --
EMBL, BC010095, AAH10095.1, --
EMBL, AF296124, AAG30413.1, --
EMBL, AF296336; CAB94787.1, --
EMBL, AL122063; CAB59242.1, --
                                                                                                                                                                                                                                                                                                                                             Nuclear protein; Polymorphism.
VARIANT 389 389 R
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Genew; HGNC:4333; GLTSCR2.
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191
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417
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hes 6; Conserv
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417
433
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01-AUG-1990
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P17280;
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Sen K., Sikkema D.J., Murphy T.F.;
Isolation and characterization of the Haemophilus influenzae tolQ,
tolR, tolA and tolB genes.";
Gene 178:75-81 (1996)
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000625; REV_protein.
PEfam; PF00424; 1.
Transcription regulation; AIDS; Phosphorylation; Nuclear protein.
SEQUENCE 124 AA; 13701 MW; FS877DIBDF65A7B2 CRC64;
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Haemophilus influenzae.
Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 68.8%; Score 33; DB 1; Length 124; Best Local Similarity 60.0%; Pred. No. 4.6; Matches 6; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     744677; P94811;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                            EMBL, X52154, CAA36405.1; -. PIR, S09988, VKLJSI.
HIV, X52154; REV$CPZ.
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TOLB OR HI0382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=EN TON NIG961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Heidelberg J.F., Eisen J.A., Nelson W.C., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                           Periplasmic; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).
-1- CATALTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = -1- CATALTIC ACTIVITY: Carboxyvinyl)-3-phosphoshikimate.
-1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3-Phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
enolpyruvylshikimate-3-phosphate synthase) (EPSF synthase)
AROA OR VC1732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                            VGS -> ITH (IN STRAIN 1479).
A -> V (IN STRAIN 1479).
T -> H (IN STRAIN 1479).
A -> G (IN STRAIN 1479).
A -> G (IN STRAIN 1479).
A -> T (IN STRAIN 1479).
A -> T (IN STRAIN 1479).
A -> V (IN STRAIN 1479).
A -> V (IN STRAIN 1479).
A -> S (IN STRAIN 1479).
W, 0882201AEE925489 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            68.8%; Score 33; DB 1; Length 427; 60.0%; Pred. No. 17; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i-SUBRINIT; Monomer (By similarity).
-i-SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i-SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                     R -> H (IN STRAIN 1479)
V -> I (IN STRAIN 1479)
                                                                                                                                                                                        TOLB PROTEIN.
                                                                                                                                                                fransport; Protein Transport;
                                                                                                                                                                                                                                                                                                                                                                   44967 MW;
                                        EMBL; U32722; AAC22040.1; -.
EMBL; U32470; AAC44597.1; -.
PIR; F64064; F64064.
                                                                                                      TIGR; HI0382; -. HAMAE; M. 0671; -; 1. InterPro. PR 0671; -; 1. InterPro. PR04052; TolB_N. Pfam; PF04052; TolB_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 OVVPSGNGYS 112
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                                                                                                                                                                                                                                                                                                          237
322
326
326
328
427 AA;
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Best Local Similarity
                                                                                        HSSP; P19935; 1CRZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholerae.
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                              SIGNAL
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AROA VIBCH
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or send an email to license@isb-sib.ch).
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"Studies of UV-inducible promoters from Clostridium perfringens in vivo and in vitro.";
Mol. Microbiol. 2:607-614 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garnier T., Cole S.T.; "Complete nucleotide sequence and genetic organization of the bacteriocinogenic plasmid, pIP404, from Clostridium perfringens."; Plasmid 19:134-150(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CPN50;
MEDLINE=87057020; PubMed=2877971;
Garnier T., Cole S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium "Characterization of a perfringens and molecular genetic analysis of the
                                                                                                                                          TIGR; VC1721; --
HAMAP; MF 00210; -; 1.
HAMAP; MF 00210; -; 1.
HAMAP; MF 00210; -; 1.

HAMAP; MF 00210; -; 1.

PROSTO; PRO01986; BPSP synth.

ProDom; PD010867; EPSP synthase; 1.

PROSTIE; PS0104; EPSP SYNTHASE 1; 1.

PROSTIE; PS001885; EPSP SYNTHASE 1; 1.

PROSTIE; PS00885; EPSP SYNTHASE 1; 1.

Aromatic amino acid bioSynthesis; 7; 1.

Aromatic amino acid bioSynthesis; 7; 1.

SROUGNCE 426 AA; 46101 MW; 38852D6483BFEIC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium perfringens.
Plasmid pIP404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                       66.7%; Score 32; DB 1; Length 426; 60.0%; Pred. No. 27; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Microbiol. 2:607-614(1988).
-!- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
-!- INDUCTION: By UV irradiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacteriocin-encoding gene.";
J. Bacteriol. 168:1189-1196(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89039249; PubMed=2460717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CPN50;
MEDLINE=88336297; PubMed=2901768;
                                                                                                              EMBL; AE004251; AAF94882.1; -. PIR; D82163; D82163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                              223 EFVIPAGOSY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 06, C
(Rel. 06, I
(Rel. 30, I
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                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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01-JAN-1988
01-OCT-1994
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Matches
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STRUCTURE BY NAR OF 2087-2142.

**REDLINE=92232684; PubMed=1567844;

**REDLINE=92232684; PubMed=1567844;

**REDLINE=92232684; PubMed=1567844;

**REDLINE** U.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,

**Archenborn A.M.;

**Thigh-resolution solution structure of the double Cys2His2 zinc

**In ADDITON; WHIS PROCUENTS SUCH AS THOSE OF SV40, CMV, OR HINT.

**Thigh-resolution structure of the double Cys2His2 zinc

**Thigh-resolution structure of the double Cys2His2 zinc

**Thigh-resolution structure of the double Cys2His2

**Thigh-resolution structure

**Thigh-reso
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-binding protein 1) (HIV-EP) (Major histocompatibility complex binding protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Biochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fan C.M., Maniatis T.; "A DNA-binding two widely separated zinc finger "A DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence."; Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PRDII-BFI).
HIVEPI OR ZNR40.
HOMO Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%; Score 32; DB 1; Length 890; 66.7%; Pred. No. 59;
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STRUCTURE BY NMR OF 2113-2142.
MEDLINE-91064333; PubMed-2248949;
MEDLINE-81064333; Clore G.M., Appella E., Sakaguchi K.,
Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96699 MW; F4E5E8971C31C6C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             HYDROPHOBIC.
                                                                                                                                                                                                          EMBL; M14481; AAA98248.1; -.
EMBL; M32882; AAA98249.1; -.
PIR; A30481; A30481.
InterPro; IPR000834; Peptidase_M14.
InterPro; IPR003646; SH3_bac.
Pfam; PF00346; Zn carbOpept; 1.
SMART; SM00287; SH3b; 3.
Antibiotic; Bacteriocin; Plasmid.
DOMAIN
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SEQUENCE FROM N.A.
MEDLINE=90169514; PubMed=2106471;
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 EVVPGGFTY 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 890 AA;
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                           MEDLINE=91260454; PubMed=1710759; Jee S.J., Romana L.K., Reeves P.R.; Jiang X.-M., Neal B., Santiago F., Lee S.J., Romana L.K., Reeves P.R.; Structure and sequence of the rfb (O antigen) gene cluster of Salmonella serovar typhimurium (strain LT2)."; Mol. Microbiol. 5:695-713(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.6%; Score 31; DB 1; Length 319;
85.7%; Pred. No. 34;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002704; Peptidase_C7.
Pfam; PF01830; Peptidase_C7; 1.
Probom; PD040949; Peptidase_C7; 1.
Hypothetical protein; Hydrolase; Thiol protease.
Rypothetical protein; Hydrolase; Thiol protease.
                                                                                                                                                                        in the cytoplasm.
-!- SIMILARITY: Belongs to peptidase family C7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
dTDP-Glucose 4,6-dehydratase (EC 4.2.1.46).
Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                  EMBL; X14524; CAA32666.1; -. PIR; S03833; S03833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 EEVVPAG.37
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MEROPS; C07.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 31
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P26391;
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RFBB_SALTY
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                                                                                                                                                                                                                                                              Gaps
SUBCELLULAR LOCATION: Nuclear.
INDUCTION: BY mitogens and phorbol ester.
DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-JUL-1989 (Rel. 11, Last sequence update)
Hypotherical protein 1 in hypovirulence-associated ds-RNA genetic element [Contains: P29 proteinase].
Cryphonectria parasitica (Chesnut blight fungus) (Endothia parasitica).
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes; Sordariomycetidae; Diaporthales, Valeaceae;
Cryphonectria-Endothia complex; Cryphonectria.
[1]
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2109 CZH2-TYPE.
2109 CZH2-TYPE.
806 POLY-SER.
2088 POLY-SER.
2095 2005
2108 2108
2108
2116
2124
2125
AA, 297217 MW, D45D3CA951FEA561 CRC64;
                                                             ZINC-FINGER IN-BETWEEN.
                                                                                                                                                                                                                                      EMBL; X51435; CAA35798.1; -.
PIR; A34203; A34203.
PDB; 3ZNF; 15-JAN-92.
PDB; 4ZNF; 15-JAN-92.
PDB; 1BBO; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ilarity 66.7%;
Conservative
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2127 213
2717 AA;
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Best Local Similarity
''^a 6; Conserv?
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AC THO THAI_CRYPA

AC 01-JUL-1989

DT 01-JUL-1989

DT 01-JUL-1989

DT 16-OCT-2001

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RESULT 11

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Gaps

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EMBL; U40630; AAA83215.1; -. HSSP; P04968; 1TDJ.
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its moch non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                               -i- PATHWAY: DTDP-L-RHAMMOSE BIOSYNTHESIS WITHIN THE O ANTIGEN
BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.
-i- SIMILARITY: BELONGY TO THE SUGAR EPIMERASE FAMILY. DTDP-GLUCOSE DEHYDRATASE SUBPAMILY.
CATALYTIC ACTIVITY: dIDP-glucose = dIDP-4-dehydro-6-deoxy-D-glucose + H(2)O.
COFACTOR: NAD.
                                                                                                                                                                                                                                                                          Pfam, PF01370; Epimerafe; 1.
TIGRPAMS; TIGR01181; dTDP gluc dehyt; 1.
Lipopolysaccharide biosynthesis; Lyase; NAD; Complete proteome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 4). Last annotation update)
Threonine dehydratase blosynthetic (EC 4.3.1.19) (Threonine
                                                                                                                                                                                                                                                                                                                                                    Length 361;
                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                     NP_BIND 7 13 NAD (POTENTIAL).
SEQUENCE 361 AA; 40718 MW; 3A574B4D917EBC57 CRC64;
                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 1;
Pred. No. 38;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burkholderia cepacia (Pseudomonas cepacia)
                                                                                                                                                                        EMBL; X56793; CAA40115.1; -.
EMBL; AE00872; AAL21001.1; -.
PTR; S12299; S12299.
PDB; IGTA; 21-MAR-01.
PDB; IKEU; 25-JAN-02.
STYGENE; SGJ0345; FEB.
INTERPRO; IPRO05888; dTDP_gluc_debyt.
INTERPRO; IPRO05888; dTDP_gluc_debyt.
                                                                                                                                                                                                                                                                                                                                                       64.6%;
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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278 DEIVPKATSY 287
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                                                                                                                                                                                                                                                                                                              -structure.
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P53607;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NBM316 / Serotype III;
MEDLINE=2224508; PubMed=1234221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek I., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence and comparative genomic analysis of an emerging human parthogen, serving V Streptococcus agalactiae.";
Proc. Natl. Acad. Sci. U.S. A. 99:12391-12396(2002).
-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP + diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCRILUTAR LOCATION: Cytoplasmic.
-!- SUMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                          SYL_STRA3 STANDARD; PRT; 833 AA.

98E3V2; 9BEXO2;
10-6CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of Streptococcus agalactiae, a pathogen causing
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                                                                                                                   64.6%; Score 31; DB 1; Length 829; 66.7%; Pred. No. 91;
                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus agalactiae (serotype III), and
Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                 51 "HIGH" REGION.
613 "KMSKS" REGION.
612 ATP (BY SIMILARITY).
93791 MW; POFOA43014F6C389 CRC64;
                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invasive neonatal disease.";
dol. Microbiol. 45:1499-1513(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=2603 V/R / Serotype V;
MEDLINE=22222988; PubMed=12200547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICBI_TaxID=216495, 216466;
                                                                                             Query Match
Best Local Similarity 60...
6; Conservative
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168 EEVLPDGTS 176
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TIGR, SAG2057; -.
HAMAP, MF_00049; -; 1.
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                                                         612 6
829 AA;
Complete proteome.
SITE 40
SITE 609
BINDING 612
SEQUENCE 829 AA;
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InterPro; IRRO0300; IRRA-synt 1a.
InterPro; IRRO0120; IRRA-synt 1a.
InterPro; IRRO0120; IRRA-synt 1a.
InterPro; IRRO0120; IRRA-synt 1.
Pram; Pr00133; IRRA-synt 1; 1.
PRINTS; PR00138; IRRA-SYNTHLEU.
TICRRAMS; TICRO0396; ISRS Bact; 1.
PROSITE; PS00178; AA TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; AIP-binding; Complete proteome.
41 52 "HIGH" PROTOM
                                                                                                                                                                                                           Gaps
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0
                                                                                                                                                                              Score 31; DB 1; Length 833;
Pred. No. 91;
1; Mismatches 2; Indels
                                                                                                                     "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
; 2C6F281AE3D3A896 CRC64;
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614 "K
613 AT
93966 MW;
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169 EEVLPDGTS 177
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Q8XXX3 Clostridium Q84031 bos taurus 000404 bomo sapien Q867a5 tragulus ja Q867a5 tragulus ja Q867a5 tragulus sapien Q7vgyo helicobacte Q7vxx8 cryptospori Q87xB brachydanio Q7vxx8 cryptospori Q81850 arabidopsis Q8445 bifldobacte Q8839 encephalito Q88415 bifldobacte Q8839 encephalito Q88415 bifldobacte Q8839 encephalito Q89415 bifldobacte Q8839 encephalito Q89415 bifldobus Q89415 bifldobus Q89415 bifldobus Q89415 bifldobus Q89415 billolos Q8415 bifldobus Q89415 billolos Q8416 bocillus an Q81440 bacillus an Q84410 bacillus an Q84410 bacillus an Q88400 clostridium Q88400 clostridium Q88400 clostridium Q8966c rhizobium m
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bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.1%; Score 37; DB 11; Length 471; 60.0%; Pred. No. 14; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Strausberg R.; Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases. Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases. MGD; MGI:2154441; Gltscr2. MGD; MGI:2154441; Gltscr2. Hypothetical protein. SEQÜÜENCE 471 AA; 54506 MW; EODA685C374A9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Bypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
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                                      Q81031
Q81031
Q867A5
Q81X7A
Q7VGYO
Q7VTH8
Q7XXX8
Q8C1D7
Q8C1D7
Q9SF93
Q868F93
Q868F93
                                                                                                                                                                                                                                                                                                     Q7V6Q4
Q81JQ6
Q814N0
Q96MU1
Q898D0
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Q8EFM1
Q889X7
Q9Y855
Q971S2
              Q81033
Q8XHX3
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                          PRELIMINARY;
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TISSUE-Liver;
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Matches 6; Conserv
Q8VD18 P Q8VD18; 01-MAR-2002 (
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Q8R126
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                                                                                                           (without alignments)
116.206 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                            June 3, 2004, 11:35:06 ; Search time 29.8667 Seconds
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Maximum Match 100%
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QBVD18
QBBX34
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QBDIH0
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Q40129
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sp_phage:*
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Gapop 10.0 , Gapext 0.5
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sp_human:*
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1: Bp_archea:*
2: Bp_bacteria:*
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faximum DB seq length: 200000000
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48
1 BEVVPXGXSYS 11
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SEQUENCE FROM N.A.
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SETALN=C57BL/60; TISSUE=Pituitary;
MEDLINE=2235460; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I annotation of
% Analyse of the mouse transcriptome based on functional annotation of
60,770 full-length oDNAs.";
Nature 420:563-573(2002).
BABL: AK077941; BAC360(1; -...
MGD; MGI:2154441; GLescr2.
SEQUENCE 484 AA; 55792 MW; EB67949BCBE92D44 CRC64;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                Score 37; DB 11; Length 484;
Pred. No. 14;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechococcus elongatus (Thermosynechococcus elongatus) Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 9:123-130(2002).

BMBL, AP005374; BAC09170.1.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR001036; Actansport; IEA.
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Pfam; PF00873; ACR tran; 1.
PRINTS; PR00702; ACRIFLAVINRP.
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Best Local 6; Conservative
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Matches 7; Conservative
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843 EEVLPNGIGYS 853
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                                                                                                                                                                                                                                                                                                                                                                                                              2 EVVPXGXSYS 11
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SEQUENCE 1044 A
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074056
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RX MEDLINE=2234683; PubMed=12466851;
RA The FANTOM Consortium,
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RA The FANTOM Consortium,
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RA The RIKEN Genome Exploration of STR 60,770 full-length consortium,
RT 60,770 full-length consortium,
RT 770 full-length consortium,
RT 80,770 full-length consortium,
RT 80,770 full-length consortium,
RT 80,770 full-length Genome Exploration of
RT 80,553-573 (2002).
RE MAD; ASSUG 61:2154441; Gltscr2.
DR 800, MG:2154441; Gltscr2.
DR 800, MG:2154441; Gltscr2.
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                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                         Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.1%; Score 37; DB 11; Length 484; 60.0%; Pred. No. 14; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                             77.1%; Score 37; DB 11; Length 484; 60.0%; Pred. No. 14; 2; Indels ative 2; Mismatches 2; Indels
             01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Samilar to glioma tumor suppressor candidate region gene 2.
GLTSCR2 OR AMS3641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBBK35;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 24, Last sequence update)
01-UNR-2003 (TrEMBLrel. 24, Last amoctation update)
01-UNR-2003 (TrEMBLrel. 24, Last amoctation update)
Similar to gliona tumor suppressor CANDIDATE region gene
                                                                                                                                                                                                                       Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC01767, AAH17637.1; -.
MGD; MGI:2154441; Gltscr2.
                                                                                                                                                                                                                                                                                                       484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 AA
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                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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239 EVIPAGASYN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 EVIPAGASYN 248
                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EVVPXGXSYS 11
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Best Local Similarity
Matches 6; Conserv
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protein. GLISCR2.

CORRECTION

Q8BK35

Q8BK35

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Gaps

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Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Rapatral V., Bhatracharyya A., Reznik G., Mikhailova N., Lapidus A.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Bhrlich S.D.,
Overbeek R., Kyrpides N.;
Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35, DB 16; Length 344;
Pred. No. 28;
1; Mismatches 3; Indels
   Indels
                                                                                                                                                                                                                                                                                Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C55268ACB7225995 CRC64;
                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter substrate-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
   5
                                                                                                                                                             344 AA
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   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 423:87-91(2003).
EMBL; AE017015; AAP12123.1; -.
InterPro; IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
                                                                                                                                                           PRT;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD005232; UPF0047; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0.
Best Local 6; Conservative
   6; Conservative
                                                                                                                                                             PRELIMINARY;
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                                                          :|||| | :|:
32 DEVVPNGKTYA 42
                                     1 REVVPXGXSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGXSY 10
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SEQUENCE 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanopyrus.
NCBI_TaxID=2320;
                                                                                                                                                             Q815A7
Q815A7;
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   Matches
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Q8TX62
                                                                                                                           RESULT 8
Q815A7
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                                                                                                                                                                                                                  "Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";
J. Bacteriol. 180.5003-5009(1998).
EMBL: AF083072, AAC62699.1;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005021; F:transporter activity; IEA.
InterPro; IPR000515; BPD_transp.
InterPro; IPR000515; BPD_transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enkaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                       Archaea; Crenarchaeota; Thermoprotei; Cenarchaeales; Cenarchaeaceae; Cenarchaeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=VESG. From "N. S. STRAIN=VESG. From "N. STRAIN=VESG. From "N. S. S. S. Gasser C.S."

MEDLINE=95375233; PubMed=7647301;

MEDLINE=95375233; PubMed=7647301;

MIlligan S.B., Gasser C.S.

Invalue and regulation of pistil-expressed genes in tomato.";

Plant Mol. Biol. 28:691-711(1995).

R EMBL, U20592; ARA80497.1; -..

R EMBL, U20592; ARA80497.1; -..

R OC; GO:0004866; F:endopeptidase inhibitor activity; IEA.

R PROSTER: STRO197; Kunitz_legume.

R PRIMYS; PRO0291; Kunitz_legume; 1.

R PRIMYS; PRO0291; Kunitz_legume; 1.

R SWART; SMO0452; STI; 1.

R PROSTER: PS00283; SOYBEAN_KUNITZ; 1.

HYPOCHELICAL DEOCENIS SIGNAL.

T SIGNAL.

T SIGNAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 1; Length 3472;
Pred. No. 2.1e+02;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           SWART; SM00320; WD40; 2.
PROSTITE, PS00402; BPD_TRANSP_INN_MEMBR; 1.
Hypothetical protein.
SEQUENCE 3472 Aa; 367058 MW; 37P80707030F9355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 UNKNUWW.
25188 MW; 1074C261D20CFDAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein precursor.
Lycopersicon esculentum (Tomato).
01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.9%; Score 35; DB 10; 54.5%; Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                              MEDLINE=98422450; PubMed=9748430;
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ilarity 54.5%;
Conservative
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2294 EDVIPRGISFS 2304
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                                                        Cenarchaeum symbiosum.
                                     Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
6; Conserv?
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Best Local Similarity
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                                                                                                          NCBI_TaxID=46770;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases 
EMBL; BC014009; AAH14009.1; -.
EMBL; BC007248; AAH07248.1; -.
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Query Match
Beet Local Similarity 60.00,
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SEQUENCE 541 AA; 60645
                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7:331-338(2000).
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                      240 EVAPAGASYN 249
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                                                                                                                                                       2 EVVPXGXSYS 11
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                                                                                                                                                                                                                                                                                   Q98BP5;
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Q9E1X6
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     TREFS
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Bukaryota; Viridiplantae; Streptophyra; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyra; Embryophyta; Tracheophyta;

Beprantophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids I; Ragales; Betulaceae; Betula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0008843; F:endochitinase activity; IEA.
GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR0012579; Glyco_hydro_18.
Pfon; PF00704; Glyco_hydro_18; I.
PROSITE; PS01095; CHITINASE_18; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillovaara-Teijo M., Korhonen M.S., Palva T.E., Kangaejarvi J.; Submitred (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ279692; CAB66334.1; -- HSSP; P23472; 2HVM.
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99CSO, Q96TT;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 22, Last annotation update)
Glioma tumor suppressor candidate region gene 2 (Fragment).
Homo sapiens (Hunan).
                                                                                           70.8%; Score 34; DB 17; Length 143; 60.0%; Pred. No. 18; arive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.8%; Score 34; DB 10; Length 174; 77.8%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                             143 AA; 15734 MW; 4C8B28A1FBBEDD0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Acidic endochithnase (EC 3.2.1.14) (Fragment)
                                                                                                                                                                                                                                                                  174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
TIGRFAMS; TIGRO0149; TIGRO0149; 1.
PROSITE; PSO1314; UPP0047; 1.
Complete proteome.
SEQUENCE 143 AA; 15734 MW; 4C8
                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 70.8
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                         1 EEVVPXGXSY 10
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75 EELVPQGAGY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Lung, and Skin;
Strausberg R.;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                  Q9M3T4;
Q9M3T4;
01-OCT-2000
01-OCT-2000
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AC 096CS
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RC SECTION
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MEDLINE=21082930; PubMed=11214968;
Raneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Kaneko T., Indemura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
McOmplete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                    70.8%; Score 34; DB 4; Length 479; 60.0%; Pred. No. 67; 1; Mismatches 3; Indels
NON TER 1 1 SEQUENCE 479 AA; 54529 MW; 0A6C3A8B476F7E8F CRC64;
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EMBL, PRO03006; BABES 927.1; -
GO; GO:0005524; F:ATP binding; IEA activity; IEA.
GO; GO:000510; F:DNA ligase (ArP) activity; IEA.
GO; GO:0006310; P:DNA recombination; IEA.
GO; GO:0006281; P:DNA repair; IEA.
GO; GO:0006261; P:DNA replication; IEA.
InterPro; IPR000977; DNA ligase.
Pfam; PF0166; DNA ligase.
Pfam; PF0166; DNA ligase A C; I.
PROSITE; PS0166; DNA LIGASE A1; I.
PROSITE; PS0166; DNA LIGASE A1; I.
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Probable DNA ligase.
MLL5481.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Ceroopithecine herpesvirus 7.
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Search completed: June 3, 2004, 11:57:34
Job time: 30.8667 secs
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Matches
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QBEWD4
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SUCHANCE FROM N.A.

MEDINE=20020109; PubMed=11756688;

DelVecchio V.G., Kapatral J., Redkar R.J., Patra G., Mujer C., Los T.,

La ruanova N., Anderson I., Bhattacharvya A., Lykidis A., Reznik G.,

Ly ruanova N., Anderson I., Bhattacharvya A., Lykidis A., Reznik G.,

Ablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Golteman B.,

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N., Overbeek R.;

The genome sequence of the facultative intracellular pathogen

Brucella melitensis."; U.S.A. 99:443-448(2002).

Embl. Abroson Sequence of the facultative intracellular pathogen

Brucella melitensis."; I.S.A. 99:443-448(2002).

Embl. Abroson Sequence of the facultative intracellular pathogen

Co. Golo005524; F.AIF binding; IEA.

GO; GO:0005247; F.AIF bending; IEA.

GO; GO:0008470; Araff bending; IEA.

GO; GO:0008470; Araff bending; IEA.

GO; GO:000840; F.AIF binding; IEA.

GO; GO:000840; F.AIF binding; IEA.

GO; GO:000840; F.AIF bending: IEA.

RICEPPO: IPRO01410; DEAD.

RICEPPO: IPRO0140; DEAD.

RICEPPO: IPRO0140; HEILC:-1.

RWART; SMO0490; HEILC:-1.

RWART; SMO0490; HEILC:-1.

RWART; SMO0490; HEILC:-1.

RWART; GO:000840; ALDEHVDE_DEHVDR_GLU; 1.
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                                                                                                                                                                          SEQUENCE FROM N.A.

Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;

"Complete Sequence of the Simian Varicella Virus Genome.";

Submitted (WAR-2001) to the BMEL/GenBank/DDBU databases.

EMBL; AF275348; AAG27217.1; --

GO; GO:00091012; P:DNA packaging; IEA.

InterPro; IPR007640; Herpes_Ull7.

Fam; PP04559; Herpes_Ull7; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brucella melitensis.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
7021_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 70.8%; Score 34; DB 12; Length 678; Best Local Similarity 50.0%; Pred. No. 98; Matches 5; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 678 AA; 75850 MW; A17809E30512FE3C CRC64;
Viruses, dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=35245;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
BMEI0275.
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Q8YJ11;
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X MEDLINE=22354719; PubMed=12466555;

X ASBARY Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., A Sasaki Y., Ishikawa J., Yamashita A., Oshimo C., Horino A., Shiba T., Sasaki T., Hattori M.;

XT "The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";

XI "Indeale Acids Res. 30:5293-530(2002).

BR InterPro: IPR008985; Cond. like_lec_gl.

DR InterPro: IPR008985; Cond. like_lec_gl.

DR InterPro: IPR008985; Cippproctain_17.

DR Pfam; PF04200; Lippproctain_17; 3.

KW Complete proteome.

SEQUENCE 1123 AA; 123636 MW; A4D707330E3DB4AC CRC64;
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                                                                                                                                                                              Mycoplasma penetrans.
Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBL_TaxID=28227;
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QBEWD4
QBEWD4;
QBEWD4;
Q1-MAR-2003 (TrEWBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
MYPB 250 paralog, 57%.
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hes 7; Conservative
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Abb80536 Hepatitis
Abb80542 Hepatitis
Abb80543 Hepatitis
Abb80543 Hepatitis
Abb80563 Hepatitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carbonyl forming keto-amide linkage with
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virucide.
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residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                ABB80546 standard; peptide; 11
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WO200208251-A2
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Modified-site
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                                                                                             3, 2004, 11:31:01; Search time 45.9333 Seconds (without alignments) 67.664 Million cell updates/sec
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                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                otal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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ABB80527
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ABB80556
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Gapop 10.0 , Gapext 0.5
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11: geneseqp1990s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
6: geneseqp2003s:*
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length: 2000000000
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52
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Match
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                                                                                                                                                                     erfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #34.
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0
                                                                                                                                  Score 49; DB 5; Length 11;
Pred. No. 0.0045;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  ABB80554 standard; peptide; 11 AA.
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                                                                                                                                  94.2%;
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                                                                                                                             Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                 1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                              1 EEVVPXGTHYS 11
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                                                                                            Sequence 11 AA;
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activity usefu
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #30.
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Pred. No. 0.0045;
0; Mismatches 1; Indels
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                                                                                   ABB80550 standard; peptide; 11 AA.
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1 REVVPXGXHYS
                       1 EEVVPXGSHYS
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RESULT 4

Score 49; DB 5; Length 11; Pred. No. 0.0045;

94.2%;

Query Match Best Local Similarity

Sequence 11 AA;

"Norvalyl carbonyl forming keto-amide linkage with 7"

residue

Misc-difference

Modified-site

'note=

/note= "C-terminal amide" 'note= "D-form residue"

WO200208251-A2

31-JAN-2002

'note= "N-terminal acetyl"

Location/Qualifiers

Key Modified-site

Synthetic

virucide

Modified-site

Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;

C virus NS3/NS4a serine protease inhibitor peptide

Hepatitis

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'note= "Norvaly1 carbony1 forming keto-amide linkage with
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                                                                                                                                                                                                                    Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide compound having hepatitis C virus protease inhibitory
lty useful for treating disorders associated with hepatitis C
                                                                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #35.
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Pred. No. 0.0045;
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/note= "C-terminal amide"
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                         standard; peptide; 11
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nilarity 90.9%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  residue 7"
                                                                                                                     (first entry
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Best Local Similarity
Matches 10; Conserv
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ABB80555
ID ABB80555
                                                                       ABB80555;
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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus

Claim 17; Page 64; 69pp; English.

protease.

Brunck TK;

(CORV-) CORVAS INT INC Lim-Wilby M, Levy OE, WPI; 2002-361643/39.

19-JUL-2001; 2001WO-US023169. 21-JUL-2000; 2000US-0220101P.

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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treat disorders associated with hepatities C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38.
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Matches 10; Conserv
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ABB80523 standard; peptide; 11 AA.

RESULT 5

1 EEVVPXGXHYS 11

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EEVVPXGSHYS

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(first entry)

08-OCT-2002

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                       /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17.
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                                                                                                                                                                                                                                                                                                                                          ; DB 5; Length.
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Pred. No. 0.007
0; Mismatches
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                 'note= "N-terminal acetyl"
                                                                          'note= "C-terminal amide"
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                                                          'note= "Oxymethionine"
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cocation/Qualifiers
                                                                                                                                                                              Brunck TK;
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                                                                                                                                           21-JUL-2000; 2000US-0220101P
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Best Local Similarity
Matches 10; Conserv
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ABB80537
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have viruside activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                            ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
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/note= "C-terminal amide"
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Best Local Similarity 90.9
Matches 10, Conservative
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                                                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Norvalyl carbonyl forming keto-amide linkage with
                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
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                                                                                                                                                                                                                                                                                92.3%; Score 48; DB 5; Length 11; 90.9%; Pred. No. 0.0072; ive 0; Mismatches 1; Indels
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           Brunck TK;
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                                                                                                                   Claim 17; Page 64; 69pp; English
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           Lim-Wilby M, Levy OE,
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                                      WPI; 2002-361643/39.
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/note= "Norvaly1 carbony1 forming keto-amide linkage with
pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus
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Pred. No. 0.0072;
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                                                                             92.3%;
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                                                 Sequence 11 AA;
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Modified-Bite
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Matches
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                                            The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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Pred. No.
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                     Claim 17; Page 65; 69pp; English.
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Conservative C
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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                  carbonyl forming keto-amide linkage with
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                                                                                                                                                          Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28.
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                                                                                                                                                                                                                                                                                                                           /note= "C-terminal amide"
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Pred. No. (
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                                                                                                                                                                                                                                                               /note= "Norvalyl
residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 65; 69pp; English
                                                                  ABB80548 standard, peptide, 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brunck
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nilarity 81.8%;
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1 EEVVPXGGHYS 11
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                                                                                                                                                                                                                                                                                                       "Norvalyl carbonyl forming keto-amide linkage with 7."
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                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #29.
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                                                  WO200208251-A2
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    Synthetic.
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"

/note= "C-terminal amide"

note= "N-terminal acetyl"

Location/Qualifiers

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
Lim-Wilby M, Levy OE, Brunck TK;
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Query Match
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Best Local Similarity 81.8%; Pred. No. 0.29;
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Sequence 4794, Ap
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Sequence 3, Appli
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                                                                                                June 3, 2004, 11:36:47; Search time 11.7333 Seconds (without alignments) 48.399 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 4794, Application US/09134001C

| Sequence 4794, Application US/09134001C
| Patent No. 6380370
| Patent No. 6380370
| GRNERAL INFORMATION:
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
| TITLE OF INVENTION: NUMBER: US/09/134,001C
| TITLE OF INVENTION: NUMBER: US/09/134,001C
| CURRENT FILING DATE: 1998-08-13
| PRIOR APPLICATION NUMBER: US 60/064,964
| PRIOR PILING DATE: 1997-08-14
| NUMBER OF SEQ ID NOS: 5674
| SEQ ID NO 4794
| LENGTH: 1037
| TYPE: PRI
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1 Sequence 21444, Application US/09252991A

2 Sequence 21444, Application US/09252991A

2 Sequence 21444, Application US/09252991A

3 Patent No. 6551795

3 TITLE OF INVENTION:

3 TITLE OF INVENTION:

4 TITLE OF INVENTION:

5 TITLE OF INVENTION:

6 TITLE OF INVENTION:

7 TITLE OF INVENTION:

8 TITLE OF INVENTION:

9 TILE REFERENCE: 107196.136

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                                      Sequence 9, Appli
Sequence 11, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 19, Appli
Sequence 32960, Ap
Sequence 41885, Ap
Sequence 7284, Ap
Sequence 15, Appl
Sequence 15, Appli
Sequence 6065, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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Pred. No. 18;
0; Mismatches 3; Indels
US-08-484-101B-7
US-08-484-101B-9
US-08-484-101B-11
US-08-714-524D-3
US-08-714-524D-7
US-08-714-524D-7
US-08-714-524D-7
US-08-714-524D-11
US-08-714-524D-11
US-09-134-001C-3950
US-09-134-001C-4185
US-09-134-001C-4185
US-09-134-001C-4185
US-09-134-001C-4185
US-09-134-001C-4185
US-09-134-048-05-7
US-09-1489-039A-8065
US-09-342-647-4
US-08-459-165-2
US-08-459-165-2
US-08-459-165-2
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.1%;
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GENERAL INPORMATION:

APPLICANT:
APPLICANT:
MATC J. RUBEnfield et al.
APPLICANT:
MATC J. RUBEnfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26615
LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                    0; Gaps
                                                                          Query Match 69.2%; Score 36; DB 4; Length 1037; Best Local Similarity 63.6%; Pred. No. 56; Matches 7; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 4; Length 277;
Pred. No. 21;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08879995A

Patent No. 598606

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hallman, Jennifer L.
APPLICANT: Hallman, Jennifer L.
APPLICANT: Matchew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Involve Pharmaceuticals, Inc.
STREET: 3174 Forter Drive
CITY: Palo Alco
STARE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER: EMACABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: LAPLICATION NUMBER: US/08/879,995A
FILING DATE: Herewith
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
RELING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                             3-09-252-991A-26615
Sequence 26615, Application US/09252991A
Patent No. 6551795
, ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.3%;
Best Local Similarity 63.6%;
Matches 7; Conservative (
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                                                                                                                                                                                                                                                 199 KEVVSNGLHYS 209
                                                                                                                                                                                          1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 EETVPGGGHTS 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
CITY: Palo Alto
COUNTRY: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 34304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastsEG for Windows Version 2.0
STREAT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0326 US
                                           PF-0326 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECHONNICATION INFORMATION:
TELECHONE: 415-85-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09215096
Patent No. 6008194
GENERAL INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION UNDRER: 36,749
REFERENCE/DOCKET NUMBER: PF-03
RELECOMMUNICATION INFORMATION:
TELERHONE: 415-855-0555
TELERAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                       ...crowody: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 163590
US-08-879-995A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
IMMEDIATE SOURCE:
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Sequence 182, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
TITLE OF INTENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSES: Human Genome Sciences, Inc.
TITLE OF INTENTION: About Avenue
STREET: 9410 KW West Avenue
STREET: Maryland
CITY: ROCKVILLe
STREE: Maryland
CITY: ROCKVILLE
STREE: MACKVILLE
STREE: MACKVILLE
STREE: MACKVILLE
COMPUTER: HP Vectra 486/33
COMPUTER: MACH SYSTEM:
MACHORITION NUMBER: US/08/961,083
FILING DATE:
REPERACE/DOCKET NUMBER: PB340P2
TELEOWANTICATION NUMBER: PB340P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 3; Length 447;
Pred. No. 89; 2; Indels
1; Mismatches 2; Indels
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62.5%;
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Matches 5; Conservative
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MOLECULE TYPE: protein
US-08-961-083-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 IVPHGGHY 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-09-107-532A-6771
Sequence 6771, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
CORRESPONDENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                   Score 34; DB 3; Length 126;
Pred. No. 14;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIF: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature;
;
; LOCATION: (B) LOCATION 1...63
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 6771:
JS-09-107-532A-6771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
                                                                                                                                65.4%;
                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                           1 EEVVPXGXH 9
                                                       5-09-215-096-3
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Squence 182, Application US/09536784
Squence 182, Application US/09536784
Squence 182, Application US/09536784
Squence 182, Application US/09536784
GENERAL INFORMATION:
APPLICANT: Choi et al.
APPLICANT: Choi et al.
APPLICANT: Choi et al.
APPLICANT: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADRESS:
ADDRESSES: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/09/536,784
FILING DATE: 30-Oct-1997
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RESULT 7 US-08-961-083-182

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Gaps

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GENERAL INFORMATION:
APPLICANT: Rey, Michael
APPLICANT: Rey, Michael
APPLICANT: Rey, Michael
APPLICANT: Golightly, Bilzabeth
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
TITLE OF INVENTION: HAVING TRIPEPTIDE AMINOPEPTIDASE
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSES: ADDRESSES:
ADDRESSES: ADDRESSES: ADDRESSES: CONTRESSES: ADDRESSES: ADDRESSE
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 58211040 No. 5821104disk of No. 5821104th America, Inc. STREET: 405 Lexington Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 600;
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Pred. No. 1.2e+02;
Pred. 2; Indels
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APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 475
ATTORNEY/ACTION:
                                                                                                          SIRELY: 405 LEXINGUM AVENUE
CITY: New York
COUNTY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASESEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
FILING DATE: JS-ARR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGESTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 31,728
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELESPAN: 212-878-9555
TELEBRAX: 212-878-9555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08821118
Patent No. 5989889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INPORMATION POR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 600 amino acide TYPE: amino acid STRANDEDNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein ; FRAGMENT TYPE: internal US-08-821-119-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VPXGXHYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-821-118-2
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| Sequence 6, Application US/09468656A
| Sequence 6, Application US/09468656A
| Sequence 6, Application US/09468656A
| GENERAL INFORMATION:
| APPLICANT: Adamou, John E. |
| TITLE OF INVENTION: Procumoniae Group A and B Having Selected Structural TITLE OF INVENTION: Motifs |
| TITLE OF INVENTION: Motifs |
| TITLE OF INVENTION: Motifs |
| FILE REFERENCE: 469201-444 |
| CURRENT APPLICATION NUMBER: 1999-12-02 |
| PRIOR APPLICATION NUMBER: 60/113,048 |
| PRIOR FILING DATE: 1998-12-21 |
| NUMBER OF SEQ ID NOS: 14 |
| SEQ ID NO SEQ ID NOS: 14 |
| SEQ ID NO SECOND SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
63.5%; Score 33; DB 4; Length 447;
Best Local Similarity 62.5%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 2; Indels
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US-08-821-119-19
US-08-821-119-19
; Sequence 19, Application US/08821119
; Patent NO. 5821104
; GENERAL INFORMATION:
; APPLICANT: Holm, Kaj Andre
; APPLICANT: Ramussen, Grethe
; APPLICANT: Lehnbeck, Jan
; APPLICANT: Lehnbeck, Jan
; TITLE OF INVENTION: Tripeptidyl Aminopeptidase
; NUMBER OF SEQUENCES: 23
                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: 0CT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGESTRATION NUMBER: 41,971
FELECOMMUNICATION INFORMATION:
TELEFRAX: (301) 309-8504
TELEFRAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
STRANDENHESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 182: US-09-536-784-182
    CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Streptococcus pneumoniae US-09-468-656A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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184 IVPHGDHY 191

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Gaps
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Sequence 66, Application US/08961083
Sequence 66, Application US/08961083
Sequence 66, Application US/08961083
Sequence 66, Application
APPLICANT: Choi et. al.
APPLICANT: Choi et. al.
APPLICANT: Choi et. al.
APPLICANT: Choi et. al.
CITIE OF INVENTION: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
STREET: 9410 Key West Avenue
STREET: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 2;
Pred. No. 1.2e+02;
0; Mismatches 2
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FILLICAL DATE.

FILLICAL DATE.

ATTORNEY AGENT INFORMATION:
NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE DOCKET WINER: PB340P2

TELECOMMUNICATION INFORMATION:
TELEFONE: (301) 309-8514

TELEFAX: (301) 309-8514

TELEFAX: (301) 309-8516

INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LENGTH: 763 amino acids

TYPE: amino acids

TYPE: TANGER: SINGLE
  4107.400-US
REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INDORMATION:
TELEPHONE: 212-867-0123
TELEFRX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                             INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal IS-08-821-118-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                         Sequence 66, Application US/09536784
Sequence 66, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et al.
TILLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: Streptococcus pneumoniae Antigens and Vaccines
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
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CONDUTE: MCCKVILLE
CONDUTE: 20850
COMPUTER: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: PORCETE 486/33
COMPUTER: HP VOCETE 486/33
FILING DATE: 30-00ct-1997
CLASSIFCATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: 07-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: MICHAEL S. MARKS
REGISTRATION NUMBER: PB340P3
TELERATION NUMBER: 41,911
TELERATION (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 763;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: procein
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-536-784-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 56, Application US/08961083 ; Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 763 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.5%;
Best Local Similarity 62.5%;
Matches 5; Conservative
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184 IVPHGDHY 191
RESULT 13
US-09-536-784-66
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RESULT 15
US-09-536-784-56
| Sequence 56, Application US/09536784
| Patent No. 6573082
| Patent No. 6573082
| TITLE TO INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
| CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: ADDRESSE: Human Genome Sciences, Inc.
| STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
| COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER READABLE FORM: MEDIUM TYPE: 30-0ct-1997 |
| CURRENT APPLICATION NUMBER: US/09/536,784 |
| FILING DATE: OCT-1997 |
| FILING DATE: OCT-1997 |
| PRIOR APPLICATION NUMBER: 08/961,083 |
| FILING DATE: OCT-20-1997 |
| CLASSIPTOTON NUMBER: OCT-20-1997 |
| CLASSIPTOTON NUMBE
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Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 2;
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NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: P8340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: BPLICATION DATA:
APPLICATION NUMBER: BPLICATION NUMBER: BTLING DATE:
ATTORNEY DATE:
ATTORNEY DATE:
ATTORNEY DATE:
ATTORNEY DATE:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 86:
SEQUENCE CRARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear ADPLECULE TYPE: protein US-08-961-083-56
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Score 33; DB 4; Length 796;
Pred. No. 1.7e+02;
1; Mismatches 2; Indels
; STRANDEDNESS: single; TOPOLOGY: linear; MOLECULB TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 56: US-09-536-784-56
                                                                                                                                                                                                                                                                                           Search completed: June 3, 2004, 12:03:09 Job time: 12.8 secs
                                                                                                                    Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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185 IVPHGDHY 192
                                                                                                                                                                                                  3 VVPXGXHY 10
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us-09-909-164-44.rapb

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June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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Sequence
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Sequence
Sequence
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Sequence
Sequence
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(cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-34
US-09-909-164-39
US-09-909-164-39
US-09-909-164-17
US-09-909-164-15
US-09-909-164-15
US-09-909-164-15
US-09-909-164-25
US-09-909-164-25
US-09-909-164-28
US-09-909-164-29
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                                                                                                                                                                                                                                                                                                                                                                                        1155919 segs, 281338677 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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52
1 EEVVPXGXHYS 11
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Match Length DB
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                                                                                                                                   Run on:
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                                                                                                                                                                                                                             Title:
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Sequence 32, Appl	Sequence 33, Appl	35	equence 36	equence 37	equence 40	equence, 41	ທ	Sequence 6, Appli	œ	6	10	12	Sequence 13, Appl	14	17	18	13	20	52	equence 23	24	equence 26	27	equence 43	45	e 46	e 47	e 48	e 49
-09-909-164-3	-09-909-16	-909-164-3	-09-909-164-3	-909-164-3	-09-909-164-	-09-909-164-	-09-909-164-	-909-164	-60-	6-60-	-09-909-164-1	164-1	6-60-	9-164-1	09-909-16	-09-909-16	39-909-164-1	09-909-164-2	-09-909-164-2	-09-909-164-2	-09-909-164-2	9-16	-09-909-164-2	-164-4	-09-909-164-4	US-09-909-164-46	-09-909-164-4	-90	-09-909-164-4
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40	40	40	40	40	40	40	39	39	33	on M	9	9	39	9	66	99	39	39	39	39	39	39	39	39	39	39	39	39	39
16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41		43	44	45

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APPLICANT: Corves International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Vilby, Marguerita
APPLICANT: Lim-Vilby, Odile B
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INOI192-US
FILE REPERENCE: INOI192-US
CURRENT APPLICATION NUMBER: 05/20,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOPTWARE: PATENTIN Version 3.1
US-09-909-164-30
. Sequence 30, Application US/09909164
. Publication No. US20020068702A1
. GENERAL INFORMATION:
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ALIGNMENTS

TYPE: PRT ORGANISM: artificial sequence SEQ ID NO 30 LENGTH: 11

OTHER INFORMATION: 11-mer synthesized according to example 1 NAME/KEY: MOD RES LOCATION: (1)..(1) OTHER INFORMATION: ACETYLATION FRATURE:
NAME KRY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION FEATURE:

DB 12; Length 11; 94.2%; Score 49; NAME/KEY: MISC_FEATURE LOCATION: (6)...(6) OTHER INFORMATION: norvaline-(CO) US-09-909-164-30 Query Match

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NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
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NAME/KEY: MISC_FEATURE
LOCATION: (8)..(9)
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LOCATION: (11)..(1
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US-09-909-164-39
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                                                      SEQ ID NO 38
                                                                                                       TYPE: PRT
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'SEQUENCE 34, Application US/09909164

Sequence 34, Application US/09909164

Sequence 34, Application US/09909164

Sequence 34, Application US/09909164

Sequence 34, Application

Publication No. US20020068702A1

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Willy, Marguerita

APPLICANT: Lim-Willy, Marguerita

APPLICANT: Brunck, Terence K

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Levy, Oddie B
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE REPERBNCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR PELING DATE: 2000-07-21
Best Local Similarity 90.9%; Pred. No. 0.0038; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE
LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
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OTHER INFORMATION: ACETYLATION
PEATURE:
NAME/KEY: MOD_RES
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OTHER INFORMATION: AMIDATION
FEATURE:
                                                                            1 EEVVPXGXHYS 11
                                                                                                             1 EEVVEXGTHYS 11
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US-09-909-164-34
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LENGTH: 11
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Sequence 39, Application US/09909164
Fublication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPL
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                                                                                                            OTHER INFORMATION: 11-mer synthesized according to example 1
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94.2%; Score 49; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 1; Indels
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COTHER INFORMATION: norvaline-(CO)
US-09-909-164-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEATURE:
NAME/FRY: MISC_PEATURE
LOCATION: (8)...(8).
OTHER INFORMATION: D-amino acid
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OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                         LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Marguerita
APPLICANT: Law, Odile B
APPLICANT: Law, Odile B
APPLICANT: Law, Odile B
APPLICANT: Law, Odile B
APPLICANT: Law, Odile R
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: 02/03-03-03-25
PRIOR PLIING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENT OF NOS: 62
SOFTWARE: PATENT OF NOS: 62
LENGTH: 11
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ORGANISM: artificial sequence
ORGANISM: artificial sequence
OTHER INFORMATION: 11-mer synthesized according to example 1
FRATURE:
NAMPICKEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB 12; Length 11;
Pred. No. 0.006;
0; Mismatches 1; Indels
     CURRENT APPLICATION NUMBER: US/09/909,164
                           CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD_RES
COCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC FEATURE
1 LOCATION: (8). (8)
2 OTHER INFORMATION: D-amino acid
US-09-909-164-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.3%;
90.9%;
                                                                                                NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
ERNOTH: 11
                                                                                                                                                                                             TYPE: PRT ORGANISM: artificial sequence
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NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Lovy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENCE: INO1192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
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Publication No. US20020068702A1
GENERAL INPOMPATION:
GENERAL INPOMPATION:
APPLICANT: Lim Wilby, Marquerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
TITLE NOT INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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                                                                      Score 49; DB 12; Length 11;
Pred. No. 0.0038;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 12; Length 11;
Pred. No. 0.006;
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LOCATION: (1)...(1)
COTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09909164
Publication No. US20020068702A1
; OTHER INFORMATION: D-amino acids JS-09-909-164-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: artificial sequence FEATURE:
                                                                      Query Match 94.2%;
Best Local Similarity 90.9%;
Matches 10; Conservative
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OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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US-09-909-164-25
US-09-909-164-25
Sequence 25, Application US/09903164
Publication No. US20020068702A1
Publication No. US20020068702A1
Publication No. US20020068702A1
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
ITTLE OF INVENTION NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
ITTLE OF INVENTION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 25
SEQ ID NO 25
LENGTH: 11
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                                                                                                                                                                                                                                           OTHER INFORMATION: 11-mer synthesized according to example 1 PRATURE:
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0.006;
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Pred. No. 0.006
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
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i OTHER INFORMATION: D-amino acid
US-09-909-164-21
                                                                                                                                                                                                                                                                               NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
FEATURE:
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LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
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OTHER INFORMATION: AMIDATION
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NAME/KEY: MISC_FEATURE
LOCATION: (6). . (6)
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                                                                                                                                                                                                                                                                               Sequence 16, Application US/09909164
; Sequence 16, Application US/09909164
; Publication No. US20200068702A1
; Publication No. US20200068702A1
; APPLICANT: Orras International, Inc.
; APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; TITLE REFERENCE: IN01192-US
; CURRENT APPLICATION NUMBER: US/09/909,164
; CURRENT FILING DATE: 2003-03-25
; PRIOR FILING DATE: 2003-07-21
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 11
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Sublication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Terence X
APPLICANT: Brunck, Terence X
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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                                                                      92.3%; Score 48; DB 12; Length 11; 90.9%; Pred. No. 0.006; tive 0; Mismatches 1; Indels
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LOCATION: (6)._(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
    ; OTHER INFORMATION: norvaline-(CO) US-09-909-164-15
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, OTHER INFORMATION: D-amino acid
US-09-909-164-16
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
                                                                                                                       10; Conservative
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Best Local Similarity
Matches 10; Conserv
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CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: US/09/909,164
PRIOR RIGHT APPLICATION NUMBER: US/09/909,164
PRIOR RIGHT APPLICATION NUMBER: US/09/909,164
PRIOR RIGHT APPLICATION NUMBER: 05/220,101
PRIOR PLING DATE: 2000-07-21
SOPTWARE: Patentin version 3.1
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GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-wilby, Marguerita

APPLICANT: Lim-wilby, Marguerita

APPLICANT: Lim-wilby, Marguerita

APPLICANT: Levy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-21

SOFTWARE: Patentin version 3.1

SEQ ID NO 28

LENGTH: 11

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ORGANISM: artificial sequence
PERATURE:
OTHER INFORWATION: 11-mer synthesized according to example 1
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NAME/KEY: MOD RES
OCHION: (11)..(11)
OCHIER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)..(9)
OTHER INFORMATION: D-amino acids
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Publication No. US20020068702A1
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NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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CTHER INFORMATION: Met(0)
US-09-909-164-44
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LOCATION: (1). (1)
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Sequence 42, Application US/09909164
Sequence 42, Application US/09909164
Sequence 42, Application No. US2020068702A1
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Version 3.1
SEQ ID NO 42
LANDTH: 11
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100.0%; Pred. No. 0.006;
iive 0; Mismatches 0
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                      OTHER INFORMATION: norvaline-(CO) FEATURE:
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LOCATION: (8)...(8)
OTHER INFORMATION: D-amino acid
IS-09-909-164-25
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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90.9%;
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THER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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CTHER INFORMATION: Met (0)
JS-09-909-164-42
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Search completed: June 3, 2004, 12:57:16
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   Publication No. US20020068702A1
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US-09-909-164-29
Sequence 29 Application US/09909164
Sequence 29 Application US/09909164
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Lievy, Odile E
APPLICANT: Brunck, Terence K
TITLE REPRENCE: IN0192-US
CURRENT APPLICANT: 2009-09,164
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 00/20,101
PRIOR PRIO
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OTHER INFORMATION: 11-mer synthesized according to example 1
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12; Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 12
Pred. No. 0.24;
0; Mismatches
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Pred. No. 0.24
0; Mismatches
                                                               NAME/KEY: MOD RES
LOCATION: (11)
CTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
CTHER INFORMATION: norvaline-(CO)
US-09-909-164-28
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US-09-909-164-31
; Sequence 31, Application US/09909164
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (1) - (1)
COTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11) - (11)
COTHER INFORMATION: AMIDATION
FEATURE:
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; OTHER INFORMATION: D-amino acid
US-09-909-164-29
OTHER INFORMATION: ACETYLATION
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81.8%;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Best Local Similarity 81.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EEVVPXGXHYS 11
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NAME/KEY: MISC_FEATURE
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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M protein - protein search, using sw model

un on:

June 3, 2004, 11:35:47 ; Search time 9 Seconds (without alignments) 117.567 Million cell updates/sec

US-09-909-164-44 52 1 EEVVPXGXHYS 11 itle: 'erfect score:

coring table: ednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues earched: otal number of hits satisfying chosen parameters:

linimum DB seq length: 0 laximum DB seq length: 2000000000

ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: * 2: pirl: * 4: pirz: * PIR 78:* atabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	DNA binding protei	proteir		ATP-dependent DNA	L-shaped tail fibe	V1 protein - tobac		_	_	6	hypothetical 92.4K	carbamoyl-phosphat	hypothetical prote	trans-regulatory s	conserved hypothet	hypothetical prote	2-methyl-branched-	hypothetical prote	TSI8.1 protein - A	cal prot	domain	conserved domain p	hypothetical prote	conserved hypothet	hypothetical profe	histidine Motit-Co	conserved hypothet	hypothetical prote	probable monoxygen
	ID	T02590	A72207	E69086	AF3286	836851	42	A25905	C75538	ന	A69284	T46758	F89892	E97985	VKLUSI	D82618	AE2001	A48702	S69046	G86430	S38143	C95136	B95136	E98004	G95115	97	8	9511	979	A70939
	DB	. 2	N	0																									7	
	Length	233	308	360	1028	1396	102	126	279	495	534	822	1057	46	124	156	252	412	460	510	743	802	819	828	839	853	855	1039	1039	162
æ	Query Match	67.3	~	67.3	5	~	65.4	ш	S	65.4	ш,	ம	S	ന	<u>ر</u>	س	m	m	m	m	m			w.		•	•	•	63.5	•
	Score	35	35	35	35	35	3.4	34	3.4	34	34	34	34	33	33	33	33	33	33	E E	33	33	33	33	33	33	33	33	33	32
	Result No.	 	N	n	4	Ŋ	w	7	80	ത				13		15	16	17	8	19	50	21	22	23	24	25	26	27	28	29

hypothetical prote prohibitin 2 [impo GMP synthetase, su	hypothetical prote fructose-bisphosph hypothetical prote probable aspartate	hypothetical prote probable non-photo probable bZIP tran aldehyde dehydroge	DNA mismatch repai phage transposase hypothetical prote	macrophage-stimula ethylene-response
S57810 C86169 H69194	AF3211 S47540 T17267 G69119	T24111 G96568 G84598 A13544	A69663 A91247 S61239	JC5061 A48246
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225 286 311	3 9 9 5 7 6 4 6 4 6 4 6 4 6 4 6 4 6 4 6 4 6 6 4 6	2442 2555 4046	627 696 701	716 738
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ALIGNMENTS

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DNA binding protein EREBP-2 - common tobacco ()Species: Nicotiana tabacum (common tobacco) ()Species: Nicotiana tabacum (common tobacco) ()Species: Nicotiana tabacum (common tobacco) ()Accession: T05590 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000 ()Accession: T05590 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000 R;Ohme-Takagi, M.; Shinshi, H. Bant Cell 7, 173-182, 1995 A;Ohme-Takagi, M.; Shinshi, H. Bant Cell 7, 173-182, 1995 A;Reference number: Z14671; MUID:95276459; PMID:7756828 A;Reference number: Z14671; MUID:95276459; PMID:7756828 A;Residues: Z14671; MUID:95276459; PMID:7756828 A;Residues: L233 cOHM> A;Residues: L233 cOHM> A;Residues: 1-233 cOHM> A;Residues: 1-233 cOHM> A;Residues: 1-233 cOHM> A;Experimental source: strain BY4; tissue-type leaf

ö Gaps ö Query Match
67.3%; Score 35; DB 2; Length 233;
Best Local Similarity 60.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 3; Indels

: ||| | || 90 QAVVPKGRHY 99 1 EEVVPXGXHY 10 ઠે 셤

freing proteinase activity modulator HfIK - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
R;Accession: A72207
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.,

Nature 399, 323-329, 1999
Aritle: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A, Reference number: A72200; MUID:99287316; PMID:10360571
A, Accession: A72200
A, Andlecule type: DNA
A, Molecule type: DNA
A, Residues: 1-308 cARN>
A, Residues: 1-308 cARN>
A, Residues: 1-308 cARN>
A, Esperimental Source: strain MSB8
C, Genetics
A, Genetics
C, Genetics
C, Superfamily: erythrocyte band 7 integral membrane protein

Gaps .. 0 Query Match 67.3%; Score 35; DB 2; Length 308; Best Local Similarity 75.0%; Pred. No. 13; Matches 6; Conservative 0; Mismatches 2; Indels

3 VVPXGXHY 10 VVPSGIHY 48

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A; Molecule type: DNA
A; Residues: 1-1396 «KML-)
A; Cross-rencess 1-1396 «KML-)
A; Cross-rencess 1-1396 «KML-)
B; Kaliman, A.V.; Kryukov, V.M.; Bayev, A.A.
Nucleic Acids Res. 16, 6230, 1988
A; Title: The nucleotide sequence of bacteriophage TS DNA at the region between early and A; Reference number: 501982; MUID:88289370; PMID:3267228
A; Reference number: S01984
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 934-985, A', 987-1396 «KA2-)
A; Cross-references: BMBL:X07559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Date: 15-Jan-1993
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yell
A;Reference number: A42452; MUID:92188538; PMID:1546458
R;Kaliman, A.V.; Kulshin, V.E.; Shlyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M. FEBS Lett. 366, 46-49, 1995
A;Title: The nucleotide sequence of the bacteriophage T5 ltf gene.
A;Reference number: 865934; MUID:95309401; PMID:7789514
A;Accession: 865934
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C.Species: Bos primigenius taurus (cattle)
C,Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A25905
R;Kotani, H.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
R;Cotani, H.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
R;Cot. Mall. Acad. Sci. U.S.A. 83, 7074-7078, 1986
A;Title: Structure and gene organization of bovine neuromedin K precursor. A;Reference number: A25905, MUID:86313713; PMID:3462746
A;Accession: A25905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: M81103; NID: 9335283; PIDN: AAA47947.1; PID: 9335284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein - tobacco yellow dwarf virus (strain Australia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 2
Pred. No. 68;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 2
Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: ltf
C,Keywords: late protein; tail fiber
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Best Local Similarity 50.0%;
Matches 5; Conservative
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Best Local Similarity 60.0°
Best Local Similarity
61.0°
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1360 KTIPAGDHYS 1369
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QVVPSGINYS 16
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A, Residues: 1-126 < KOT>
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A; Residues: 1-102 < MOR>
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R. Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; S.; Church, G.M.; Daniels, C.G.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A. Patteriol. 179, 7135-7155, 1997
A. Patteriol. Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A. Reference number: A69000; MuID: 98037514; PMID: 9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-dependent DNA helicase BME10275 [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C;Accession: AF3286
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 11028 4KUR>
A;Coss-references: GB:AE008917; PIDN:AAL51457.1; PID:g17982167; GSPDB:GN00190
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                             cell division protein - Methanobacterium thermoautotrophicum (strain Delta H) C.Species: Methanobacterium thermoautotrophicum C.Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-shaped tail fiber protein - phage TS
N;Alternate names: ltf protein
S;Species: phage TS
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 17-Nov-2000
C;Accession: S65934; S01984; $36851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.3%; Score 35; DB 2; Length 360;
45.5%; Pred. No. 16;
ive 4; Mismatches 2; Indels
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A, Gene: MTH1642 C, Superfamily: cell division protein MJ0174

5; Conservative

Query Match Best Local Similarity Matches 5; Conserv

|::|| |:: EDLVPMGSHHT 108 1 EEVVPXGXHYS 11

ò g 49;

67.3%;

2; Mismatches Score 35; Pred. No.

6; Conservative

Query Match Best Local Similarity Matches 6; Conserv

C;Genetics: A;Gene: BMEI0275 A;Map position: I

Accession: AF3286

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Score 34; DB 2; Length 126; Pred. No. 8.2; 1; Mismatches 2; Indels

65.4%;

6; Conservative

Query Match Best Local Similarity Matches 6; Conserv

28 EQVVPGGGH 36

1 EEVVPXGXH 9

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coenzyme F420-quinome oxidoreductase (EC 1.6.5.+) 56K chain - Archaeoglobus fulgidus
NyAlternate names: sarcosine oxidase alpha chain soxA homolog
C;Species: Archaeoglobus fulgidus
C;Daccession: A62284; S45665;
C;Accession: A62284; S45665;
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
S;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: A69284
A;Status: nucleic acid sequence not shown; translation not shown
A;Accession: A69284
A;Accession: A69284
A;Kubow, J.; Linder, D.; Stetter, K.O.; Thauer, R.K.
Bur. J. Biochem: 223, 503-511, 1994
A;Title: F(420)H(2): quinone oxidoreductase from Archaeoglobus fulgidus. Characterizatio
A;Reference number: 845665; MUID:94333340; PMID:8055920
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Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Staphylococous aureus
Cjate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F89892
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 62;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.4%; Score 34; DB 2; Length 534;
45.5%; Pred. No. 39;
ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical 92.4K protein - Streptococcus agalactiae
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75.08;
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Best Local Similarity 45.5
Best Local Si Conservative
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Matches
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F89892
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(Species: Deinococcus radiodurans)
(Species: Deinococcus radiodurans)
(Species: Os-10-1999 #sequence_revision 03-De-1999 #text_change 28-Jul-2000)
(Accession: C75538
(Multe, O.) Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; White, O.) Eisen, J.A.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M. Smith, H.O.; Venter, J.C.; Fraser, C.M.
(Since 286, 1571-1577, 1999)
(Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.)
(Arcession: C75538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .Molecule type: DNA.
.;Residues: 1-279 «WHI».
.;Cross-references: GB:AE001889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795
.;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1,Status: preliminary; translated from GB/EMBL/DDBJ
1,Molecule type: DNA
1,FResidus: 1-455 cGRA
1,FResidus: 1-455 cGRA
1,Cross-references: EMBL:AF022972; PIDN:AAC48234.1; GSPDB:GN00023; CESP:Fl0D2.3
1,Experimental source: strain Bristol N2; clone Fl0D2
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Space: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Superfamily: Deinococcus radiodurans hypothetical protein DR0271

", Map position: 1

Status: preliminary

Query Match 65.4%; Score 34; DB 2; Length 279; Best Local Similarity 75.0%; Pred. No. 19; Matches 6; Conservative 0; Mismatches 2; Indels

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65.4%; Score 34; DB 2; Length 495; 50.0%; Pred. No. 36; ive 2; Mismatches 3; Indels

Query Match
Best Local Similarity 50.0
Matches 5; Conservative

1:|| |: 218 ENIVPTGKHH 227 1 EEVVPXGXHY 10

≿

XESULT 10 169284

i,Map position: 5 i,Introns: 37/2; 90/1; 113/1; 183/3; 356/3; 380/3; 428/2

Gene: CESP:F10D2.3

Graves, T.; Wohldmann, P.; Gillam, B.
ubmitted to the EMBL Data Library, September 1997
Upbescription: The sequence of C. elegans cosmid F10D2.
Upbecenumber: 220515
Upbecession: T28717

pothetical protein F10D2.3 - Caenorhabditis elegans

100 VPLGRHYS 107

4 VPXGXHYS 11

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Cydecession: T46758
R;Spellerberg, B.; Rozdzinski, E.; Martin, S.; Weber-Heynemann, J.; Schnitzler, N.; Luet R;Spellerberg, B.; Rozdzinski, E.; Martin, S.; Weber-Heynemann, J.; Schnitzler, N.; Luet R;Spellerberg, B.; Rozdzinski, E.; Martin, S.; Weber-Heynemann, J.; Schnitzler, N.; Luet A;Tele: Lmb, a protein with similarities to the LraI adhesin family, mediates attachmen A;Reference number: 224091, MUID:99115568; PMID:9916102
A;Recession: T46758
A;Racession: T46758
A;Racession: T46758
A;Residues: L822 <SPEA
A;Residues: L822 <SPEA
A;Residues: L822 <SPEA
A;Residues: BMBL:AF062533; NID:94249622; PIDN:AAD13797.1; PID:94249624
A;Residues: Strain R268
C;Superimental source: strain R268
C;Superfamily: Streptococcus agalactiae hypothetical 92.4K protein
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ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
A,Accession: $45665
A,Molecule type: protein
A,Residues: 2,'X',4,'X',6-7,'X',9-10,'XX',13-14 <XUN>
A,Note: the authors could not distinguish between glutamate and cysteine for residues 5-
C,Superfamily: glutemate synthase small chain
C,Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N315
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Gaps

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A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule (type: DNA
A;Residues: 1-156 6sINA
A;Residues: 1-156 6sINA
A;Residues: 1-156 6sINA
A;Residues: 1-156 6sINA
A;Cross-references: GB:AE004014; GB:AE003849; NID:g9107044; PIDN:AAF84752.1; GSPDB:GN00
A;Reperimental Source: strain 9ac.
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Canargo, M.S. Alvarenga, R.; Rsimpson, A.J.G.; Reinach, F.C.; Arruda, P.A.; Canargo, L.S.A.; Carrarc, D.M.; Carrer, I Briones, M.R.S.; Bueno, M.R.P.; Canargo, A.A.; Fraga, J.S.; Pranca, A.J.S.
submitted to Genbank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.P.; Krieger, J.B.; Kuramae, B.J.; Laig'
J.D.; Junquelra, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, B.S.; Laig'
J.D.; Junquelra, M.A.; Madeira, M.M.B.; Marcho, C.L.; Marcques, M.V.; Martins, J.A.; Marchors: Marcques, L.S.; Laig'
A;Authors: Martins, E.M.F.; Maseukuma, A.Y.; Menck, C.F. M.; Miracca, B.C.; Mayaki, C.Y.; F.C.; Numes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; Pelmieri, D.Sawasal
R;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr.; W.A.; da Silva, A.; Sawasal
A;Reference number: A59328
A;Contents: annotation
A;Reference number: A59328
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Dates: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Dates: 10-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515, MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: D52618
C;Superfamily: AIDS trans-regulatory splicing protein
C;Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                          Score 33; DB 1; Length 124;
Pred. No. 13;
1; Mismatches 3; Indel8
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Pred. No. 17;
2; Mismatches
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                                                                                                                                        63.5%;
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Best Local Similarity 55.6
Matches 5, Conservative
                                                                                                                                                                                    Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 107 ETVPAGGNYS 116
                                                                                                                                                                                                                                                                                                                             2 EVVPXGXHYS 11
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                                                                                                                                             Query Match
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A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-6ep-1991 #sequence_revision 30-5ep-1991 #text_change 16-Jul-1999
C;Accession: 809988
R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: 809983; MUD:90259077; PMID:2188136
A;Accession: 809988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gispecies: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: 32-9985
C;Accession: B37985
C;Accession: B37995
C;Accession: B379985
C;Accession: B379985
C;Accession: B37985
C;Accession: B379875
C;
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C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin
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                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1057 «KUR>
A;Cross-references: GB:BA000018; PID:g13701002; PIDN:BAB42298.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
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;Molecule type: DNA
:Residues: 1-46 «XUR»
;Cross-references: GB:AEC07317; PIDN:AAK99713.1; PID:g15458516; GSPDB:GN00174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein spr0909 [imported] - Streptococcus pneumoniae (strain R6)
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Tile: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUD:21311952; PMID:11418146
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A.Gene: spr0909
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Gape

ò g A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-124 <HUE> A;Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36405.1; PID:9763085

A;Gene: rev; trs; art A;Introns: 27/1

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(c) 1993 - 2004 Compugen Ltd.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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STRAIN=RIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=12620739;
MEDLINE=22508454; PubMed=12620739;
MEAKING K., Oshima K., Kurckawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancet 36:743-749(2003).

-I. CATALTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
phosphate + 5-0-(1-carboxyviny1)-3-phosphoshikimate.
-I. PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0870X9;
0870X9;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation u
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InterPro; IRROD1986; ERSP synth.
PEAM; PF00275; ERSP synthase; 1.
PROSITE; PS00104; EPSP SYNTHASE_1; 1.
PROSITE; PS00885; ERSP SYNTHASE_2; 1.
Aromatic amino acid blosynthesis; Transferase; Complete proteome.
SEQUENCE 426 AA; 46094 MW; 373D39CC5BA1F70F CRC64;
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    Score 36; DB 1; Length 426;
Pred. No. 5.6;
1; Mismatches 3; Indels
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-- SUBUNIT: Monomer (By similarity).
-- SUBURIT: Monomer (By similarity).
-- SUBURITUAR LOCATION: Cytoplasmic (Probable).
-- SIMILARITY: Belongs to the EPSP synthase family.
-- SIMILARITY: Belongs to the EPSP synthase family.
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                                                 SLS1_YARLI
TOLB HABIN
YL15_VIBPA
DHP1_SCHPO
PDRB_YEBZI
PDRB_YEBZI
A10A HUYAN
POLG_PERVM
ILLIA_BOVIN
ILLIA_BOVIN
ILLIA_SKHEBP
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             NCBI_TaxID=670;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

Zhang Y.-Q., Miao Y.-G., Rang W.-Y. Chen R.-S., Shen Y., Chen Z.,

Yuan Z.-H., Zhao G.-P., Qu D., Danchin A.-N.,

Yuan Z.-H., Zhao G.-P., Qu D., Danchin A.-Y., Wen Y.-M.;

Genome-based analysis of virulence genes in a non-biofilm-forming

XT Genome-based analysis of virulence genes in a non-biofilm-forming

XT Staphylococcus epidermidis strain (ATCC 12228).";

Mol. Microbiol. 49:157-1593 (2003).

-I- CATALYITC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +

phosphate + L-glutamate + carbamoyl phosphate.

-I- CATALYITC ACTIVITY: 2 ATP + L-glutamine | COFACTOR: Binde 3 manganese inns per subunit (By similarity).

-I- PATHWAY: Arginia biosynthesis.

-I- PATHWAY: Arginial biosynthesis.

-I- PATHWAY: Composed of two chains; the small (or glutamine) chain

promotes the hydrolysis of glutamine to ammonia, which is used by

the large (or ammonia) chain to synthesize carbamoyl phosphate (By
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Pfam; Proz.
Pfam; Proz.
Pfam; Proz.
Pfam; Proz.

                                                                                                               15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-
phosphate synthetase ammonia chain).
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MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
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HANAP, MF 02105, -; 1.
INCEPPO; IRR006275; CRAL L glu.
INCEPPO; IRR006493; CPASE L.
INCEPPO; IRR006493; CPASE L. D2.
INCEPPO; IRR006493; CPASE L. D2.
INCEPPO; IRR006481; CPASE L. D3.
INCEPPO; IRR006481; CPASE L. D3.
INCEPPO; IRR004581; CPASE L. D3.
INCEPPO; IRR004069; SHPTOT ASSICE.
PEAN; PP002089; CPSASE L. ChAĪN; 2.
PÉAN; PP027089; CPSASE L. D2; 2.
PÉAN; PP027087; CPSASE L. D3; 1.
                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis.
                                                              STANDARD;
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STRAIN=ATCC 12228;
PubMed=12950922;
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                                                    CARB STAEP
Q8CPJ4:
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NP_BIND
METAL
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DOMAIN
DOMAIN
REPEAT
RESULT 2
CARB STAEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21886534; PubMed=11889109;
RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Materal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Materal V., Anderson I., Ivanova N., Grechkin G., Zhu L.,
RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
A Larsen N. D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Rostein M., Kyrpides N., Overbeek R.;
Ronstein M., Kyrpides N., Overbeek R.;
Ronstein M., Kyrpides N., Overbeek R.;
T. Gengence and analysis of the oral bacterium Fusobacterium
RT Genome sequence and analysis of the oral bacterium Fusobacterium
RT Genome sequence and analysis of the oral bacterium Fusobacterium
RT Genome sequence and analysis of the oral bacterium Fusobacterium
RT Genome sequence and analysis of the oral bacterium Fusobacterium
L. CATALYIC ACTIVITY: 2 AFP + L-glutamine + CO(2) + H(2)O = 2 ADP +
Diosphate + L-glutamiate + Garbamoyl phosphate (By Similarity).
L. CATALYIC ACTIVITY: 2 AFP + L-glutamine (By Similarity).
L. PATHMAY: Arginiae biosynthesis.
L. PATHMAY: Arginiae biosynthesis function ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By Similarity).
L. SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (BC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
                                                                                                                                                                       Score 36; DB 1; Length 1057; Pred. No. 14; Mismatches 3; Indels
300 300 MANGANESE 2 (BY SIMILARITY).
820 820 MANGANESE 3 (BY SIMILARITY).
832 832 MANGANESE 3 (BY SIMILARITY).
1057 AA, 117391 MM, 89447708DB1CAES9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE010554; AAL94625.1; ALT_INIT.
HAWAP; MF 01210; -; 1.
ThierPro; IRR006575; Caral_L glu.
InterPro; IRR00549; CPase_L D2.
InterPro; IRR00540; CPase_L D3.
InterPro; IRR00540; CPase_L D3.
InterPro; IRR00540; CPase_L D3.
InterPro; IRR00540; CPase_L N.
InterPro; IRR005481; CPase_L N.
InterPro; IRR004362; MGS_ING.
Pfam; PF00289; CPSase_L Chain; 2.
Pfam; PF02787; CPSase_L D3; 1.
Pfam; PF02142; MGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00098; CPSASE.
TIGRFAMS; TIGR01369; CPSaseII_lrg; 1.
                                                                                                                                                                                   69.2%;
                                                                                                                                                                                                                       63.6%;
                                                                                                                                                                           Query Match 69.2
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=ATCC 25586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC
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                                                                           METAL
SEQUENCE
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CARB_FUSNN
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PIR; S65934; S36851.
Late protein.
CONFLICT 986 98
SEQUENCE 1396 AA;
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TECK BOVIN
ID TECK BOVIN
AC PO8858;
                                                                                                                                                                                                                     Y11K TYDVA
P31619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAC3 OR NKNB
                                                                                Query Match
                                                                                                          Matches
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                                                                                                                                                                                                                                                                                     0; Gaps
                                                                          OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage T5.
Viruses; dsDNB viruses, no RNA stage; Caudovirales; Siphoviridae;
T5-like viruses.
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis, Ligase; Repeat;
Arginine biosynthesis; Pyrimidine biosynthesis, Ligase; Repeat;
Arginine biosynthesis; Complete protecome.
CARPOTERIC DOMAIN.
CARDOTERIA DOMAIN.
                                                                                                                                         ATP (POTENTIAL).

ATP (POTENTIAL).

ANGANESE I (BY SIMILARITY).

MANGANESE I (BY SIMILARITY).

117451 MW; ED7037AP77C1E39F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaliman A.V., Kryukov V.M., Bayev A.A.;
"The nuclectide sequence of bacteriophage T5 DNA at the region between early and late genes.";
Nucleic Acids Res. 16:6230-6230(1988).
-! - FUNCTION: Nonessential protein that mediates binding to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide sequence of the bacteriophage T5 ltf gene."; Lett. 366:46-48(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-95309401; PubMed=7789514;
Kaliman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.
                                                                                                                                                                                                                                                         Score 35; DB 1; Length 1058;
Pred. No. 23;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                      ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                         01-7AN-1990 (Rel. 13, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
L-shaped tail fiber protein (LTF protein).
                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1396 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88289370; PubMed=3267228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X69460; CAA49220.1; -.
EMBL; AJ001191; CAA04591.1; -.
PIR; S01982; S01982.
                                                                                                                                                                                                                                                           67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymannose O antigen.
                                                                                                                                                                                                                                                                   Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                             190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                              2 EVVPXGXHYS 11
                                                                                                                                                                                                                        832
                                                                                                                                          153
302
302
302
302
300
820
832
1058 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               P13390; 048502;
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                                                                                                                                                                                                      METAL
METAL
SEQUENCE
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NP_BIND
NP_BIND
METAL
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                                                                          DOMAIN
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REPEAT
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                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92188838; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
The nucleotide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
infecting monocotyledonus plants.";
Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Ammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoídea,
Bovidae, Bovinae, Bos.
NCBI_TaxID=9913;
                                                                                                                                   ö
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                                                                        67.3%; Score 35; DB 1; Length 1396; 50.0%; Pred. No. 31; tive 2; Mismatches 3; Indels
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Pred. No. 3.4;
2; Mismatches 2; Indels
986 986 V -> A (IN REF. 2).
1396 AA; 147989 MW; 18CD2192F65FFFC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A42452, A42452.
InterPro; IPR002621; Gemini mov.
Pfam; PF01708; Gemini mov; I.
Mypotherical protein.
SEQUENCE 102 AA; 11178 MW; A40ECFIEOAF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-CTT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurokinin B precursor (NKB) (Neuromedin K).
                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.4%;
                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                  1360 KTIPAGDHYS 1369
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                     2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EVVPXGXHYS 11
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                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=31599;
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CARB_STAAW
ID CARB_STAAW
AC P58940;
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SEQUENCE
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NP_BIND
NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
 STATE TETTETETETE BRANK BRANK STARK
                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-aib.ch/announce) or send an email to license@isb-sib.ch).
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Gaps
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STRAIN=MASO / ATCC 700699, and N315;
MEDLINE=21311952; Pubmed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
Cati L., Oguchi M., Mateumaru H., Maruyaman A., Murakami H., Hosoyama A.,
Mizuteni-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
                                                                                                                                                                                                                                                                                                                                                                                EMBL; M14351; AAA30723.1; -.
EMBL; M14348; AAA30723.1; -.
EMBL; M14348; AAA30723.1; JOINED.
EMBL; M14348; AAA30723.1; JOINED.
EMBL; M14349; AAA30723.1; JOINED.
EMBL; M14350; AAA30723.1; JOINED.
EMBL; M14369; AAA30725.1; JOINED.
EMBL; M14369; AAA30725.1; JOINED.
EMBL; M14369; AAA30725.1; JOINED.
EMBL; M14369; AAA307267.1; JOINED.
EMBL; M14369; AAA307267.1; JOINED.
EMBL; M14369; AAA307267.1; JOINED.
EMBL; M14369; AAA307723.1; JOINED.
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION (G-96 PROVIDE AMIDE GROUP) 446EF433498EC059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamcyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamcyl-phosphate synthetase ammonia chain).
CARB OR PYRAB OR SAV1203 OR SA1046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.4%; Score 34; DB 1; Length 126; 66.7%; Pred. No. 4.3; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus (strain MuSO / ATCC 700699), and Staphylococcus aureus (strain N315).

Bacteria; Firmicutes; Bacillales; Staphylococcus.

NCBI_TaxID=158879;
                                                                                                                                                                               -!- SUBCELLUTAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the tachykinin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 AA; 13871 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                      Lancet 357:1225-1240(2001).

-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + Dosphate + L-glutamate + carbamoyl phosphate.

-!- CATALYTIC ACTIVITY: 3 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + Dosphate + L-glutamate + carbamoyl phosphate.

-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis, first step.
-!- PATHWAY: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; "Whole genome sequencing of meticillin-resistant Staphylococcus aurents.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRINIS, KANONS, CESABELI LIG; 1.
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 1; Length 1057;
Pred. No. 38;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1057 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            gimilarity).
-!- SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BMBL; AP003361; BAB57365.1; -...
BMBL; AP003132; BAB42298.1; -...
FISP; P00968; 1050.
HAMAP; MF 01210; -; 1...
InterPro; IPR006575; CarA L glu.
InterPro; IPR0065475; CarA L glu.
InterPro; IPR005479; CPase L D2.
InterPro; IPR005480; CPase L D3.
InterPro; IPR005481; CPase L D3.
Pfam; PP02788; CPSase L Chain; 2.
Pfam; PP02788; CPSase L D2; 2.
Pfam; PP02788; CPSase L D3; 1.
Pfam; PP02787; CPSase L D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.4%;
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Les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00098; CPSASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 EIVSNGLHYS 199
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                                                                                                                                                                                                                                                                                                         Lancet 359:1819-1827(2002).

-i-CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.

-i-COFACTOR: Binds 3 manganese ions per subunit (By similarity).

-i-PATHWAY: Arginine biosynthesis.

-i-PATHWAY: Arginine biosynthesis, first step.

-i-SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).

-i-SIMILARITY: Belongs to the carB family.
                                                                                                                                                                                               MEDLINE-22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manganese; Complete proteome.

1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

02 546 OLIGOMERIZATION DOMAIN.

47 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

10 1057 ALLOSTERIC DOMAIN.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamcyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamcyl-phosphate synthetase ammonia chain).
CARB OR PYRAB OR WM1086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (POTENTIAL).

ATP (POTENTIAL).

ANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS, PRO0098, CPSASE.
TIGREAMS, TIGR01369; CPSASE.1, 2.
PROSITE, PSO0866; CPSASE.1, 2.
PROSITE; PSO0867; CPSASE.2, 2.
Arginine biosynthesis, Pyrimidine biosynthesis, Ligase, Repeat;
ATP-binding, Manganese, Complete proteeme.
                                                                                                                                                                                                                                                        Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 1057;
Pred. No. 38;
1; Mismatches 3; Indels
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                                                                                                           Staphylococcus aureus (strain MM2).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF 01210; -; 1.
InterPro; 1PR006275; CarA L glu.
InterPro; 1PR006479; CPase L D2.
InterPro; 1PR005480; CPase L D2.
InterPro; 1PR005480; CPase L D3.
InterPro; 1PR005481; CPase L D3.
Pfam; PP00289; CPSase L Chain; 2.
Pfam; PP02787; CPSase L D3; 1.
Pfam; PP02787; CPSase L D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP004825; BAB94951.1; -.
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Best Local Similarity 60.0
Matches 6; Conservative
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1057
546
1057
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300 30
820 82
832 83
                                                                                                                                              NCBI TaxID=196620;
                                                                                                                                                                                                                                                                                           acquired MRSA.
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NP_BIND
NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 345:1205-1394 LIPYU).

-I- FUNCTION: REV APPEARS.

-I- FUNCTION: REV APPEARS.

NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.

-I- SUBCELLILAR LOCATION: Nuclear; accumulates in the nucleoli.

-I- PTM: Phosphoprotein whose state of phosphorylation is mediated by a specific serine kinase activity present in the nucleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90259077; PubMed=2188136;
Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-359(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Transcription regulation, AIDS; Phosphorylation; Nuclear protein.
SEQUENCE 124 AA; 13701 MW; FS877DIBDF65A7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-1900 (Rel. 14), Last annotation update)
REP-2003 (Rel. 41, Last annotation update)
REV protein (Anti-repression transactivator protein) (ARI/TRS).
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Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBI_YEAST STANDARD; PRT; 460 AA. Q03010; PST330; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 110-0CT-2003 (Rel. 42, Last annotation update) UMBI OR WIM3 OR YPI139C OR LPI7C.
                                                                                                                                                                                                                                                                                                                                                        124 AA
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HIV; X52154; REV$CPZ.
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Best Local Similarity 60.0.
Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                 190 EIVSNGLHYS 199
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2 EVVPXGXHYS 11
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                 REV_SIVCZ
ID REV_SIVCZ
AC P17280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAC OOC OOR REPRESENTATION OF THE STATE OF T
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Multidrug resistance-like ATP-binding protein mdlB
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P36148;
01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66827 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%;
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Best Local Similarity Su.v.,
Best Local Similarity
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NP BIND
SEQUENCE
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YK47 YEAST
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RX MEDLINE-2288C / AB972;

RX MEDLINE-29131371; PubMed=9169875;

RX BUSINES-9731371; PubMed=9169875;

RX Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

RX Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

RX Bursher C.M., Coster F., Davis R.W.,

Chung B., Churcher C.M., Coster F., Davis R.W.,

RX Duncan M., Flockin M., Friesen J.D., Fritz C., Goffeau A.,

RX Duncan M., Hebling U., Heumann K., Hilbert H., Hillier L.W.,

RA Hall J., Hebling U., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,

RA Marathe R., Messenguy F., Mewes H.W., Mirtipati S., Moestl D.,

RA Marathe R., Messenguy F., Mewes H.W., Mirtipati S., Moestl D.,

RA Petel F.X., Pohl T.M., Purnelle D., Schäfer M., Scharfe M.,

Scherens B., Schramm S., Schreder M., Sdicu A.M., Tettelin H.,

RA Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler E., Winnett E.,

RA Malsh S.V., Wang Y., Wedler E., Wedler H., Winnett E.,

RA Malsh S.V., Wang Y., Wedler E., Wedler H., Winnett E.,

RA Malsh S.V., Wang Y., Wedler E., Wedler H., Winnett E.,

RA Marues 397:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the BNED custatation the Buropean Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: TRANSCRIPTIONAL MODULATOR WITH ROLES IN MEIOTIC REGULATION AND SILENCING. NEGATIVE REGULATOR OF MEIOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005634; C:nucleus; IDA.
GO; GO:0003714; F:transcription co-repressor activity; IDA.
GO; GO:0003714; F:transcription of meiosis; IGI.
InterPro; IPR001080; WD40.
Pfam; PF00400; WD40; 3.
SMART; SM00320; WD40; 4.
PROSITE; PS00673; WD REPEATS_1; FALSE_NEG.
PROSITE; PS00623; WD REPEATS_2; FALSE_NEG.
PROSITE; PS50294; WD REPEATS_REGION; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.5%; Score 33; DB 1; Length 460; 62.5%; Pred. No. 26; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51022 MW; AA6F60448B7BCBA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulation, Melosis, Repeat, WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 4 WD repeats.
-!- SIMILARITY: STRONG, TO YEAST WIM1 AND WIM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6666
14264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U10280; AAB40937.1; -. EMBL; U43703; AAB68221.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 62.8
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 42, (Rel. 42, 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S69046; S69046.
GermOnline; 144121; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 IVPLGLHY 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S0006060; UME1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GermOnline; 14412
TRANSFAC; T04309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ranscription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
MDLB BUCGBP
ID MDLB BUCGBP
AC Q89A36;
DT 10-OCT-2003
DT 10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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SOLUTION SOLUTION SERVICE SERV

REPEAT REPEAT

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                                                                                                                                                                                                                                                             MEDINE-22426901; PubMed=12522265; Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F., Van Ham R.C.H.J., Kamerbeek J., Postigo M., Silva F.J., Bastolla U., Pernandez J.M., Jimenez L., Postigo M., Silva F.J., Tamames J., Viguera B., Latorre A., Valencia A., Moran F., Moya A.; Reductive genome evolution in Buchmera aphidicola."; Proc. Natl. Acad. Sci. U.S.A. 100:581-586 (2003).
-i. SUBCELUTAR LOCATION: Integral membrane protein (Potential).
-i. SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Buchnera aphidicola (subsp. Balzongia pistaciae).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
NCBI_TaxID=135842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S288;
van Vliet-Reedijk J.C., Planta R.J.;
van Vliet-Reedijk J.C., Planta R.J.;
submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELJULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBL011W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kDa protein in CCP1-MET1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE014017; AA027134.1; -.
InterPro; IPR001140; ABC_TM_transpt.
InterPro; IPR00343; ABC_Transporter.
Pfam; PF00664; ABC membrane; 1.
Pfam; PF00005; ABC_tran; 1.
PROSTIE; PS00211; ABC_TRANSPORTER 1; FALSE_NEG.
PROSTIE; PS00211; ABC_TRANSPORTER 2; 1.
ATANSPORTER 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 1; Length 578;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3B84848CE196ADF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABC TRANSPORTER.
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or send an email to license@isb-sib.ch/
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                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
GAAB METTH
ID GAAB METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetase)
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SEQUENCE
                                                                                                                                        ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     026806;
  SON REAR REPORTED
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                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Lucopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                         GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0004366; F:glYcerol-3-phosphate O-acyltransferase acti. . .; IDA.
GO; GO:0008654; P:phospholipid biosynthesis; IDA.
InterPro; IPR002123; Acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Peptide methionine sulfoxide reductase msrA (EC 1.8.4.6) (Proteinmethionine-S-oxide reductase) (Peptide Met(O) reductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Protecobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBL_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.5%; Score 33; DB 1; Length 743; ilarity 75.0%; Pred. No. 43; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                               31 55 POTENTIAL.
69 85 POTENTIAL.
502 524 POTENTIAL.
539 555 POTENTIAL.
743 AA, 83644 MW, 84B9946ES6B82FIS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 AA
                                                                                                                                                                                                                                                                                                                                                                            protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                  Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; PlsC; 1.
                                                                                                                                                                           EMBL; Z28292; CAA82146.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio parahaemolyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 VVPCGLHY 301
                                                                                                                                                                                              PIR; S38143; S38143.
GermOnline; 140046; -
SGD; S0001775; GPT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSRA OR VP0306.
                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
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9
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SEQUENCE
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Matches
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WEDLINE=98037544; PubMed=9371463;

MEDLINE=98037544; PubMed=9371463;

MEDLINE=98037544; PubMed=9371463;

Aldredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K.,

Aldredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K.,

A Harrison D., Hoang L., Keagle P., Lumm W., Pothier-B., Qiu D.,

A Harrison D., Hoang L., Wierer B., Gilbert R.,

A Juani N., Caruso A., Bush D., Safer H., Patwell D., Prabakar S.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

A Daniels C.J., Man O.J.-I. Rice P., Noelling U., Reeve J.N.;

T. Complete genome sequence of Methanobacterium thermoautotrophicum

deltaH: functional analysis and comparative genomics.";

T. GATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine +

H(2)0 = AMP + diphosphate + GMP + L-glutamate.

- I - PATHMAY: GMP biosynthesis.

- I - PATHMAY: GMP biosynthesis.

- I - SUBUNIT: Heterodimer composed of a glutamine amidotransferase

subunit (A) and a GMP synthase subunit (B) (Potential).
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (EC 6.3.5.2) (GMP
                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanobacterium thermoautotrophicum.
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRPAMs; TIGRO0884; guad Cterm; 1.
Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding; complete protecme.
                                                                                                                                                                                                                                              61.5%; Score 32; DB 1; Length 212; 55.6%; Pred. No. 19; 2; Indels iive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMP-BINDING (BY SIMILARITY).
                                                                                                                                                                                  212 AA; 23616 MW; 1967AFEC3C735EC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IP (BY SIMILARITY).
F2DCF6ED202CAEC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 AA.
                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000850; AAB85215.1; ALT_INIT.
HSSP; P04079; IGPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                    Pfam; PP01625; PMSR; 1.
Oxidoreductase; Complete proteome.
ACT SITE 51 BY S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP005074; BAC58569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 35 A
308 AA; 34403 MW;
                                                                                                                                                                                                                Query Match
Query Match
Best Local Similarity 55.00,
Best And 5, Conservative
                                 HAMAP; MF_01401; -; 1.
InterPro; IPR002569; PMSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          171 EIVPAGPYY 179
                                                                                                                                                                                                                                                                                                                                                                              2 EVVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=187420;
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                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and characterization of a full-length cDNA coding for ovine aldolase B from fetal mesonephros.";
Biochim. Bioch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY STMILARITY.

C-1-PHOSPHATE GROUP OF THE SUBSTRATE.

C-1-BHOSPHATE GROUP OF THE SUBSTRATE.

SCHIFF-BASE WITH DIHYDROXYACETONE-P.

ESSENTIAL FOR ENHANCED ACTIVITY OF THE

BYZYME TOWARD FUCTOSE 1,6-BISPHOSPHATE.

PCOMPARED WITH FRUCTOSE 1-PHOSPHATE.

FC8B45666821E2BD CRC64;
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Mesonephros;
MEDLINE=94368863; PubMed=8086469;
Gianquinto L., Pailhoux E.A., Bezard J., Servel N., Kirszenbaum M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, vomeep).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Octartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.5%; Score 32; DB 1; Length 363; Best Local Similarity 62.5%; Pred. No. 34; Matches 5; Conservative 1; Mismatches 2; Indels
61.5%; Score 32; DB 1; Length 308; 63.6%; Pred. No. 29; 4; Indels ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 229372; CAA82563.1; -.
PIR; S47540; 547540.
HSSP; POOR83; 1A0.
InterPro; IPRO00741; Aldolase I.
Pfam; PF00274; Glycolytic_enzy; 1.
PRODIN; PD001128; Aldolase I; 1.
PROSITE; PS00158; ALDOLASE_CLASS I; 1.
Lyase; Schiff base; Glycolysis; Multigene family.
INIT_MET
                                                                                                                                                                                                                                                                                                                                           363 AA
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Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                    216 EEVVESGLHES 226
                                                                                                                         1 EEVVPXGXHYS 11
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                                                                                                                                                                                                                                                                                                                                        ALFB SHEEP
P52210;
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2 EVVPXGXH 9

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Search completed: June 3, 2004, 11:49:55
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189 EVIPDGSH 196
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029966 archaeoglob

089772 streptococc

0864u1 streptococc

086281 streptococc

080282 streptococc

08059xv4 streptococc

081b11 plasmodium

0967h5 sulfolobus

0967d5 xylella fas

097d4 homo sapien

081031 bos taurus

081031 hos taurus
Q9rxn9 deinococcus
Q9hlh8 thermoplasm
O16912 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (UTV-2002) to the EMBL/GenBank/DDBJ databases. Submitted (UTV-2002) to the EMBL; BC032195; AAH32195.1; -MGD; MGI:1915724; Tada31. MGD; MGI:1915724; Fada31. MGD; MGI:1915724; Figand-dependent nuclear receptor transcrip. GO; GO:0005515; F:protein binding; IPI. SEQUENCE 413 AA; 46621 MW; A9BBAIDC70CDA0D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 11; Length 413;
Pred. No. 2.7;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence AI987856.
TADA3L OR 1110004819RIK.
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Last sequence update)
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                                                                       Q9ZHG7
Q8E4U1
Q8DZ81
Q8NZ82
Q8K5Q1
Q99XV4
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Q96YH5
Q8CYU7
Q9XST4
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Q87D36
Q81033
Q81031
Q00404
Q87XD7
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Q867A5
Q8HXY9
Q7VP43
Q9UEE9
Q8IGN5
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Local Similarity 63.6%;
Les 7; Conservative 1
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      PRELIMINARY;
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    01-NOV-1996
01-NOV-1996
01-OCT-2003
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Matches 7
      Q46486
Q46486;
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                                                                                                       June 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                              )M protein - protein search, using sw model
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Q46486
Q46486
Q40479
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Q50W50
Q9HU5
Q9X2E2
Q8X317
Q8X317
Q7XTG3
Q7XTG3
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Q8W111
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sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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1: SP_archea:*
2: SP_bacteria:*
3: SP_tungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mammal:*
7: SP_mammal:*
8: SP_organelle:*
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52
1 BEVVPXGXHYS 11
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Perfect score:
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Q9LW50
ID Q9LW
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A Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Oin Z.,
A Chen Z., Wen Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Oin Z.,
A Chen Z., Wen Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Oin Z.,
Chen Z., Wen Y., Corporation of the EMBL, GenBank/DDBJ databases.

EMBL; AE016746; AA004476.1; -.

R GO; GO:000524; F:ATP binding; IEA.

GO; GO:0004108; F:Carbamoyl-phosphate synthase activity; IEA.

GO; GO:0004108; F:Carbamoyl-phosphidase activity; IEA.

R GO; GO:0006526; F:arginine biosynthesis; IEA.

GO; GO:0006526; P:arginine biosynthesis; IEA.

R GO; GO:0006509; P:proceolysis and peptidolysis; IEA.

R InterPro; IRR005479; CPase_L.

R InterPro; IRR005490; CPase_L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEPECTES—C. STITISTURY, STRAIN=M82B,
MEDILINE=20194806; PubMed=1073568;
MEDILINE=20194806; PubMed=1073568;
Tauch A., Krieft S., Kalinowski J., Puhler A.;
"The 51,409-bp R-plasmid pTP10 from the multiresistant clinical
isolate Corynebacterium striatum M82B is composed of DNA segments
initially identified in soil bacteria and in plant, animal, and human
pathogens.",
Mol. Gen. Genet. 253:1-11(2000).
BMBL; M2024666; AAG03390.1; -.
GO; GO:0046861; Cextrachromosomal DNA; IEA.
Hyporbetical protein, Plasmid.
SEQUENCE. 208 AA; 23012 MW; FISO4BEIECDE85A6 CRC64;
                                                                                                                                                                                                                                                                                    SPECIES=C.xerosis; STRAIN=M82B;
MEDLINE=96117603; PubMed=8559800;
Tauch A., Kassing F., Kalinowski J., Puhler A.;
Tauch A., Kassing F., Kalinowski J., Puhler A.;
The Corynabacterium xerosis composite transposon In5432 consists of two identical insertion sequences, designated IS1249, flanking the erythromycin resistance gene ermCX.";
Plasmid 34:119-131(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                      Corynebacterium xerosis, and Corynebacterium striatum. Bacteriam Striatum. Bacteria; Actinobacteria; Actinobacterias, Corynebacterinese; Corynebac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.2%; Score 36; DB 2; Length 208; 50.0%; Pred. No. 15; 2; Indels ative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8CPJ4 PRELIMINARY; PRT; 1057 AA.
Q8CPJ4;
Q8CPJ4;
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Bacteria, Firmicutes, Bacillales, Staphylococcus
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Hypothetical protein (GcrA)
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130 DVIPEGKHYA 139
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Best Local Similarity
Matches 5; Conserv
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Bukaryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
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GO; GO.0003700; F:transcription factor activity; IEA.
GO; GO.000355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPRO1471; FE ERF.
Pfam; PF00847; AP2-domaIn; 1.
PRINTS; PR00367; ETHRSPELENNT.
PRINTS; PR001457; TE_RF; 1.
SMART; SM00380; AP2; 1.
SMART; SM00380; AP2; 1.
SEQUENCE 233 AA; 25563 MW; 6CD16783582C0CB5 CRC64;
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Pred. No. 88;
1; Mismatches 3; Indels (
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 AA.
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InterPro; IPR00166; SHprot acsite.
Pfam; PF00289; CPSase_L Chain; 2.
Pfam; PF002786; CPSase_L LD2; 2.
Pfam; PF002786; CPSase_L D3; 1.
Pfam; PF002787; CPSase_L D3; 1.
Pfam; PF002142; MGS; 1.
Pfam; PF00142; MGS; 1.
PROSTE; PS00086; CPSASE_1; 2.
PROSTE; PS00866; CPSASE_1; 2.
PROSTE; PS00639; THIOL_FROTEASE_HIS; 1.
Complete protecome.
SEQUENCE 1057 AA; 117391 MW; 8944D7D8DE
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01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                63.2%;
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Best Local Similarity 60...
Best G; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                             189 KEVVSNGLHYS 199
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Score 35;
Pred. No. 3
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            67.3%;
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Best Local Similarity 75.0
Matches 6; Conservative
          Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                    Bacteria, Thermo
NCBI_TaxID=2336;
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Q38317;
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                                                                  Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledone; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.
NCSI TaxID=4096;
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                                                                                                                                                      MEDINE=20399450; PubMed=10945353;
Xitalima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;
Xitalima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;
Characterization of gene expression of NSEREs, transcription factors
of basic PR genes from Nicotiana sylvestris.";
Plant Cell Physiol. 41:817-824 (2000).
EMBL, ABO16264; BAA97122.1;
HSSP, 080337; 2GCC.
                                                                                                                                                                                                                                                      GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPRO1471; TERF.
Pfam; PF00847; AP2-domain; 1.
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GO: 0005746; C:mitcochondrial electron transport chain; IEA.
GO: 0005489; F:electron transporter activity; IEA.
GO: GO: 0005189; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                  67.3%; Score 35; DB 10; Length 237; 60.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 AA; 30961 MW; 31D9CDE2711747EE CRC64;
                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0367; ETHRSPELEMNT.
ProDom; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
SMART; SM00380; AP2; 1.
SEQUENCE 237 AA; 26243 MW; 01BC3EBS1E46298 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Ethylene-responsive element binding factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR002325; Cyt_Cl.
Edan, PP00167; Cytcohrome_Cl; 1.
PRINTS; PR00603; CYTOCHROME_C.
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                        Nicotiana sylvestris (Wood tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7:331-338(2000).
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Matches 6; Conservative
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                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE 285 AA
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KERWOODD X BUNGEL BERKKKKKKKKKKKKK
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CK MEDLINE-SP9287316; PubMed=10360571;

CK MEDLINE-CF FROM N.A.

CK MEDLINE-CF PLOWER A. M. Gill S.R., Gwinn M.L., Dodson R.J.,

Melson K.B., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

A McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrent K.M.,

CA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

CA Stewart A.M., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

CA Slazberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

CHICAL PART S.L., Smith H.O., Venter J.C., Fraser C.M.;

CHARLES S.L., SMITH S.L., T.M., MAILES S.L., T.C., T.M., MAILES S.L., T.C., T.M., MAILES S.L., T.C., T.C., MAILES S.L., T.C., MAILES S.L., T.C., MAILES S.L., T.C., T.C.
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Bacteria, Thermotogae, Thermotogales, Thermotogaceae, Thermotoga.
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16; Length 285
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
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SWART; SW00244; PHB; 1.
Protease; Complete proteome.
SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-NOV-1999 (TrEMBLrel. 24, Last annotation update) FTSH protease activity modulator HFLK.
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     35;
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(TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last seq
(TrEMBLrel. 25, Last ann
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Les 5, Conservative
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433 IVPSGDHYA 441
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01-MAR-2001
01-OCT-2003
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Q7XTG3;
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Q9E1X6
ID Q9E1X
AC Q9E1X
DT 01-MA
DT 01-WA
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                                                                                                                                                                                                                                                                                                Engel G., Altermann E., Klein J., Henrich B.;

Engel G., Altermann E., Klein J., Henrich B.;

"Structure of a genome region of the Lactobacillus gasseri temperate
T phage phi adh covering a repressor gene and cognate promoters.";

Gene 210:67-70(1998).

R EMBL; AJ131519; CAB52540.1;

R GO, GO:0003796; F:1yeozyme activity; IEA.

R GO, GO:000396; F:1yeozyme activity; IEA.

R GO; GO:000396; F:1yeozyme actabolism; IEA.

R GO; GO:0009253; P:peptidoglycan catabolism; IEA.

R InterPro; IPR003646; SH3 bac.

R InterPro; IPR003646; SH3 bac.

R ProDom; PD004620; Glyco_hydro_25; 1.

R SMART; SM00641; Glyco_bydro_25; 1.

R SMART; SM00641; Glyco_bydro_25; 1.
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MEDLINE=98037514; PubMed=9371463;
Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Vicare R., Wang Y., Marzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
                                                                                                                                                                                                                             encoding integrative
                                  Altermann E., Klein J., Henrich B.; Primary structure and features of the genome of the Lactobacillus gasseri temperate bacteriophage phi-adh."; Gene 236:333-346(1999)
                                                                                     [3]
SEQUENCE FROM N.A.
MEDLINE=95138034; PubMed=7836307;
Henrich B., Binishofer B., Blaesi U.;
"Primary structure and functional analysis of the lysis genes of Lactobacillus gasseri bacteriophage phi-adh.";
J. Bacteriol. 177:723-732(1995).
                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=33231538; PubMed=8472961;
Fremaux C., De Antoni G., Raya R., Klaenhammer T.;
"Genetic organization and sequence of the region encoding integra
"Genetic organization and sequence of the region encoding integra
functions from Lactobacillus gasseri temperate bacteriophage phi-
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Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 9; Length 317;
Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34703 MW; 9FF271SEE43561C7 CRC64;
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[2]
SEQUENCE FROM N.A.
MEDLINE=99384014; PubMed=10452953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                 Gene 126:61-66(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 AA;
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SEQUENCE FROM N.A.

Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia G., Wang S.Y., Ren S.Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Mang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Fen G.W., Huang Y.C., Li Y. Zhu J.Z., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H., Olan Y.M., Xing Y., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X., Chan R.M., Ying Y., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Hong G.F., Shang M.Q., Guan J.P., Hong G.F., Ewell, Aleosets: Ewell, Aleosets: System R. Shang R.Q., Shang
"Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

B. MEL; AE000923; AAB66115.1; -.

PIR; E69086; E69086.

GO; GO:0000910; P:Cytckinesis; IEA.

RO; GO:0000910; P:Cytckinesis; IEA.

RO; GO:0000910; P:Cytckinesis; IEA.

RO; GO:0000910; P:Cytckinesis; IEA.

RITHETPO; IPRO0141; RFF1_2.

RITHETPO; IPRO0141; RFF1_2.

RITHETPO; IPRO0141; RFF1_2.

RITHETPO; IPRO0141; PEIA.

RITHETPO; IPRO0141; PEIA.

REAM; PF00463; RFF1_2; 1.

REAM; PF00465; RFF1_2; 1.

REQUENCE 360 AA; 40814 MW; ZA000CB4B3CEF469 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
03991214-12.4.
0ryza saīiva (Rice).
0ryza saīiva; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae, Streptophyta; Embryophyta; Poaceae; Birhartoideae; Oryzaa, Oryzaa.
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45.5%; Pred. No. 46;
tive 4; Mismatches 2; Indels
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SEQUENCE FROM N.A.
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Q8YJ11
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MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

MAMMARIAGE R.A., Lewis S.E., Holt R.A., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Holt R.A., Andrag Q., Chen L.X.,

MARIAGO R.C., Rogers Y.H., Balazel R.G., Nelson C.R., Feiffer B.D.,

Abril J.F., Agbayani A., An H.J., Andrews Pfannkor G.L.,

Abril J.F., Agbayani A., Baxendale J., Bayasker Fannkor G.R.,

Ballew R.M., Basu A., Baxendale J., Bayasker Fannkor G.L.,

Abril J.F., Agbayani A., Butler H.J., Andrews Pfannkor G.L.,

R. Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakoy S.,

Borkova D., Botchan M.R., Bouck J., Barckerier P., Brottier F.,

Borkova D., Botchan M.R., Bouck J., Bayasker Fannkor G.L.,

RA Gherry J.M., Cawley S., Dahlke C., Davaphort L.B., Davies P.,

Borkova D., Botchan M.R., Bouck J., Bayaska A.D., Dew I., Discretz S.M.,

RA Gherry J.M., Cawley S., Dahlke C., Davaphort L.B., Davies P.,

Booson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn R.A.

RA Dodson K.J. Evangelista C.C., Ferraz C., Balai M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibeyam C.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibeyam C.,

RA Jalai M., Kalush P., Razpen G.H., Kazvitz S., Kulp D., Lai Z.,

Liu X., Mattei B. M. Murphy B., Murphy L., Murphy L., Murphy L., Murphy L., Murphy L., Murphy C., Palaz D., Puri V., Resee M.G.,

RA Rainzcho M., Pittman G.S., Pan L.,

RA Rainzcho M., Pittman G.S., Pan H.,

RA Rainzch K., Remingron M., Sunderer F., Shen H.,

Shue B.C., Siden-Khamos I., Simpson M., Skupski M.P., Smith T.,
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                                                                                                                                                         Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.; "Complete Sequence of the Simian Varicella Virus Genome."; Submitteed (WAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275348; AAG271217.1.
GO; GO:0019012; C:virion; IEA.
GO; GO:0019012; C:virion; IEA.
InterPro; IPR007640; Herpes UL17.
Ffam; PF04559; Herpes UL17.
Hypothetical protein.
SEQUENCE 678 AA; 75850 MW; A17B09E30512FE3C CRC64;
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CG30437 OR CG10398 OR CG10408.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Endopterty, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                 67.3%; Score 35; DB 12; Length 678; 50.0%; Pred. No. 90; ive 2; Mismatches 3; Indels
     Cercopithecine herpesvirus 7.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=35245;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 50...
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Hypothetical protein.
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SEQUENCE FROM N.A.

BERTIES C.A., Gocayne U.D., Amanatides P.G., Brandon R.C., Rogers Y., Buranc G.A., Gocayne U.D., Amanatides P.G., Brandon R.C., Rogers Y., Barach J., An H., Baldwin D., Barach J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., A Dodson K., Dersett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Golle R.P., Garg N.S., George R.A., Ibock J., Hockkin R.A., Hockstin D., Mostin D., Howland T.J., A Gonzalez M., Houck J., Hoskin R.A., Hostin D., Howland T.J., A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., A Pacleb J., Paragas V., Park S., Patel S., Pitchards S., Scheler P., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., A Williams S.M., Zaveri J.G., Puri, V., Kichards S., Scheler P., Stapleton M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome."
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.Y. Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodsey, Warlisher K.C., Wu D., Yang S., Yao Q.A., Ye J., Zheng R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.M., Zhoug W., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
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Mistra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Mistra S., Crosby M.A., Matthews B.B., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Carlang M., Dryddale R., Bammert D., Frise B., de Grey A., Harris N., Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield B., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Shannotation of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR001117; Cu-cxidase.
InterPro; IPR002355; Cu ox copper BS.
PRam; PF00194; Cu-cxidase; 3.
PROSITE; PS00009; MULTICOPPER CXIDASE1; 1.
SEQUENCE 855 AA; 94532 MW; 39BD5A516D6312DB CRC64;
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Last annotation update)
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01-MAR-2002 (TYEMBLrel. 20,
01-MAR-2002 (TYEMBLrel. 20,
01-OCT-2003 (TYEMBLrel. 25,
ATP-dependent DNA helicase.
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Beet Local Similarity 66.70,
Beet Local Similarity 66.70,
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TIGRFAMS; TIGR00915; 2A0602; 1.

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 23456 / Biotype 1;

STRAIN-16M / ATCC 23456 / Biotype 1;

A DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

A DelVecchio V.G., Kapatral V., Redkar R.J., Lykidds A., Reznik G.,

A Jablonski L., Laren N., D'Souza M., Bernal A., Mazur M., Goltsman B.,

A Jablonski L., Larer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

A Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

RA selkov E., Kryrides N., Overbeek R.;

Raucella melltensis ";

Brucella 
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KX MAKAMURE 22225144; PubMed=12240834;

KA NAKAMURE Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,

RA MATANDEA A., Iriguchi M., Ravashima K., Kimura T., Kishida Y.,

RA Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N.,

RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RY Complete genome structure of the thermophilic cyanobacterium

RI Thermosynechococcus elongatus BP-1.";

DN RE MBL; APO05374; BAC09170.];

DR GO; GO:0005021; F:transporter activity; IEA.

DR GO; GO:000510; P:transporter activity; IEA.

DR GO; GO:000510; P:transporter activity; IEA.

DR HOUSTO, IPRO01036; Activinin_res.

InterPro; IPRO04764; HAEI.
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Pred. No. 1.4e+02;
2; Mismatches 3; Indels C
                                  Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
NCBI_TaxID=29459,
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Bacteria: Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Multidrug efflux transporter.
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PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
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les 6, Conservative
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                       Srucella melitensis.
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SEQUENCE 1028 AP
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SEQUENCE FROM N.A.

SEQUENCE 22827954; PubMed=12910271;

MEDLINE=22827954; PubMed=12910271;

MEDLINE=22827954; PubMed=12910271;

Parkiall J.S., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Achran M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A Richingworth T., Collins M., Cronin A., Davis P., Doggett J.,

B Achran M., Atkin R., Hamlin N., Hauser H., Davis P., Doggett J.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Leather S., Simmonds M., Skalton J., Squares B., Seeger K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

Under Laborative analysis of the genome sequences of Bordetella pertussis,

R Dordetella parapertussis and Bordetella bronchiseptica.";

Nat. Genet. 35:32-40(2003).
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                                                                                                                                                                                                                                                                                                                                                                                         Borderella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=518;
                                                  Length 1044;
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Complete proteome.
SEQUENCE 1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation updat
                                                  Score 35; DB 16;
Pred. No. 1.4e+02;
1; Mismatches 3
                                                                                                                                                                                                                                                                        262 AA
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Job time : 29.8667 secs
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                                                      Query Match 67.3%;
Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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Q7WNB7
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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Abb80560 H
Abb80527 H
                       Abb80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80555 RABB80550 RABB80550 RABB80550 RABB80550 RABB80555 RABB8055 RABB805 RABB805 RABB805 RABB805 RABB805 RABB805 RABB805 RABB805 RA
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(c) 1993 - 2004 Compugen Ltd.
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RESULT 4

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Query Match Best Local Similarity

Sequence 11 AA;

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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virucide.
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                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31
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                                                                                                                                                                    note= "N-terminal acetyl"
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORV-) CORVAS INT INC
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Modified-site
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activity usefu
                                                                                                                                                                                                                                                                                      Modified-site
                                                                                 08-OCT-2002
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Gaps

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Synthetic

(first entry)

08-OCT-2002

ABB80551;

ESULT 5

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Length 11; 1; Indels

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Misc-difference
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                                                       /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) proctease inhibitory activity. The peptides of the invention are alpha *ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Norvaly1 carbony1 forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide,
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
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Pred. No. 0.02;
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                                     'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "N-terminal acetyl"
                                                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                 'note= "D-form residue"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                       Brunck TK;
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Best Local Similarity 90.5
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                                                                                                                                                                                                                                                                                                                                                                                                       Levy OE,
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                                                                                                               Misc-difference
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  Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                   peptide compound having hepatitis C virus protease inhibitory
ity useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22
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Pred. No. 0.02;
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                                        /note= "C-terminal amide"
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/note= "D-form residue"
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                                                                                                                                                                                                                                                                                                          Brunck TK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 65; 69pp; English.
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                               (CORV-) CORVAS INT INC
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Modified-site
                     Modified-site
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activity 1
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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
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               Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                   ABB80524 standard; peptide; 11 AA.
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                                                                                                          Claim 17; Page 65; 69pp; English
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90.9%;
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les 10, Conservative
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             Levy OE,
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                                    WPI; 2002-361643/39.
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               Lim-Wilby M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                             ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                  Gaps
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virucide.
                                                                                                                                                                                                                                                            pharmaceutical composition comprising the peptide as an active ing is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                       Score 46; DB 5; Length 11;
Pred. No. 0.02;
0; Mismatches 1; Indels
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/note= "C-terminal amide"
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                                                                                 Brunck TK;
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                                                                                                                                                                            Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; peptide; 11
           19-JUL-2001; 2001WO-US023169.
                                  21-JUL-2000; 2000US-0220101P.
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90.9%;
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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                                                       (CORV-) CORVAS INT INC
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                                                                                                      WPI; 2002-361643/39.
                                                                                  Levy
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                                                                                                                                                                                                                                                                                                  Sequence 11 AA;
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                                                                                                                              Novel peptide
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                                                                              Lim-Wilby M,
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
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virucide.
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Pred. No. 0.02;
0; Mismatches 1; Indels
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Sequence 11 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                        Matches
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                                    The sequence represents a peptide compound of the invention having the peptides of virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmacceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #13.
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                                                                                                                                                                                    Score 46; DB 5; Length 11;
Pred. No. 0.02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note≂ "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               ABB80533 standard; peptide; 11 AA.
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             Claim 17; Page 64; 69pp; English
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                                                                                                                                                                                    92.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residue 7º
                                                                                                                                                                                                  Local Similarity 90.3
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                                                                                                                                                         Sequence 11 AA;
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                        Gaps
                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         btide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C ^{\circ}
                                                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9
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Length 11;
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                          Mismatches
                                                                                                                                                                                                                                                                                                                                  note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "D-form residue"
Score 46;
Pred. No.
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                                                                                                                                       ABB80529 standard; peptide; 11 AA.
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92.0%;
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                        10; Conservative
                                                 EEVVPXGXDYS 11
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                                                                        EEVVPXGGDYS
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Query Match
Best Local Similarity
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Matches 10; Conserv
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketocamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C '
                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                'note= "D-form residue"
                                                                                                                                                                                                               Location/Qualifiers
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ABB80538 standard; peptide; 11 AA.
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                                                              (first entry)
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                 Misc-difference
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Modified-site
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                               ABB80538;
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ABB80562
ID ABB8
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                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Norvaly1 carbony1 forming keto-amide linkage with
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                                                                                                                                                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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Pred. No. 0.02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                  note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "D-form residue"
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                                                                                                                             ABB80528 standard; peptide; 11 AA.
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                                     EEVVPXGMDYS 11
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              EEVVPXGXDYS
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Best Local Similarity
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Gaps

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Length 11; 1; Indels

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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.

Best Loc Matches

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The sequence represents a peptide compound of the invention having the peptides of the peptides of the peptides of the invention are alpha *ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                             /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                     'note= "N-terminal acetyl"
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                                                                                                                                                                                                'note= "D-form residue"
                                                                                                                                                                                                                         note= "D-form residue"
                                                                                                                                                                      note= "Oxymethionine"
                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 Brunck TK;
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                                                 Synthetic
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Gapa ö Score 46; DB 5; Length 11; Pred. No. 0.02; 0; Mismatches 1; Indels 92.0%; 90.9%; Query Match
Best Local Similarity 90.9
Matches 10; Conservative

Sequence 11 AA;

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1 REVVPXGXDYS 11

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1 EEVVPXGMDYS 11

3, 2004, 11:48:24 Search completed: June Job time: 45.9333 secs

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STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IP PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
US-09-134-000C-4848
Query Match
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Sequence 76, Appl
Sequence 82, Appl
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14, Appli
43, Appli
4318, Ap
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                                                               June 3, 2004, 11:36:47; Search time 11.7333 Seconds (without alignments) 48.399 Million cell updates/sec
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1  /ogn2_6/ptodata/2/iaa/5A_COMB.pep:*
2:  /ogn2_6/ptodata/2/iaa/5B_COMB.pep:*
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5:  /ogn2_6/ptodata/2/iaa/PoTUS_COMB.pep:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-134-000C-4318
US-08-459-146-2
US-08-459-066-2
US-09-413-814-86
US-09-617-594A-2
US-08-617-594A-2
US-09-621-976-4604
US-09-621-976-4604
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US-09-134-001C-5124
US-09-830-217-14
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                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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US-09-523-263B-18
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US-08-879-995A-1
US-09-215-096-1
                                                                                                                                                                          389414 segs, 51625971 residues
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                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                     US-09-909-164-45
50
                                                                                                                         1 EEVVPXGXDYS 11
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Match Length DB
                                                                                                                                             Scoring table:
                                                                                                       litle:
Perfect score:
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                                                                                                                         Sequence:
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                                                                 Run on:
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Sequence 4848, Application US/09134000C

Sequence 4848, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR PAPLICATION NUMBER: US 60/055,778

PRIOR PAPLING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NO 4848

LENGTH: 181

LENGTH: 181
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                                    sequence seq
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TILLS OF INVENTION: HUMANISED ANTIBODIES
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSE: No GEB0377ris, LLP
STREET: One Liberty Place - 46th Floor
                                                                        US-09-093-448-1
US-09-093-448-2
US-09-093-448-3
US-09-813-555-1
US-09-813-555-2
US-09-813-555-2
US-09-813-555-3
US-09-523-263B-4
US-09-523-263B-17
US-09-523-263B-17
US-09-252-991A-22164
US-09-294-272-10
US-08-429-054A-11
US-08-718-777-7
JS-09-252-991A-25088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-051-341-7
US-09-394-272-8
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US-08-569-147-76
US-08-569-147-76
Sequence 76, Application US/08569147
Patent No. 6180377
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT

ORGANISM: Enterococcus faecalis
US-09-134-000C-4848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 70.0
Matches 7; Conservative
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1068
1068
1068
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us-09-909-164-45.rai

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ORGANISM: Staphylococcus aureus US-09-830-217-14
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55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.0
Lac 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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                                                                  122 VVPTGFDY 129
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US-09-830-217-14
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COUNTRY: U.S.A.

ZIP: 19103
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,147
FILING DATE: 25-March-1996
JCLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yacko
REGISTRATION NUMBER: 35,719
REPERENCE/DOCKET NUMBER: 35,719
REPUBLICE/DOCKET NUMBER: 35,71
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/569,147
FILLING DATE: 25-March-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INNORMATION:
    NAME: Trujillo, Doreen Yatko
    REGISTRATION NUMBER: 35,719
    REPERENCE/DOCKET NUMBER: 35,719
    REPERENCE/DOCKET NUMBER: GARP-0047
    TELECOMMUNICATION INFORMATION:
    TELECHONE: (215) 568-3100
    TELECHONE: (215) 568-3100
    INFORMATION: POR SEQ ID NO: 76:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.0%; Score 33; DB 3; Length 140; 75.0%; Pred. No. 24; 1.1ve 0; Mismatches 2; Indels
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Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 82. Application US/08569147
Fatent No. 6180377
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6180377ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-147-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserva
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340 Kingsland Street

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Sequence 4318, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICATY: Lynn boucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BATE: 02796-032

CURRENT FILING DATE: 1998-08-13

CURRENT FILING DATE: 1998-08-13

FRIOR PAPLICATION NUMBER: US 60/055,778

FRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 4318

LENGTH: 303
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                 APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Ronald V.
APPLICANT: Peldman, Robert A.
APPLICANT: Peldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP. 002A
CURRENT APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PastSEQ for Windows Version 3.0
SSC TANKE: PastSEQ for Windows Version 3.0
LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (2). [(2)]
; OTHER INFORMATION: Amino acid 2 is Xaa wherein Xaa = any amino acid. US-09-134-000C-4318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.0%; Score 32; DB 4; Length 3472; 45.5%; Pred. No. 1.5e+03; Live 3; Mismatches 3; Indels
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APPLICANT: Choi, Gil Ho
APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION: Hypovirulence
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.0%; Score 31; DB 4; Length 303; Best Local Similarity 40.0%; Pred. No. 1.5e+02; Matches 4; Conservative 3; Mismatches 3; Indels
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Patent No. 5866405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|:| :|
2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 45.5
nes 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGXDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-408-020-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Gaps
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Fatent No. 5832642

GENERAL INFORMATION:
APPLICANT: Choi, Gil Ho
APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Hypovirulence
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: 3
CORRESPONDENCE ADDRESSE: George M. Gould, Esq., Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITT: Nutley
STATE: Nusley
COUNTRY: U.S.A.
ZITE: O'110

COUNTRY: U.S.A.
ZITE: PO'110

COUNTRY: FRAAABLE FORM:
MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1, Indels
                                                                        "MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,146
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,117
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, CAPPACION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,065
FILING DATE: 02-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Endothia parasitica (Cryphonectria ORGANISM: parasitica)
STRAIN: EP713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 2;
Fred. No. 3.3e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                          NAME: ROSEMEN, Catherine R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 34,240
TELECOMMUNICATION INFORMATION:
TELEPAK: (201) 235-6208
TELEPAK: (201) 235-3500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 622 amino acida
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 62.0
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-JUN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
STREEL. Nutley CITY: New Jersey CTATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 EEVVPAG 37
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                                                COUNTRY: U
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STRAIN:
US-08-459-146-2
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Sequence 2, Application US/09617594A

Patent No. 6541458

GENERAL INFORMATION:
FINERMATION:
FINERMATION:
FILE REPRENCE: 444313-151.1

FILE REPRENCE: 445431-315.1

CURRENT APPLICATION NUMBER: 05/09/617,594A

CURRENT PILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/193,332

PRIOR FILING DATE: 2000-03-30

PRIOR PRIING DATE: 2000-02-11

PRIOR APPLICATION NUMBER: France 00 01761

PRIOR PRILING DATE: 1999-07-16

NUMBER OF SEQ ID NOS: 26

SEQ ID NOS: 26

SEQ ID NO 2

LENGTH: 669
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4.5e+02;
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Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: VAN DER OSTEN, CLAUS
APPLICANT: HALKIER, TORDEN
APPLICANT: HALKIER, TORDEN
APPLICANT: BAUDITZ, DETER
APPLICANT: BAUDITZ, PETER
APPLICANT: HANSEN, PETER RAMP
ITILE OF INVENTION: PROTEAGE VRIIANTS AND COMPOSITIONS
ITILE OF INVENTION: PROTEAGE 1997, 908/963,851
CURRENT FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FALLEGO FOR WINDOWS VERSION 3.0
SEQ ID NO 14
LENGTH: 59
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CURRENT APPLICATION NUMBER: US/09/621,976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08963851 Patent No. 6300116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Enterococcus faecalis
US-08-963-851-14
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Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Feline calicivirus
US-09-617-594A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 EELTPAG-DYS 437
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US-09-621-976-4604
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APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Brever, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Bloecker, Helmut
APPLICANT: Bloecker, Helmut
APPLICANT: Hooly Faul M
APPLICANT: Goldberg, Steven L
APPLICANT: Mueller, Joachim
APPLICANT: Metler, Joachim
APPLICANT: Heichenbach, Hans
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: POT/US 99/23535
CURRENT APPLICATION WUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
FILE REFERENCE: POS: 107
SARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOUTHARE: PATENTION: HOWER: DE 198
SEQ ID NOS: 107
SEQ ID NO 96
FURNIT HOUSE
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Pred. No. 4e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.0%; Score 31; DB 2; Length 622; 85.7%; Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Endothia parasitica (Cryphonectria ORGANISM: parasitica)
STRAIN: EP713
US-08-459-065-2
         APPLICATION NUMBER: US 07/832,117
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROSSEMBA, CATHERINE R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8899
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-6208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 86, Application US/09413814 Patent No. 6225064 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT CRGANISM: Sorangium cellulosum US-09-413-814-86
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Best Local Similarity 62.5
---nhes 5; Conservative
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Matches 6; Conservative
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Gaps

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RESULT 11 US-09-617-594A-2

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EARLIER FILING DATE: 1998-03-12
ERALIER PELING DATE: 1998-03-12
ERALIER APPLICATION NUMBER: 60/040,762
ERALIER PILING DATE: 1997-03-14
ERALIER PILING DATE: 1997-03-14
ERALIER PILING DATE: 1997-03-14
ERALIER PILING DATE: 1997-03-30
ERALIER PILING DATE: 1997-05-30
ERALIER FILING DATE: 1997-05-30
ERALIER FILING DATE: 1997-05-30
ERALIER FILING DATE: 1997-05-30
ERALIER FILING DATE: 1997-06-30
ERALIER FILING DATE: 1997-06-30
ERALIER PILING DATE: 1997-06-05
ERALIER APPLICATION NUMBER: 60/048,970
ERALIER PILING DATE: 1997-06-05
ERALIER PILING DATE: 1997-06-05
ERALIER PILING DATE: 1997-06-05
ERALIER PILING DATE: 1997-01-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Pred. No. 83;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                           Query Match 60.0%; Score 30; DB 4; Length 120; Best Local Similarity 50.0%; Pred. No. 82; Matches 5; Conservative 2; Mismatches 3; Indels
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WE-COLUT 14

US-09-152-060-68

Sequence 68, Application US/09152060

Partent No. 6448230

Partent No. 6448230

Partent No. 10448230

APPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REPERENCE: P7003P1.US

CURRENT APPLICATION NUMBER: US/09/152,060

CURRENT APPLICATION NUMBER: D71/US98/04858

ERALIER APPLICATION NUMBER: 06/040,762

ERALIER FILING DATE: 1998-03-14

ERALIER FILING DATE: 1997-03-14

ERALIER FILING DATE: 1997-03-14

ERALIER FILING DATE: 1997-03-16

ERALIER APPLICATION NUMBER: 60/040,710

ERALIER PILING DATE: 1997-05-30

ERALIER PILING DATE: 1997-05-30

ERALIER FILING DATE: 1997-05-30

ERALIER FILING DATE: 1997-05-30

ERALIER FILING DATE: 1997-05-30

ERALIER FILING DATE: 1997-05-30

ERALIER PILING DATE: 1997-12-19
           2000-07-21
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CURRENT FILING DATE: 2000-C
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4604
LENGTH: 120
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-09-621-976-4604
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LOCATION: (67)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FRATURE:
                                                                                                LOCATION: (89)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                      60.0%; Score 30; DB 4; Length 121; 85.7%; Pred. No. 83; ive 0; Mismatches 1; Indels
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                      NAME/KEY: SITE
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Sequence 85, Application US/09152060
Setent No. 6448230
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REPERENCE: PZ003P1.US

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RESULT 15 US-09-152-060-85

us-09-909-164-45.rapb

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                         June 3, 2004, 11:57:42 ; Search time 33.7333 Seconds
(without alignments)
91.741 Million cell updates/sec
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Sequence 40,
Sequence 41,
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUBL.pepp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-12
US-09-909-164-13
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                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seg length: 200000000
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1 EEVVPXGXDYS 11
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Perfect score:
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Maximum DB
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ALIGNMENTS

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Sequence 31, Application US/09909164
; Sequence 31, Application US/09909164
; Publication No. US20020068702A1
; Deblication No. US20020068702A1
; GENERAL INFORMATION:
    APPLICANT: Corvas International, Inc.
    APPLICANT: Lim-Wilby, Marguerita
    APPLICANT: Brunck, Terence K
    TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
    TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
    TITLE OF INVENTION NUMBER: US/09/909,164
    CURRENT PEPLICATION NUMBER: 60/220,101
    PRIOR FILING DATE: 2000-07-21
    NUMBER OF SEQ ID NOS: 62
    SOFTWARE: Patentin Version 3.1
    SEQ ID NO 31
    LENGTH: 11
    LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEX: MISC_FEATURE
LOCATION: (6)...(6)
CTHER INFORMATION: norvaline-(CO)
US-09-909-164-31
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
  US-09-909-164-31
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DB 12; Length 11;

94.0%; Score 47;

Query Match

Sequence

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US-UY-DUY-184-40
| Sequence 40, Application US/09909164
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Corvas International, Inc.
| APPLICANT: Levy, Odile E
| APPLICANT: Levy, Odile E
| APPLICANT: Levy, Odile E
| TILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
| TILE REFERENCE: IN01192-US
| CURRENT FILING DATE: 2003-03-25
| PRIOR APPLICATION NUMBER: 60/220,101
| PRIOR PLING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: PATENTIAL OF ACTION OF A
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                                                                                                                                                                                                                     OTHER INFORMATION: 11-mer synthesized according to example 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 12; Length 11;
Pred. No. 0.0049;
0; Mismatches 1; Indels
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MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: norvaline-(CO)
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NAME/KEY: NISC FEATURE

LOCATION: (9)...(9)

CTHER INFORMATION: D-amino acid
US-09-909-164-35
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THER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                      NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
                 SOFTWARE: Patentin version 3.1 SEQ ID NO 35 LENGTH: 11
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Best Local Similarity 90.9%;
Matches 10; Conservative (
                                                                                                                                   TYPE: PRT
ORGANISM: artificial sequence
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NAME/KEY: MOD RES
LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
FEATURE:
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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NUMBER OF SEQ ID NOS: 62
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US-09-909-164-32
Sequence 32, Application US/09909164
Fublication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
ITILE OF INVENTION NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
LEGGTH: 11
LEMETH: 11
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Sequence 35, Application US/09909164
Sequence 35, Application US/09909164
Sequence 35, Application No. US20020068702A1
Sublication No. US20020068702A1
Sublication No. US20020068702A1
APPLICANT: Lim Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PILING DATE: 2000-07-21
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                                       0; Gaps
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Pred. No. 0.0049;
0; Mismatches 1; Indels
   Pred. No. 0.0049;
0; Mismatches 1; Indels
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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; LOCATION: (9)...(9)
; OTHER INFORMATION: D-amino acid
US-09-909-164-32
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: artificial sequence
   Best Local Similarity 90.9%;
Matches 10; Conservative
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OTHER INFORMATION: AMIDATION
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Sequence 12, Application US/09909164

Sequence 12, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile B
APPLICANT: Loure B
APPLICANT: Levy, Odile B
APPLICANT: NUMBER: 00/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Version 3.1
SEQ ID NO 12
LENGTH: 11
APPE: PATENT: Levy CONTANT: Levy CO
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FRATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(1)
FRATURE:
PEATURE:
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CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 8
LENGTH: 11
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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NAME/KRY: MISC_FEATURE
LOCATION: (9)..(9)
OTHER INFORMATION: D-amino acid
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OTHER INFORMATION: ACETYLATION
FEATURE:
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ORGANISM: artificial sequence
FEATURE:
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.5
Matches 10; Conservative
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NAME/KEY: MOD_RES
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Sequence 41, Application US/09903164

Publication No. US2002068702A1

Publication No. US2002068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wibby, Marguerita

APPLICANT: NUMBER: US/09/909,164

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

LENGTH: 11

LENGTH: 11
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Odile E
APPLICANT: Brunck TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
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94.0%; Score 47; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                                            Score 47; DB 12; Length 11;
Pred. No. 0.0049;
                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (6). (6) COTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: MISC_FEATURE
; LOCATION: (8)..(9)
; OTHER INFORMATION: D-amino acids
US-09-909-164-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD_RES
LOCATION: (1) .. (1)
OCHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11) .. (11)
FEATURE:
                 ; OTHER INFORMATION: D-amino acid JS-09-909-164-40
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                                                                                                                Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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us-09-909-164-45.rapb

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Sequence 18 Application US/09909164
; Sequence 18 Application US/09909164
; bublication No. US20202068702A1
; GENERAL INFORMATION:
    APPLICANT: Corvas International, Inc.
    APPLICANT: Law.Wilby, Warguerita
    APPLICANT: Levy, Odile E
    APPLICANT: Levy, Odile E
    APPLICANT: Levy, Odile E
    APPLICANT: NOVEL PEFTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
    TITLE OF INVENTION: NOVEL PEFTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
    TITLE OF INVENTION: NUMBER: 06/220,101
    PRIOR APPLICATION NUMBER: 60/220,101
    PRIOR APPLICATION NUMBER: 60/220,101
    PRIOR APPLICATION NUMBER: 60/220,101
    PRIOR PRILING DATE: 2000-07-21
    NUMBER OF SEQ ID NOS: 62
    SOFTWARE: Patentin version 3.1
    SEQ ID NOS: 62
    SOFTWARE: PATENTE IN TYPE: PRI
    TYPE: PRI
    TYPE: PRI
    TYPE: PRI
    TYPE: PRI
    TYPE: PRI
    SEQ CONSANISM: artificial sequence
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATCHIN VEYEGON 3.1
SEQ ID NO 17
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92.0%; Score 46; DB 12;
Best Local Similarity 90.9%; Pred. No. 0.008;
Matches 10; Conservative 0; Mismatches 1
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; OTHER INFORMATION: norvaline-(CO)
US-09-909-164-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
LOCATION: (1). (1)
OTHER INFORMATION: ACETYLATION
PEATURE:
NAME/KEY: MOD RES
LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
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THER INFORMATION: D-amino acid
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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NAME/KEY: MISC_FEATURE
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LOCATION: (11)..(11)
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US-09-009-164-13

US-09-909-164-13

US-09-909-164-13

US-09-909-164-13

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Cim-wilby, Marguerita

APPLICANT: Lim-wilby, Marguerita

APPLICANT: Lim-wilby

APPLICAN
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OTHER INFORMATION: 11-mer synthesized according to example 1
                                                                                                                                                                                                                                                  Score 46; DB 12; Length 11; Pred. No. 0.008;
                                                                                                                                                                                                                                                                                                                         1; Indels
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Pred. No. 0.008
0; Mismatches
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Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
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NAME/KEY:
NAME/KEY:
NAME/KEY:
(6)..(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (1)..(1)
LOCATION: (1)..(1)
PEATURE: NFORMATION: ACETYLATION
PEATURE: LOCATION: (11)..(11)
OCHER_INFORMATION: AMIDATION
           OTHER INFORMATION: norvaline-(CO)
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                                         FEATURE:
NAME/ERE:
LOCATION: (8). (8)
OTHER INFORMATION: D-amino acid
US-09-909-164-12
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ORGANISM: artificial sequence
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Best Local Similarity 90.5
Matches 10; Conservative
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Sequence 27, Application US/0909164

| Sequence 27, Application US/0909164
| Publication No. US20020068702A1
| Publication No. US20020068702A1
| APPLICANT: Lim-Wilby, Marguerita
| FILE REPRENCE: INVINIA-US
| CURRENT PRING DATE: 2000-07-21
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SEQ, ID NO 27
| Lim-Wilby, Marguerita
| Lim-Wilby, M
          APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRENCACE: INOLID3-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PELING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 11
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Pred. No. 0.008;
0; Mismatches 1; Indels
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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NAME/KEY: MOD_RES
LOCATION: (1) .. (1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative
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NAME/KEY:
MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FEATURE:
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Levy, 'Odile E
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NAME/KEY: MISC FEATURE
LOCATION: (8). (8)
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Sequence 22, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FURRENT PEPERENCE: IND132-US
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
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OTHER INFORMATION: 11-mer synthesized according to example 1
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Best Local Similarity 90.9%; Pred. No. 0.008;
Matches 10; Conservative 0; Mismatches
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Best Local Similarity 90.9%; Pred. No. 0.008;
Matches 10; Conservative 0; Mismatches
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                                                   NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
COTHER INFORMATION: norvaline-(CO)
US-09-909-164-18
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: D-amino acid
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NAME/KEY: MOD RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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OTHER INFORMATION: AMIDATION
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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LENGTH: 11
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US-09-909-164-46

Sequence 46, Application US/09909164

Sequence 46, Application US/09909164

Sequence 46, Application US/09909164

Sequence 46, Application No. US20020068702A1

SEQUENCE 1 Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

SETTE OF INVENTION: NOWER: US/09/909,164

CURRENT FILING DATE: 2000-07-21

SUMMER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3:1

SEQUENCE: AND NOS: 62

SOFTWARE: Patentin version 3:1
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ORGANISM: artificial sequence
PEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
PEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(11)
OTHER INFORMATION: AMIDATION
OTHER INFORMATION: AMIDATION
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Job time: 34.7333 secs
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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OTHER INFORMATION: D-amino acids
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COTHER INFORMATION: Met(0)
US-09-909-164-46
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NAME/KEY: MISC_FEATURE
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US-09-909-164-45
US-09-909-164-45
Sequence 45, Application US/09909164
Sequence 45, Application US/09909164
Sequence 45, Application No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TILLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINB PROTEASE INHIBITORS OF HEPATITIS C
TILLE REPRENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 45
LENGTH: 11
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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92.0%; Score 46; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                              Score 46; DB 12; Length 11; Pred. No. 0.008;
                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                      | FEATURE | MISC FEATURE | MAMEKEY: MISC FEATURE | LOCATION: (6) ... (6) | OTHER INFORMATION: norvaline-(CO) | FEATURE | NAME/KEY: MISC_FEATURE | LOCATION: (8) ... (9) | OTHER INFORMATION: D-amino acids | US-09-909-164-27
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NAME/KEY: MISC FEATURE

LOCATION: (8)..(8)

FOTHER INFORMATION: D-amino acid

FEATURE:

NAME/KEY: MISC_FEATURE

COCATION: (8)..(8)

COCATION: (8)..(8)

US-09-909-164-45
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MOD RES
LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
OTHER INFORMATION: AMIDATION
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5.1.6 Compugen Ltd.	
Gencore Version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.)M protein - protein search, using sw model

3, 2004, 11:35:47 tun on:

, Search time 9 Seconds
 (without alignments)
117.567 Million cell updates/sec

US-09-909-164-45 50 Perfect score:

1 EEVVPXGXDYS 11 scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Ainimum DB seq length: 0
Aaximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
4: pir4:* Jatabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	conserved hypothet	6-0-methylgnanine-		11	disease resistance	818		hypothetical prote	conserved hypothet	unknown protein [i	ferrisiderophore r	peptidoglycan-bind	fat facets (faf) s		thiol peroxidases	thiol peroxidases	conserved hypothet	hypothetical prote	hypothetical prote		probable alkaline	ATP-dependent DNA	probable chitinase	hypothetical prote	plastocyanin b - L		plastocyanin b pre	conserved hypothet	hypothetical prote
QI	955	AG3104	D98182	13	CD.	T48899	A42452	S54619	A96001	A96546	F82491	H87660	B49132	VKLJSI	AG1272	AH1635	AD0454	S57810	S40753	DERTCM	H72784	AF3286	D82246	T20173	500210	3825	N	I093	995
DB	2	N	N	(1	~	0	(1	N	N	N	(7	(1)	(1	Н	7	(1	7	~	~	Н	ď	7	7	N	N	N	N	(1	N
Length	363	290	290	587	906	806	102	156	247	257	394	433	2747	124	165	165	196	225	327	421	440	8	1088	15	66	155	168	196	301
* Query Match	72.0	70.0	70.0			70.0		68.0	68.0	68.0	68.0	68.0	68.0	0.99	66.0	0.99	0.99	0.99	0.99	0.99	66.0	66.0	0.99	66.0	64.0	64.0	64.0	64.0	64.0
Score	36	35	35	35	35	35	34	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	33	32	32	32	32	32
Result	:	7	m	4	Ŋ	Q	7	œ	σı	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote hypothetical prote probable hexosyltr	I-lactate dehydrog hypothetical prote tolb protein - Hae ABC transporter AT	oligopeptidase lim protein B0212.3 [i probable membrane hypothetical 367K	projectin - fruit response regulator S-adenosylmethioni conserved hypothet hypothetical prote
F84330 AH1912 G69290	G69350 T24111 F64064 E86665	H84350 G88651 F69009 T31308	T13931 A69487 H97247 B72330 F72745
0 0 H	01010101	0000	00000
307 314 357	366 425 565	632 672 1474 3472	6658 117 202 233 296
64.0 64.0	64.0 64.0 64.0	64.0 64.0 64.0 64.0	64.0 62.0 62.0 62.0 0
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3310 3310	64 64 62 64	6 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 4 4 1 ር 6 4 4 1

ALIGNMENTS

RESULT 1 D69551		100 to 10	פיילה[המפלמדה	-
COMPETAGO	INDOCTION OF	DIOCUIL AFALL	ų	77

ö Gaps Score 36; DB 2; Length 363; Pred. No. 9.1; 2; Mismatches 3; Indels 72.0%; Query Match 72.0 Best Local Similarity 54.5 Matches 6; Conservative

120 ENIVPYGIDFS 130 1 EEVVPXGXDYS 11 g ð

G-0-methylguanine-DNA methyltransferase [imported] - Agrobacterium tumefaciens (strain C c; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C; Accession: AG3104
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, L.
R; Marp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
Shauthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

Bter, E.W.

A;Tille: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Tille: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Recession: AG3104

A;Status: preliminary

A;Rotale: preliminary

A;Residues: 1-290 <KMIR>

A;Residues: 1-290 <KMIR>

A;Cross-references: GB:AE0008689; PIDN:AAL45253.1; PID:g17742937; GSPDB:GN00187

A;Experimental source: strain C58 (Dupont)

C; Genetics:

A;Gene: ada A;Map position: linear chromosome

|:: | | || 9 EDITPIGSDY 18

1 EEVVPXGXDY 10

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disease resistance protein RPP8 [validated] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C;Accession: T48898
R;McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dang
Plant Cell 10, 1861-1874, 1998
A;Title: Intragenic recombination and diversifying selection contribute to the evolutio
A;Reference number: Z24999; MUID:99030193; PMID:9811794
A;Accession: T48898
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-906 cMCD>
A;Cross-references: EMBL:AF089710; NID:g3928861; PIDN:AAC83165.1; PID:g3928862
A;Experimental source: Landaberg erecta
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Introns: 293/1; 342/1
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Vad 452

Val protein - tobacco yellow dwarf virus (strain Australia)

C; Species: tobacco yellow dwarf virus

C; Species: 15-dan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999

C; Accession: A42452

R; Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.

A; Tricle: The nucleotide sequence of the infectious cloned DNA component of tobacco yell: A; Reference number: A42452

A; Accession: A42452

A; Accession: A42452

A; Molecule type: DNA

A; Residues: 1-102 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease resistance protein rpp8 [similarity] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 0.2-Unn-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C;Accession: T48899
R;McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dang Plant Cell 10, 1861-1874, 198
A;Title: Intragenic recombination and diversifying selection contribute to the evolution A;Reference number: 224999; MUID:99030193; PMID:9811794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Gene: rpp8
A/Introns: 293/1; 342/1
C/Function:
A/Description: susceptible allele of a gene that promotes resistance to Peronospora par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-908 «MCD
A;Coss-references: EMBL:AF089711; NID:G3901293; PIDN:AAC78631.1; PID:G3901294
A;Experimental source: Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 10.0%; Score 35; DB 2; Length 906; Local Similarity 60.0%; Pred. No. 40; es 6; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Description: promotes resistance to Peronospora parasitica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |::|| | ||
881 EKLVPGGEDY 890
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883 EKLVPGGEDY 892
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C'Species: Neisseria meningitidis
C'Date: 31 Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C'Accession: F81138
R'Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; Ve A;Reference number: A81000; WUID:20178755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                O6-methylguanine-DNA methyltransferase PA2118 [imported] - Agrobacterium tumefaciens (st
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: D98182
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-587 <TET>
A;Crosi-references: GB:AE002446; GB:AE002098; NID:g7226185; FIDN:AAF41356.1; PID:g722618
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: NMB0950
C;Superfamily: fumarate reductase flavoprotein; 3-oxosteroid 1-dehydrogenase homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 25;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 70.0%; Score 35; DB 2; Length 290; Best Local Similarity 50.0%; Pred. No. 12; Matches 5; Conservative 2; Mismatches 3: Indele
                                                         Score 35, DB 2; Length 290;
Pred. No. 12;
2; Mismatches 3; Indels
                                                         Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Genetics:
A,Gene: AGR L_818
A,Map position: linear chromosome
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Best Local Similarity 70.0%;
Matches 7; Conservative
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1 EEVVPXGXDY 10 EDITPIGSDY 18

A,Status: preliminary A,Molecule type: DNA A,Residues: 1-290 <KUR> A;Accession: D98182

RESULT 5 T48898

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Ansorae in [imported] - Arabidopsis thaliana (C.) Species arabidopsis thaliana (mouse-ear cress) (C.) Accession: A96546 (M.) A.) Rocker, J. R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Huddes, B.; Hudzar, L. Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, M.; A; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Manit, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziali, A; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.B.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Reference and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ferrisiderophore reductase VCA0183 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: R82491
C;Accession: R82491
J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardeon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross references: GB: AB004358; GB: AB003853; NID: 99657566; PIDN: AAF96096.1; GSPDB: GN001
A; Experimental source: serogroup O1; strain N16961; blotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 2
C;Superfamily: flavohemoglobin; cytochrome-b5 reductase homology; globin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: AE005173; NID: g11094688; PIDN: AAG29624.1; GSPDB: GN00141
                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.0%; Score 34; DB 2; Length 257; 54.5%; Pred. No. 17; ive 2; Mismatches 3; Indels
                                                                                                                         Length 247;
                                                                                                                                                                                                 Indels
                                                                                                                         ;
;
                                                                                                                    Score 34; DB
Pred. No. 16;
1; Mismatches
                                                                                                                    68.0%;
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                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                      1 EEVVPXGXDY 10
                                                                                                                                                                                                                                                                                                                                                                            48 EDVEPRGADY 57
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Best Local Similarity
Matches 6; Conserv
                                                                                                                    Ouery Match
Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-257 <STO>
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A.Molecule type: DNA
A.Residues: 1-394 <HEI>
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A;Gene: SMb21444
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Map position: 1
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Gene: F8A12.12
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A;Molecule type: DNA
A;Cross-references: strain 1021, megaplasmid psymB
A;Experimental source: strain 1021, megaplasmid psymB
A;Experimental source: strain 1021, megaplasmid psymB
A;Experimental source: strain 1021, megaplasmid psymB
A;Cross-references: T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Palain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
A; Cocience 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Rebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A; Reference number: A96039; MUID:21368234; PMID:11474104
A;Concents: annotation
C;Genetics:
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R.Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A.Title: The complete sequence of the 1,683-kb psym8 megaplasmid from the N2-fixing endo A;Reference number: A95842; WUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cross-references: EMBL:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR01; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein, homolog to osmotically inducible sensory protein SMC22-1
C,Species: Sinorhizobium meliloti
C,Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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(Alternate names: hypothetical protein 02612; hypothetical protein YOL303.3

(Alternate names: hypothetical protein 02612; hypothetical protein YOL303.3

(Species: Saccharomyces cerevisiae

(Species: Saccharomyces cer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yeast (Saccharomyces cerevisiae)
protein O2612; hypothetical protein YOL303.3
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A;Residues: 1-156 <DEH>
A;Residues: 1-156 <DEH>
A;Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
A;de Haan, M.; Grivell, L.A.; Maarse, A.C.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66877
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    4; Cross-references: GB: M81103; NID: 9335283; PIDN: AAA47947.1; PID: 9335284
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                                                                                68.0%; Score 34; DB 2; Length 102; 60.0%; Pred. No. 6.1;
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Pred. No. 9.6;
1; Mismatches
                                                                                                                                                                      2; Mismatches
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C;Superfamily: hypothetical protein YOR013w
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                        2 EVVPXGXDYS 11
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50 EVMPLGMDY 58
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                                                                                                                             Best Local Similarity
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NiAlternate names: anti-repression trans-activator; art protein; rev protein; trs prote C, Species: simian immunodeficiency virus SIVCpZ A; Mote: bost Pan troglodytes (chimpanzee) C, Dacession: S0988 #squence_revision 30-Sep-1991 #text_change 16-Jul-1999 C, Accession: S0988 #squence not a chimpanzee lentivirus related to HIV-1. A; Reference number: S09983; MUD:90259077; PMID:2188136 A; Accession: S09988 #squence not shown; translation not shown A; Release incleic acid sequence not shown; translation not shown A; Release I-124 cHUS> C, Accession: S0988 A; 
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Grander, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke, Grander, P.; Farageul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, F.D.; Fsihi, H.D.; Jones, L.M.; Karst, U.D.; Jones, L.M.; Karst, U.D.; Jones, L.M.; Karst, U.D.; Jones, L.M.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.; Alauthors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Reference number: Alionomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
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A;Cross-references: GB:NC 003210; PIDN:CAC99661.1; PID:g16411012; GSPDB:GN00177
A;Experimental source: strain EGD-e
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Superfamily: thioredoxin peroxidase
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Conservative
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ses 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                               peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus C; Species: Caulobacter crescentus C; Species: Caulobacter crescentus C; Species: Caulobacter crescentus C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C; Accession: H87660
C; Accession: H87660
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A.Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MuID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fat facets (faf) splice form 1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 19-Dec-1933 #sequence_revision 25-Apr-1997 #text_change 01-Dec-2000
C;Accession: B49132; A49132
R;Fischer-Vize, J.A.; Rubin, G.M.; Lehmann, R.
Bevelopment 116, 985-1000, 1992
A;Title: The fat facets gene is required for Drosophila eye and embryo development.
A;Reference number: A49132; MUID:93202020; PMID:1295747
A;Contents: isogenic st
A;Accession: B49132
A;Accession: B49132
A;Accession: Breliminary
A;Molecule type: nucleic acid
A;Molecule type: nucleic 
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A;Molecule type: nucleic acid
A;Residues: 1-2704, VT', 2707, ANNV' <PI2>
A;Crose references: GB:L04958; NID:g1S7410; PIDN:AAF01346.1; PID:g6013475
A;Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:129029)
C;Keywords: alternative splicing
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A.Molecule type: DNA
A.Residues: 1-433 <STO>
A.Cross-references: GB.AE005673; NID:gl3425020; PIDN:AAK25284.1; GSPDB:GN00148
C.Genetics:
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Pred. No. 2.2e+02;
2; Mismatches 3; Indels
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8 셤 trans-regulatory splicing protein - simian immunodeficiency virus SIVcpz

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Copyright (c) 1993 - 2004 Compugen Ltd.
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EMBL, AB015468, BAB10695.1; -.
EMBL, AK17163, BAG1841.1; -.
Interpro, IPR000767; Disease_resist.
Interpro, IPR001611; LR.

RPPB/HRT subfamily.
--- SIMILARITY: Contains 3 leucine-rich (LRR) repeats.
--- SIMILARITY: Contains 1 NB-ARC domain.
--- DATABASE: NAME-MIB-LRRS.
--- DATABASE: NAME-MIB-LRRS.
NOTE-Functional and comparative genomics of disease resistance gene

homologs; WWW="http://niblrrs.ucdavis.edu".

This .

34 30 60.0 203 35 30 60.0 231 36 30 60.0 231 37 30 60.0 232 39 30 60.0 232 39 30 60.0 225 41 30 60.0 421 42 30 60.0 423 43 30 60.0 453 44 30 60.0 453 45 30 60.0 453 46 30 60.0 423 47 30 60.0 453 48 48 48 48 49 60.0 453 48 49 60.0 453 49 50 60.0 453 40 60.0 423 41 30 60.0 453 42 30 60.0 453 42 30 60.0 453 43 60.0 453 45 48 48 48 48 45 10-OCT-2003 (Rel. 42, La 11 Brasslcales 11 Brasslcales 11 Brasslcales 12 Republe 12 Republe 13 Res. 5:297-308 (1998) 14 Res. 5:297-308 (1998) 15 Republe 15 Republe 16 Republe 17 Republe 18 Republe 18 Republe 18 Republe 19 Republe 19 Republe 19 Republe 10 Republe 10 Republe 10 Republe 11 Republe 11 Republe 12 Republe 13 Republe 14 Republe 15 Republe 16 Republe 17 Republe 18 Re	P14194 bacillus su P08203 escherichia P06190 salmonella Q92183 helicobacte P56006 helicobacte P06308 lymnaea sta P38174 saccharomyc O52250 halomonas e Q92eu7 halomonas e Q05865 bacillus su O15231 homo sapien P53998 kluyveromyc	INTS	908 AA.	date) update) morenin 4		ko m. Korani H Mivalima N.,	iana chromosome 5. VII.	, Akiyama K., Ishida J., saka M., Carninci P., Kawai J.,	11. A.; 111.length cDNA."; the EMBL/GenBank/DDBJ databases. the EMBL/GenBank/DDBJ databases. ats probably act as specificity determinant of (By similarity). to the disease resistance NB-LRR family.
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STRAIN-CV. Columbia, and cv. Landsberg erecta;
MEDLINE-99030193; PubMed-9911794;
MCDLINE-99030193; PubMed-9911794;
MCDOWell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
Holub E.B., Dangl J.L.;
"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cooley M.B., Pathirana S., Wu H.J., Kachroo P., Klessig D.F., "Members of the Arabidopsis HRT/RPP8 family of resistance genes confer resistance to both viral and comycete pathogens."; plant Cell 12:663-676 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tabata S., "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                     RPP8 ARATH STANDARD;
QUWA59, QGWG51, Q9MSA1, Q9ZSY3; Q9ZSY4;
QUWA579, GGWG51, Q9MSA1, Q9ZSY3; Q9ZSY4;
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Disease resistance protein RPP8 (Resistance to Peronospora parasitica protein 8).
                                                                                                                                                                                                                        Gaps
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STRAIN=cv. Columbia;
MEDLINE=22954850; PubMed=14593172;
Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopeis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids; eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                        .
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   10 45 LEUCINE-ZIPPER.

146 459 NB-ARC.

575 599 LRR 1.

600 623 LRR 2.

842 867 LRR 3.

192 199 ATP (POTENTIAL).

908 AA; 104448 NW; 3111991B17239693 CRC64;
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SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS.
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RPP8 OR HRT OR ATSG43470 OR MWP20.19.
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MEDLINE=20271766; PubMed=10810142;
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                                                                                                                                                                                     70.0%;
InterPro; IPR002182; NB-ARC.
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DNA Res. 7:31-63(2000).
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RPP8_ARATH
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WINTERACTION WITH TIP.

WEDLINE-20496823; PubMed=11041886;

Ren T., Qu F., Morris T.J.;

REn T., Qu F., Morris T.J.;

REn T., Qu F., Morris T.J.;

RI "HRT gene function requires interaction between a NAC protein and properties to confer resistance to turnip crinkle virus.";

RI viral capial parients confer resistance to turnip crinkle virus.";

RI Plant Call 12.1917-1926(2000).

- :- FUNCTION: Disease resistance protein. Resistance proteins quard the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive contexponse, which restricts the pathogen growth. The interaction with TIP (TCV-interacting protein) may be essential for the recognition of the avirulence proteins, and the triggering of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Note=Has been shown to exist only in cv. Columbia so far;
-!- DOWAIN: The LRR repeats probably act as specificity determinant of
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J., Chan M.M., Tang C.C., Omodera C.S., Deng J.M., Akiyama K., Ansari Y., Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P., Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.P., Hayashizaki Y., Johnson-Hopson C., Hayashizaki X., Karnes M., Khan S., Koesema B., Ishida J., Jiang P.X., Jones T., Kawi J., Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Saton M., Tanse R., Wapberg M., Wallender E.K., Wong C., Yamamura Y., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., Tamamura Y., "Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOPORM 2).
SERIALNS-CV. COlumbia;
Serki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.,
"Arabidopsis thaliana [ull-length CDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
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WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome.";
Science 302:842-846(2003).
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T -> I (in cv. Di-17).
S -> R (in cv. Di-17).
S -> R (in cv. Di-17).
H -> Q (in cv. Di-17).
I -> L (in cv. Landsberg erecta).
K -> R (in cv. Landsberg erecta).
K -> N (in cv. Landsberg erecta).
PRFEEDYW -> WDEDFG (in cv. Landsberg
                                                                                                              ATP (POTENTIAL).
WRMLLTSRNEGVGIH -> ELLWYIHBALFLLNS (in
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                                                                                                                                                                                                                                                                                                               C -> R (in cv. Di-17 and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                               Landsberg erecta).

E197YS -> KITYOE (in cv. Di-17).

A -> V (in cv. Landsberg erecta).

E -> Q (in cv. Landsberg erecta).

DNYLSWQ -> NYKIRWH (in cv. Di-17).

NY -> SH (in cv. Landsberg erecta).
                                                                                                                                                                                                                                                                                                                                   erecta).
DSEISTYSLFY -> YSKISAYDLFN (in cv.
                                                                PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat;
Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                    F -> S (in cv. erecta).
                                                                                    LEUCINE-ZIPPER
EMBL; AF089711; AAC78631.1; -.
EMBL; AF234174; AAF3697.1; -.
EMBL; AB025638; BA497426.1; -.
EMBL; AX06514; AAL32592.1; -.
EMBL; AX18862; BAC4349.1; -.
InterPro; IPR001671; Disease_resist.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                          erecta).
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                                                                                           NB-ARC.
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                                                    Pfam; PF00560; LRR; 2.
Pfam; PF00931; NB-ARC; 1.
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Arabidopsis.";
Plant Cell 10:1861-1874(1998).
Liplant Cell 10:1874(1998).
Liplant Cell 10:1874(19:1874(19).
Liplant Cell 10:1874(19).
Liplant Cell 10:1874(19:1874(19)
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STRAINS.v. Landsbeege erecta,
MEDLINE-99030193; PubMed=9811794;
MCDOwell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
Hollub E.B., Dangl J.L.;
"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
PRF -> SRFK (in cv. Di-17).
Y -> F (in cv. Di-17).
S -> Y (in cv. indebberg erecta).
C -> S (in cv. Di-17 and cv. Landsberg
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mww=http://niblrrs.ucdavis.edu".

InterPro; IPR000767; Disease_resist.

InterPro; IPR000767; Disease_resist.

InterPro; IPR000161; LRR.

R pfam; PR000560; LRR; 2.

R PFINTS; PR00364; DISEASERSIST.

R PRINTS; PR00364; DISEASERSIST.

R PRINTS; PR00364; DISEASERSIST.

T DOMAIN 146 459 LECINE_ZIPPER.

T REPEAT 602 625 LRR 1.

T REPEAT 844 869 LRR 2.

T REPEAT 844 869 LRR 2.

T NP_BIND 192 199 ATP (POTENTIAL).

T NP_BIND 192 199 ATP (SIENTIAL).
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                                                                                                                                                                                              Score 35; DB 1; Length 908;
Pred. No. 18;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last ancotation update)
Disease resistance protein RPH8A (RPP8 homolog A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 910 AA.
                                                                                                                                             erecta).
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Best Local Similarity 60.0%;
Matches 6; Conservative
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883 EKLVPGGEDY 892
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Best Local Similarity
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              558
564
595
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RP8H ARATH
ID RP8H ARATH
AC P59584;
          VARIANT
VARIANT
VARIANT
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I --> K (in cv. Di-17 and cv. Landsberg
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C -> S (in cv. Di-17 and cv. Landsberg
erecta).
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ALLOSTERIC DOMAIN.

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HMPA VIBCH
Q9KMY3;
16-OCT-2001 (
16-OCT-2001 (
28-FEB-2003 (
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P31619;
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HMPA_VIBCH
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      Gaps
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CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
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PRINTS; PRODUCTS CPSASE.

TIGREAMS; TICROID69; CPSASE.

PROSITE; PSOU866; CPSASE.1; 2.

PROSITE; PSOU867; CPSASE.2; 2.

PROSITE; PSOU867; CPSASE.2; 2.

Arginine blosynthesis; Pyrimidine blosynthesis; Ligase; Repeat; Arginine blosynthesis; Complete protecome.

ATP-binding; Manganese; Complete protecome.

CARBOXPHOSPHATE SYNTHETIC DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
   Indels
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                                                                                                                                                                                                                                                               PRT; 1058 AA
   2; Mismatches
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InterPro; IPR005275; CarA L glu.
InterPro; IPR005483; CP86E.L.

InterPro; IPR005480; CP86E.L.

InterPro; IPR005481; CP86E.L.

InterPro; IPR005481; CP86E.L.

InterPro; IPR005481; CP86E.L.

Pfam; PF00289; CP886E.L.

Pfam; PF00289; CP886E.L.

Pfam; PF02786; CP886E.L.

Pfam; PF02786; CP886E.L.

Pfam; PF02786; CP886E.L.

Pfam; PF02187; CP886E.L.

Pfam; PF02187; MGS; 1.
      6; Conservative
                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                   885 EKLVPGGEDY 894
                                                           1 EEVVPXGXDY 10
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QBRG86;
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CARE_FUSNN
      Matches
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ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E., "The nuclectide sequence of the infectious cloned DNA component tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants."; virology 187:633-642(1992).
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0
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Pred. No. 22;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses, ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=92188538; PubMed=1546458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A42452; A42452.
InterPro; IPR002621; Gemini mov.
Pfam; PF01708; Gemini mov. I.
Hypotherical protein.
SEQUENCE 102 AA; 11178 MW; A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                             70.0%;
                                                                                                                                                                                          1058 AA; 117451.
                                                                                                                                                                                                                                                                      60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                                                                  2 EVVPXGXDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EVVPXGXDYS 11
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                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=31599;
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                                                                                                                                                                                         ESQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAINNEL TOT NIG561 / Serotype O1;

STRAINNEL TOT NIG561 / Serotype O1;

MEDLINE-20406833; PubMed=10952301;

MEDLINE-20406833; PubMed=10952301;

MEDGINE-20406833; PubMed=10.3. Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nalson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 406:477-483(2000).

-!- DOMAIN: CONSIGNS OF TWO DISTINCT DOMAINS; ONE IS A HEME-CONTAINING OXYGEN BINDING DOMAIN IN THE N-TERMINAL REGION AND THE OTHER IS AN FAD-CONTAINING REDUCTASE DOMAIN FOUND IN THE C-TERMINAL REGION.
-!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY. TWO-DOMAIN FLAVOHERORPOTEINS SUBFAMILY.
-!- SIMILARITY: TO A NUMBER OF FAD/NAD(P) FLAVOPROTEIN OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
IRON (HEME PROXIMAL LIGAND)
(BY SIMILARITY).
NDD (RIBOSE PART) (BY SIMILARITY)
DDA3490FAE28823A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008333; FAD_binding_6.
InterPro; IPR008333; FAD_binding_6.
InterPro; IPR00097109; FPN cyt_redctse.
InterPro; IPR0009733; Oxed FAD/NAD(P).
InterPro; IPR001221; Phe_hydroxylase.
Pfam; PF00047; FAD_binding_6; 1.
Pfam; PF00047; Pfam; PF0CR.
Pfam; PF00175; NAD_binding_1; 1.
PRINTS; PR00311; PFNCR.
PRINTS; PF00131; PFNCR.
PROSITE; PS01033; GLOBIN; 1.
Oxidoreductase; NADP; Heme; Flavoprotein; FAD; Iron transport;
   Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin).
                                                                                   Bacteria; Protechacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio. Vibrionaceae; Vibrio. Vibrionaceae; Vibrio. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.0%; Score 34; DB 1; Length 394; 66.7%; Pred. No. 13; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HEME DISTAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxygen transport; Transport; Complete proteome. DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE004358; AAF96096.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 AA; 44191 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR, F82491, F82491.
HSSP, P39662, 1CQX.
FIGR, VCA0183; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                               HMP OR VCA0183.
Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
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P55824; Q9V9T6; Q3V0Z7;
01-NOV-1997 (Rel. 35, Created)
15-MAR-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Porbable ubjquitin carboxyl-terminal hydrolase FAF (EC 3.1.2.15)
PAF (Ubjquitin thiolescerase FAF) (Ubjquitin-specific processing protease FAF) (Deubiquitinating enzyme FAF) (Wiquitin-specific processing protease FAF) (Deubiquitinating enzyme FAF) (Fat facets protein).
PAF OR BCUNA.1502283 OR CG1944.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prerygota; Neoplera; Endopteryzota; Diptera; Brachycera; Muscomorpha; NCBL TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22426069; PubMed-1257572;
Mister S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mister S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Eye imaginal disk;
MEDLINE-93202020; PubMed-1295747;
Fischer-Vize J.A., Rubin G.M., Lehmann R.;
"The fat facets gene is required for Drosophila eye and embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          development.";
Development 116:985-1000(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
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Gaps

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Conservative

2 EVVPXGXDY 10

194 EVTPEGSDY

2778 AA

STANDARD;

FAF_DROME

FAF_DROME ID FAF D RESULT 7

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TPX LISIN
Q92BC5;
28-FEB-2003 (
28-FEB-2003 (
28-FEB-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REV SIVCZ
P17280;
                                                                                                            CONFLICT
CONFLICT
SEQUENCE
                              VARSPLIC
                                                                                                                                                                                                                               Query Match
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TPX LISIN
                                                                                                                                                                                                                                                          Best Loc
Matches
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   STATETOS
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B Frient PF00443; UCH 2 1; 1.

DR PROSITE; PS00972; UCH 2 2; 1.

DR PROSITE; PS00973; UCH 2 3; 1.

DR PROSITE; PS50255; UCH 2 3; 1.

DR PROSITE; PS50255; UCH 2 3; 1.

DR PROSITE; PS50275; UCH 2 3; 1.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                 IsoId=P55824-3; Sequence=VSP_005269; TISSUE SPECITY: Eye disks and ovaries. DEVELOPMENTAL STACE: Expressed both maternally and zygotically. SIMILARITY: Belongs to peptidase family C19.
Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flyase, FBgn0005632, faf.

GO; GO:0005737, C:cytoplasm; IDA.

GO; GO:0007349; P:cellularization; IMP.

GO; GO:0007459; P:embryonic morphogeneels; IMP.

GO; GO:0007456; P:eye morphogeneels (sensu Drosophila); IMP.

GO; GO:0007939; P:mystery cell fate differentiation (sensu Dr.

GO; GO:000797; P:mystery cell fate differentiation (sensu Dr.

GO; GO:000797; P:protein deubiquitination; IMP.

GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IGI.

InterPo; FRR001394; P:eptidase_C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ubiquitin + a thiol.

LATERNATURE PRODUCTS

Event-Alternative splicing; Named isoforms=3;

Comment-Experimental confirmation may be lacking for some
                                    systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                  1089-2778 FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isold=P55824-2; Sequence=VSP_005270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [sold=P55824-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, L04959; AAF01345.1; -.
EMBL, L04958; AAF01346.1; -.
EMBL, L04960; AAF01347.1; -.
EMBL, AE003779; AAF57198.1; -.
EMBL, AE003779; AAF57198.1; -.
EMBL, AF19577; AAF57198.1; -.
EMBL, AF19677; AAF57198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       soforms;
                                                                                                                  SEQUENCE OF
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MEDINES-053077; Pubmed=2188136;
MEDINES-053077; Pubmed=2188136;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-135910.

-1- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
-1- SUBCELLIAGAR LOGATION: Nuclear; accumulates in the nucleoli.
-1- PTM: Phosphoprotein whose state of phosphorylation is mediated by
a specific serine kinase activity present in the nucleus.
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
/FTId=VSP_005269.
IATAATLBPĀGMSELTTMVEKNLIISQENPQAKSSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X52154; CAA36405.1; -.
PIR; S09988; VKLJSI.
HIV; X52154; REVSCPE.
InterPro; IPR000625; REV_protein.
Pfam; PF00424; REV; 1.
Transcription regulation; AIDS; Phosphorylation; Nuclear protein.
SEQUENCE 124 AA; 13701 MW; FS877DIBDF65A7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FBB-2003 (Rel. 41, Last amnotation update)
REV protein (Anti-repression transactivator protein) (ART/TRS).
                                                                                                                                                                                                                                                                            ;
0
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                                                                                                                                                                                                                 Score 34; DB 1; Length 2778;
Pred. No. 97;
2; Mismatches 3; Indel8
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Pred. No. 6.2;
1; Mismatches 3; Indels
                                                     Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11723,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.0%;
                                                                                                                                                                                                                    / Match 68.0%;
Local Similarity 54.5%;
Les 6; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.v.,
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                 1394 EVIVPDGODFS 1404
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                                                                                                                                                                                                                                                                                                                                 1 EEVVPXGXDYS 11
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MEDLINE=94150718; PubMed=7906398;
MEDLINE=94150718; PubMed=7906398;
MEDLINE=94150718; PubMed=7906398;
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Claxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Fahih H., Garcia-del Portillo F., Garrido P., Jackson D., Jones L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Matlournam A., Mata Vicente J., Ny E., Noedjari H., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vossell R., Vorgarative genomics of Listeria species.", Consart P., Comparative genomics of Listeria species.", Science 294:849-852(2001)
-!- FUNCTION: Has antioxidant activity. Could remove peroxides or H(2)0(2) (By similarity).
-!- SIMILARITY: Belongs to the abpC/tsa family. Tpx subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antioxidant, Oxidoreductase, Peroxidase, Complete proteome.
SEQUENCE 165 AA; 18133 MW; 77705B7CC46D424D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 66.0%; Score 33; DB 1; Length 165; Local Similarity 66.7%; Pred. No. 8.4; es 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C15H7.4 in chromosome III.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL591979; CAC99661.1; -. PIR; AG1272; AG1272. Listilist; LMO01583; -. HAMAP; MF 00269; -1 1. InterPro; IPR002066; AhpC-TSA. InterPro; IPR002065; TPX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00578; AhpC-TSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 EVVPEGSDH 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EVVPXGXDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00578; Ah
PROSITE; PS01265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YK14 CAEEL
P34338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elegans.
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Matches
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           PACOCCO OD THE STANT OF THE STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the burpopan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-CLIP 11262 / Serovar 6a;

STRAIN-CLIP 11262 / Serovar 6a;

STRAIN-CLIP 11262 / Serovar 6a;

MEDLINE-21537279; PubMed=11679669;

A Glaser P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,

A Glaser P., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jussurget O.,

Brian K.-D., Fshi H., Gomez-Lopez N., Hain T., Hauf J., Jussurget O.,

Charbit C., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jussey G.,

A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jussey G.,

Madueno E., Maicournam A., Mata Vicente J., Kubr M., Kurnsk F., Kurzpkat G.,

Mordsiek G., Novellas A., Mata Vicente J., Simoes N., Tierrez A.,

Nordsiek G., Novellas A., Weshland J., Cossart P.,

Comparative genomics of Listeria species.",

Science 294:894-852(2001).

Science 294:894-852(2001).

Science 294:894-852(2001).

C. I. SIMILARITY: Belongs to the ampC/tsa family. Tpx subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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MEDLINE=21537279; PubMed=11679669;
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Glaser P., Teangeul L., Bocker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antioxidant; Oxidoreductase; Peroxidase; Complete proteome.
SEQUENCE 165 AA; 18162 MW; 77705B7CD9BC8F4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.0%; Score 33; DB 1; Length 165; 66.7%; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable thiol peroxidase (EC 1.11.1.).
Listeria monocytogenes.
Listeria monocytogenes.
Bacteria monocytogenes, Bacillales, Listeriaceae, Listeria.
NCBI_TaxID=1639;
                                                                                                                 Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 AA
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       Probable thiol peroxidase (EC 1.11.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ListLiist; LINO1625; -.
HAMAP; MF_00269; -; 1.
InterPro; IPR000866; AbpC-TSA.
InterPro; IPR002065; TPX.
Pfam; PF00578; AbpC-TSA; 1.
PROSITE; PS01265; TPX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL596169; CAC96856.1; -. PIR; AH1635; AH1635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.78;
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                          Listeria innocua.
                                                                                                                                                    NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPX LISMO
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RESULT 10 TPX_LISMO

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               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED custstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
28-78B-2003 (Rel. 41, Last annotation update)
48-71-CoA dehydrogense, medium-chain specific, mitochondrial precursor (EC 1.3.99.3) (MCAD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Homotetramer.
SUBUNITLUTAR LOCATION: Mitochondrial matrix.
SUBCELLANBOUS: A number of straight-chain acyl-CoA dehydrogenases of different substrate specificities are present in mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101. Chem. 262:10104-10108(1987).
FUNCTION: This enzyme is specific for acyl chain lengths of 4 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87280028; PubMed=3611054; Mateubara Y., Kraus J.P., Ozasa H., Glassberg R., Finocchiaro G., Ikeda Y., Mole J., Rosenberg L.E., Tanaka K.; "Mole J., Rosenberg L.E., Tanaka K.;" "Mole Coning and nucleotide sequence of cDNA encoding the
                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
                                                                                                                                                                                                                                                                                                     Score 33; DB 1; Length 327;
Pred. No. 17;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entire precursor of rat liver medium chain acyl coenzyme A
                                                                                                                                                                                               PIR; S40753; S40753.
WormPep; C15H7.4; CE00082.
Hypothetical protein.
SEQUENCE 327 AA; 35566 MW; 716BC2BDD2E9607E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chem. 262:10104-10108(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                EMBL; Z22173; CAA80126.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J02791; AAA40670.1; -.
PIR; A28436; DERTCM.
                                                                                                                                                                                                                                                                                                        Query Match 66.0%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGXDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P11310; 1EGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: FAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dehydrogenase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=SSI-1 / Serotype M3;
MEDLINE=22683278; PubMed=12799345;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Nakagawa I., Kawabata S., Yamasaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
                                                                                                                                                                                                                ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN
SPECIFIC.
FORMS A HYDROGEN-BOND WITH THE FLAVIN
N(5) OF THE FAD COFACTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
ARGS OR SPYM3_1809 OR SPS1807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MGAS315 / Serotype M3;
MEDIINE=2133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlitevert P.M., Musser J.M.,
Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            into phage evolution.";

Genome Res. 13:1042-1055(2003).

Genome Res. 13:1042-1055(2003).

-1- CATALYTC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +

diphosphate + L-arginyl-tRNA(Arg).

-1- SUBUNIT: Monomer (By similarity).

-1- SUBCELULAR LOCATION: Cytoplassmic.

-1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                              ..
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R InterPro; IPR006089; Acyl-CoA dh.
R InterPro; IPR006099; Acyl-CoA_dh_C.
R InterPro; IPR006091; Acyl-CoA_dh_M.
R InterPro; IPR006092; Acyl-CoA_dh_M.
R Pfam; PP00441; Acyl-CoA_dh; 1.
R Pfam; PP00771; Acyl-CoA_dh; 1.
R Pfam; PP00771; Acyl-CoA_dh M; 1.
R PROSITE; PS00073; Acyl-CoA_Dh 1; 1.
R PROSITE; PS00073; Acyl-CoA_Dh 1; 1.
R Mitchcantage; FlavoproteIn; FAD; Patty acid metabolism; Mitchchodrion; Transit peptide.
R MITCCHONDRION.
                                                                                                                                                                                                                                                                                                                                       Score 33; DB 1; Length 421;
Pred. No. 22;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus_pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                         2CF076F8C919BDE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 AA
                                                                                                                                                                                                                                                                                                         46555 MW;
                                                                                                                                                                                                                                                                                                                                            66.08;
                                                                                                                                                                                                                                                                                                                                                           50.08;
                                                                                                                                                                                                                                                                                                                                                           Local Similarity 50.0
                                                                                                                                                                                                                                                        193
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                                                                                                                                                                                                                                                                                            401
                                                                                                                                                                                                                                                                                                           421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=198466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
                                                                                                                                                                                                                                                        193
                                                                                                                                                                                                                                                                                            401
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SEQUENCE
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us-09-909-164-45.rsp

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                                                                                                                                                                                                                                                      EMBL; AE014171; AAM80416.1; -.

R EMBL; AP0015146; BAC64902.1; -.

R HAMAPP MF 00123; -; 1.

R InterPro; IPR001278; Arg_tRNA-synt_1c.

R InterPro; IPR001248; Nag_tRNA-synt_1d_C.

InterPro; IPR001412; tRNA-synt_1d_C.

InterPro; IRR001412; tRNA-synt_1d_1.

R Pfam; PF00750; tRNA-synt_1d; 1.

R Pf00750; tRNA-synt_1d; 1.

R Pf00750; tRNA-synt_1d; 1.

R Pf00750; tRNA-synt_1d; 1.

R Pf00750; tRNA-synt_1d;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SITE 121 131 "HIGH" REGION.
SEQUENCE 563 AA; 63134 MW; B0B7DEC31A9DCF63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
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0; Gaps Query Match 66.0%; Score 33; DB 1; Length 563; Best Local Similarity 45.5%; Pred. No. 30; Matches 5; Conservative 3; Mismatches 3; Indels |:|: | ||: 94 EQVITAGSDYA 104 1 EEVVPXGXDYS 11 셤

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STRPB

PRT; 563 AA.

28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginyl--FRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
ARGS OR SPYM18_2183. Streptococcus pyogenes (serotype M18). Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; STANDARD; Streptococcus. NCBI_TaxID=186103; RESULT 14
SYR STRP8
DT 28-FED
DT 28-

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=MGASS232 / Serctype M18;

STRAIN=MGASS232 / Serctype M18;

STRAIN=MGASS232 / Serctype M18;

STRAIN=MGASS232 / Serctype M18;

A MEDLINE=21927533; PubMed=11917108;

Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,

A Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,

Kapur V., Daly J.A., Vasy L.G., Musser J.M.,

"Genome sequence and comparative microarray analysis of serctype M18

"Genome sequence and comparative microarray analysis of serctype M18

"Group A Streptococcus strains associated with acute rheumatic fever

"The couple of the sequence of the seque

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EMBL; AE010119; AAL98627.1; -. HAMAP; MF_00123; -; 1.

ö InterPro; IPR001278; Arg_tRNA-synt_lc.
InterPro; IPR005148; N.
InterPro; IPR005909; tRNA-synt_ld_C.
InterPro; IPR0019412; tRNA-synt_ld_C.
InterPro; IPR001412; tRNA-synt_ld_C.
Pfam; PF00748; N-Arg; 1.
Pfam; PF00748; tRNA-synt_ld; 1.
Pram; PF00748; tRNA-synt_ld; 1.
PRINTS; PR01038; TRNASYNTHARG.
TIGRRO465; args; 1.
PR057178; PS00178; AA TRNA, LIGARE I; FALSE NEG.
Aminoacyl_tRNA synthetase; Protein biosynthesis; Ligase; AIP-binding; Query Match 66.0%; Score 33; DB 1; Length 563; Best Local Similarity 45.5%; Pred. No. 30; Matches 5; Conservative 3; Mismatches 3; Indels SITS 121 131 "HIGH" REGION. SEQUENCE 563 AA, 63134 MW; PECAF176A68D8858 CRC64; Complete proteome. 

28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS) ARGS OR SPY2151. Streptococcus pyogenes. Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, 563 AA. STANDARD; NCBI_TaxID=1314; SYR STRPY Q99XL5; RESULT 15 SYR STRPY

|:|: | ||: 94 EQVITAGSDYA 104

g

1 EEVVPXGXDYS 11

REPUBLICE FROM N.A.

RECORDING ATCC 700294 / Serotype M1;

REAIN=SF370 / ATCC 700294 / Serotype M1;

REAIN=SF370 / ATCC 700294 / Serotype M1;

RA PERMEAL ST 1926-84; PubMed=112956296;

RA PERMEAL ST 21926-84; PubMed=112956296;

RA PATHEAL ST 21926-85; Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

RA Dian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,

RA Dian X., Clifton S.W., Roe B.A., McLaughlin R.,

RA COMPIECE Genome sequence of an M1 strain of Streptococcus pyogenes.";

RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

RT "Complete Genome sequence of an M1 strain of Streptococcus pyogenes.";

RT "Complete Genome sequence of an M1 strain of Streptococcus pyogenes.";

RT "Complete Genome sequence of an M1 strain of Streptococcus pyogenes.";

RT "Complete Genome sequence of an M1 strain of Streptococcus pyogenes.";

RT "Complete Genome sequence of B1 an M1 and Arm (Arg) = AMP +

CC -1 STBUILT: Monomer (By similarity).

CC -1 STBUILT: Monomer (By similarity).

CC -1 STBUILT: M1 STBUILT: ATP + L-arginine + tRNA(Arg) = AMP +

CC -1 STBUILT: M1 STG COPYTIGHT. It is produced through a collaboration complete of B1 on on control of B1 on the B1

HSSP; Q05506, 1852.

HAMAP; MF_00123; -; 1.

InterPro; IPR001278; Arg_tRNA-synt_lc.

InterPro; IPR005148; N.

InterPro; IPR005909; tRNA-synt_ld_C.

Pfam; PF03485; N-Arg; 1.

Pfam; PF03485; N-Arg; 1.

Pfam; PF00750; tRNA-synt_ld; 1.

Pfam; PF00750; tRNA-synt_ld; 1.

Pfam; PF00750; TRNA-synt_ld; 1.

Pfam; PF00748; TRNA-Synt_ld_C; 1.

PINTE; PR01038; TRNA-SYNTHARG. EMBL; AE006633; AAK34788.1; -. HSSP; O05506: 1BS2. 

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DR PROSITE; PS00178; AA TRNA LIGASE I; FALSE NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 121 131 "HIGH" REGION.
SQ SEQUENCE 563 AA; 63120 MW; ROF2CAC28D03B613 CRC64;
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SEQUENCE 563 AA; 63120 MW; E0F2CAC28D03B613 CRC64;

Query Match
Best Local Similarity 45.5%; Pred. No. 30;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps

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1 BEVVPXGXDYS 11 |:|: | ||: 94 EQVITAGSDYA 104

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Search completed: June 3, 2004, 11:49:56 Job time: 5.86667 secs

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74.0%; Score 37;
      Q12479
Q8VX88
                   Q859A6
Q92U66
Q9C6J0
Q8NR16
                                              Q82DT4
Q9A382
                                                          096YH5
08TX62
08ZA09
065890
                                                                                                                       083NN9
083G59
                                                                                                                                   Q8KL43
Q7VGY0
Q9YF13
Q8R126
                                                                                                  Q40129
Q8XPA8
Q8FPY9
                                                                                                                                                                       QBBTX4
QBBK35
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Q9DDJ4
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                                                                                                                                                                Q8VD18
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ProDom; PD007253; MS_channel; 1.
TIGRPAMS; TIGR00220; mscL; 1.
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Q82ZB4
                                                                                                                                                                                                                                     RESULT 1
QBEEV7 oceanobacil
QBEEV7 oceanobacil
QBGihO synechococc
Q9xet4 canis famil
QBIG33 bos taurus
QBIG31 bos taurus
00404 homo sapien
QBCAS tragulus ja
QBU7j0 agrobacteri
QBNy9 bos taurus
QBNy9 bos taurus
QBNy9 bos taurus
QBNy9 meisseria m
Q9y190 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                Q82zb4 enterococcu
O52367 rhizobium t
                                            June 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
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                                                                                                                                      1017041
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                        1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_phage:*
sp_plant:*
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Perfect score:
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ESQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STATC 700802;

MEDLINE=22550857; PubMed=12663927;

MEDLINE=22550857; PubMed=22595071-7074(2003)

MEDLINE=22550856; AAO828281;

MEDLINE=22550856; AAO828281;

MEDLINE=22550856; AAO828281;

MEDLINE=22550856; AAO828281;

MEDLINE=22550856; AAO828281;
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI TaxID=1351;
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01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-UTN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MSCL OR BF3152.
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GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001185; MS channel.
Pfam; PF01741; MscL; 1.
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Length 149;

DB 16;

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Nucleic Acids Res. 30:3927-3935(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                 189 EQLVPHGIDY 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaeoglobus fulgidus.
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Matches
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094617
ID 0946
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DT 01-D
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GO; GO:00046821; C:extrachromosomal DNA; IEA.
GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008270; F:zinc_ion_binding; IEA.
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STRAIN=HTBB31 / DSM 14371 / JCM 11309;
STRAIN=HTB31 / DSM 14371 / JCM 11309;
TAKBILINE=22220767; PubMed=12235576;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosenblueth M., Hynes M.F., Martinez-Romero E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!-COPACTOR: ZINC (BY SIMILARITY).
-!-SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gabs
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pRtrCFN299a.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.0%; Score 36; DB 2; Length 298; 50.0%; Pred. No. 19; ive 3; Mismatches 2; Indels
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 AA; 31092 MW; 49B2F8117C33AE87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 01-UUN-1998 (TrEMBLrel. 06, Created)
01-UUN-1998 (TrEMBLrel. 06, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Aryl-allochol dehydrogenase homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical conserved protein.
080509
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InterPro; IPR002085; AbH zinc.
InterPro; IPR002085; AbH zinc.
InterPro; IPR002085; AbH zinc.
InterPro; IPR002085; AbH zinc.
InterPro; IPR001070; AbH zinc.
InterPro; IPR002085; Abh zinc.
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      Pred. No. 5.2;
); Mismatches
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01-MAR-2003 (TrEMBLrel. 23, Created)
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      Best Local Similarity 70.0%;
Matches 7; Conservative
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les 5; Conservative
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                                                                                          1 REVVPXGXDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium tropici
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XR MEDLINE-98049343; PubMed=9389475;

XR TLERK H.-P., Clayton R.J., Tomb U.-F., White O., Nelson K.E.,

XR Atchum K.A., Dodson R.J., Gwinn M., Hickey B.K., Peterson J.D.,

XR Atchum R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

XR Tixhese B.F., Dougherty B.R., McKenney K., Adams M.D., Loftus B.,

XR Tixhese B.F., Dougherty B.R., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., Mowidl L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

A Cotton M.D., Spriggs T., Arriach P., Kaine B.P., Sykes S.M.,

A Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
BMBL; AE001109; AAB91255.1; -.
PIR; D69551; D69551.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annocation update)
3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34).
HMGR1.
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                                                                                                                                                                                     72.0%; Score 36; DB 16; Length 319; 60.0%; Pred. No. 20; 2; Mismatches 2; Indels
EMBL; AP004594; BAC12465.1; -.
InterPro; IPR001279; Blactmase-like.
Pfam; PF00753; Jactamase B; I.
Hypotherical protein; Complete proteome.
SEQUENCE 319 AA; 35617 MW; 3BDAE4BF13E79E37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaeea; Buryarchãeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBL_TaxID=2234;
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Pfam; PR00296; bac_luciferase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein AF2411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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6; Conservative
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SECUENCE FROM N.A.

SECUENCE TROW N.A.

TISSUBE-Thyroid;

MEDLINE=20422104; PubMed=10964405;

Bichon B., Marcan D., Pouillon V., Christophe-Hobertus C.,

Christophe D.;

A method for the large-scale cloning of nuclear proteins and nuclear targeting sequences on a functional basis.";

Anal. Biochem. 284:231-239(2000).

EMBL; AJ389531; CAP46833.1; -.

NOM TER 78

SEQÜENCE 78 AA, 8895 MW; B62486313555FBAI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q81033;
01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Human-type bcnt protein.
Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                       72.0%; Score 36; DB 16; Length 1044; 63.6%; Pred. No. 79; 3; Indels (1)
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Pred. No. 6.8;
2; Mismatches 3; Indels
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STRANTH-Jersey;
Iwashita S., Itch T.,
"A LINE-mediated gene diversity.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB081003; BAC11552.1;
SEQUENCE 175 AA; 19529 WW; CE7283CB98393BE
   Complete proteome.
SEQUENCE 1044 AA; 113205 WW; 00E9C13F0F636D2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrewBirel. 12, Created)
01-NOV-1999 (TrewBirel. 12, Last sequence update)
01-DEC-2001 (TrewBirel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                              Local Similarity 63.6%;
tes 7; Conservative
                                                                                                                                                                                                                                                                      843 EEVLPNGIGYS 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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EDYVPSGGEYS 26
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                                                                                                  Query Match
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Matches
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081033
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                                                                                                                                                                                                                                                     Krishnan S., Banerjee N.S.;

"3-hydroxy-3-methylglutaryl coenzyme A reductase gene from
"3-hydroxy-3-methylglutaryl coenzyme A reductase gene from
Andrographis paniculata.";

"3-hydroxy-3-methylglutaryl coenzyme A reductases.

"B. Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

"B. Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

"B. Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

"B. GOJ GO:0016021; C:integral to membrane; IEA.

"GOJ GO:0004420; F:hydroxymethylglutaryl-CoA reductase activity; IEA.

"GOJ GO:0006629; F:lipid metabolism; IEA.

"GOJ GO:0006629; F:lipid metabolism; IEA.

"B. InterPro; IPR004554; HMG CoA_NDD bind.

"InterPro; IPR004559; HMG CoA_NDD bind.

"B. InterPro; IPR004559; HMG CoA_NDD bind.
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Andrographis paniculata.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicocyledons; core eudicots; asterids;
lamiids; Lamiales; Acanthaceae; Acanthoideae; Ruellieae;
Andrographinae; Andrographis.
NCBI_TaxID=175694;
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MEDLINE=2225144; PubMed=12240834;
MEDLINE=22255144; PubMed=12240834;
Nakamala 2.7 Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watamabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Kiyokawa C., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.0%; Score 36; DB 10; Length 595; 70.0%; Pred. No. 42; tive 0; Mismatches 3; Indels
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Multidrug efflux transporter.
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EMBL, APROS134; BACO3170.1. -

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005215; P:transporter activity; IEA.

GO; GO:0005215; P:transport, IEA.

InterPro; IPR001036; Activin_res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPROJ IPROOFSS4; HNG_COA_RNADP.
INTERPRO, IPROOFSS4; HNG_COA_RNADP.
INTERPRO, IPROOFSS9; HNG_COA_RUB_bind.
PROSTIE; PROOFSS; HNG-COA_REBUCTASE.
TIGREAMS; TIGROOFSS3; HNG-COA_REBUCTASE_1; I.PROSTIE; PSOOLOGE; HNG-COA_REBUCTASE_2; I.PROSTIE; PSOOLSS; HNG-COA_REBUCTASE_3; I.PROSTIE; PSOOLS; HNG-COA_REBUCTASE_3; I.PROSTIE; PSOOLS; HNG-COA_REBUCTASE_4; I.CAA_COA_REBUCTASE_4; I.CAA_COA_REBUCTASE_5; I.CAA_COA_REB
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PRINTS; PR00702; ACRIFLAVINRP.
TIGRFAMs; TIGR00915; 2A0602; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.0
Best Local Similarity 70.0
Matches 7; Conservative
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SEQUENCE FROM N.A.
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MEDINE=21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okuta V.K., Zhou Y., Chen L., Wood G.E., Almaida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Essen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Rutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Shang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Mester E.W.;

"The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUELLY.
TISSUELLY.
Ubon S., Kimura J., Kurohmaru M., Fukuta K., Iwashita S.;
"Gene organization of the chevrotain bont whose paralogue in
ruminantia includes an endonuclease domain of RTE-1 in the protein.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB103377; BACS7061.1; -.
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                                                                                                                                                                                                                                                                      Tragulus javanicus (Tesser Malay chevrotain).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Tragulina,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JTN-2002 (TrEMBLrel. 21, Created)
01-JTN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
6-O-methylguanine-DNA methylransferase.
ADA OR ATU4459 OR AGR L 818 (strain CS8 / ATCC 33970).
Bacteria, Protoobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiam-Agrobacterium Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 70.0%; Score 35; DB 6; Length 281; Local Similarity 54.5%; Pred. No. 29; lndels is 6; Conservative 2; Mismatches 3; Indels
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NON TER 281 281
SEQUENCE 281 AA; 31557 MW; 8133A9BAFF7509A6 CRC64;
                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Human-type Bont (Fragment).
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                                              281 AA.
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                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                            Tragulidae; Tragulus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9849
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ID Q8U7J0
AC Q8U7J0;
Q867A5

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DT Q1-JUN:

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MEDLINE=97160586; PubMed=9006920;
MEDLINE=97160586; PubMed=9006920;
Mobukuni T., Kobayaahi M., Oomori A., Ichinose S., Iwanaga T.,
Takahashi I., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.;
"An Alu-linked repetitive sequence corresponding to 280 amino acids is expressed in a novel bovine protein, but not in its human homologue.";
J. Biol. Chem. 272:2801-2801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%; Score 35; DB 6; Length 215; 54.5%; Pred. No. 22; 3; Indels ative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRAINERED #750;
Iwashita S., Itoh T., Sezaki M., Oshima K., Hashimoto E. Kitagawawa Y., Takahashi T., Masui T., Hashimoto K.;
"A LINE-mediated gene diversity ";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB081095; BAC15593.1;
NON_TER 215
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                                                                                                                                                                                                                                                                          Q81031 PRELIMINARY; PRT; 215 AA.
Q81031.
Q81031.
Q1-MAR-2003 (TYENBLrel. 23, Created)
O1-MAR-2003 (TYENBLrel. 23, Last sequence update)
H-type bcnt protein (Fragment).
H-TYPE BCNT.
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01-JTU-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
P97 homologous protein.
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Best Local Similarity 54...
6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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            EEVVPXGXDYS 11
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RESULT 10

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SEQUENCE

RESULT 11

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STRAIN=MCE FROM N.A.

STRAIN=MCS8 / Serogroup B;

STRAIN=MCS8 / Serogroup B;

MEDLINE=2017555; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gawinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parkeey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                      MEDLINE-98267221; PubMed-9602175;
Takahashi I., Nobukuni T., Ohmori H., Kobayashi M., Tanaka S.,
Ohshima K., Okada N., Masui T., Hashimoto K., Iwashita S.;
"Existence of a bovine LINE repetitive insert that appears in the cDNA
of bovine protein BCNT in ruminant, but not in human, genomes.";
Gene 211:387-394(1998).
                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 4; Length 299; Pred. No. 32; Mismatches 3; Indels
Eutheria; Primates; Catarrhini; Hominidae; Homo
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GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR003953; FAD bind2.
InterPro; IPR001327; FAD_pyr_redox.
                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33593 MW; F4A9E928B669451A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Succinate dehydrogenase, flavoprotein subunit.
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-1- COFACTOR: FAD (BY SIMILARITY).
EMBL; AEO02446; AAF41356.1; -.
PIR; F81138; F81138.
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Best Local Similarity 54.00,
Best Local 6; Conservative
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TIGR; NMB0950; -.
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                                                                                                                                                                                                                               TISSUE=Placenta;
                  NCBI_TaxID=9606
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SEQUENCE
                                                         SEQUENCE
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                                                                                  This, December 2016 of Contracellular, IEA.

GO; GO:0003908; F:methylated-DNA-[protein]-cysteine S-methylt. . .; IEA.

GO; GO:0003908; F:methylated-DNA-[protein]-cysteine S-methylt. . .; IEA.

GO; GO:000309; F:menscription factor activity; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO; GO:000658; P:reansferase activity; IEA.

GO; GO:000658; P:reansferase activity; IEA.

InterPro; IPR000005; HTHAAC.

InterPro; IPR001497; Methylransf_1.

Pfam; PF00165; HTH AraC; 2.

Pfam; PF00165; Methylransf_1; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBL-1. 25, Last annocation update)
BCNT protein (CRANIOFACIAL development protein 1).
BCNT Homo saplens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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TISSUE=Kidney;
TIMENTE=Kidney;
TALINE-mediated gene diversity.";
"A LINE-mediated gene diversity.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO81004; BACI1953.1;
SEQUENCE 297 AA, 33354 WW; D4A944BC8740373C CRC64;
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TIGREAMS; TIGR00589; ogt; 1.
PROSITE; PS01124; HTH ARAC FAMILY 2; 1.
Methyltransferase; Transferase; Complete proteome,
SEQUENCE 290 AA; 31587 MW; B626592EF519977F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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              EMBL, AE009374; AAL45253.1; --
EMBL, AE008340; AAX88982.1; --
PIR, AG3104; AG3104
PIR, D98182; D98182.
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Matches 5; Conservative
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Matches 6; Conservative
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NCBI_TaxID=9913;
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9 EDITPIGSDY
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70.0%; Score 35; DB 16; Length 587;
Best Local Similarity 70.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 3; Indels
InterPro; IPR003952; FRD/SDH FAD_BS.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR004110; Succ_DH flav_C.
Ffam; PP00890; FAD_binding_2; 1.
Ffam; PP02910; succ_DH flav_C; 1.
PRINTS; PR00411; PNDRDTASEI.
PROSTE; PR006411; PNDRDTASEI.
PROSTE; PS00664; FRD_SDH FAD_BINDING; 1.
FROSTE; PS00664; FRD_SDH FAD_BINDING; 1.
FAD; Flavoprotein; Oxidoreductase; Complete proteome.
SEQUENCE 587 AA; 64502 MW; 9581701B08069003 CRC64;
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Search completed: June 3, 2004, 11:57:34 Job time: 29.8667 secs

366 EVVVPQGEDY 375

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
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                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28
                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
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                                ABB80535
ABB80567
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                                                                                                                                                                                                                                                                                  ABB80548 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brunck
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   Misc-difference
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Copyright (c) 1993 - 2004 Compugen Ltd
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                                                                                                      Gaps
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RESULT

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31.
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                                                                                                                                                                    'note= "N-terminal acetyl"
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                                                                                                                                                                                                       Synthetic
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                                                 ABB80557;
                                                                                                                                                                        virucide
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Gaps

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Best Loc Matches

ઠ 셤 RESULT 5

Misc-difference 8

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                                  /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha *ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
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                          'note= "N-terminal acetyl"
                                                                                                               /note= "C-terminal amide"
                                                                                      note= "D-form residue"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB80561 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                     21-JUL-2000; 2000US-0220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.0%;
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                                                                          Misc-difference
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Modified-site
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Best Local Simi
Matches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22.
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                                 /note= "C-terminal amide"
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           'note= "D-form residue"
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                                                                                                              19-JUL-2001; 2001WO-US023169.
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                    (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                           protease.
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Brunck

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                    otide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB80543 standard; peptide; 11 AA.
                                                                                                                                                                                       Claim 17; Page 65; 69pp; English.
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             19-JUL-2001; 2001WO-US023169
                                     21-JUL-2000; 2000US-0220101P
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                                                                                    Levy OE,
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                                                             (CORV-) CORVAS INT INC
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                                                                                                            WPI; 2002-361643/39
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                    Novel peptide activity usefu
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Modified-site
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                                                                                                                                                                protease
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'note= "N-terminal acetyl"

Location/Qualifiers

/note= "C-terminal amide"

'note= "D-form residue" 'note= "D-form residue"

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                                                                                                                               The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating adsorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Norvaly1 carbony1 forming keto-amide linkage with
                                                        ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
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Pred. No. 0.02;
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          Brunck TK;
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                                                                                                         English
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residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                         Claim 17; Page 65; 69pp;
                                                                                                                                                                                                                                                                     Local Similarity 90.9
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           Levy OE,
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                                   WPI; 2002-361643/39.
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                                                                                                                                                                                                                                   Sequence 11 AA;
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                                                         Novel peptide
activity usefu
           Lim-Wilby M,
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Modified-site
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Gaps

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Mismatches

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Score 46; DB 5; Length 11; Pred. No. 0.02;

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Sequence 11 AA;
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                                         of the
                           The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #13.
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                                                                                                                                     92.0%; Score 46; DB 5; Length 11; 90.9%; Pred. No. 0.02; 1; Indels iive 0; Mismatches 1; Indels
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          Claim 17; Page 64; 69pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           residue 7'
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                             Conservative
                                                                                                                                                                                 1 EEVVPXGXDYS 11
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                                                                                                                                                   Similarity
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                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9
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Pred. No. 0.02;
0; Mismatches
  5,
                       0.02;
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  Score 46;
Pred. No.
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                                                                                          1 EEVVPXGXDYS
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ABB80538 standard; peptide; 11
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                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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Pred. No. 0.02;
0; Mismatches 1
                                                                                                                                                                                                                                                                              note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                                         /note= "D-form residue"
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                                                                                            ABB80528 standard; peptide; 11 AA
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                                                                                                                                                                                                                                                                                                                    residue 7"
                                                                                                                                           (first entry
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Best Local Similarity 90.9
Matches 10; Conservative
          1 EEVVPXGXDYS 11
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                               EEVVPXGMDYS
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                    /note= "Norvalyl carbonyl forming keto-amide linkage with residue ?"
                                                               Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.
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                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
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The sequence represents a peptide compound of the invention having the peptides of the inveptions c virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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                                                                                                      'note= "N-terminal acetyl"
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                                                                        Location/Qualifiers
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Search completed: June 3, 2004, 11:48:25 Job time : 46.9333 secs

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OPERATING SYSTEM:
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-523-263B-18
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                                                                                                                                                                                                                                                                                                                                                                                                    389414 seqs, 51625971 residues
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Listing first 45 summaries
                                                                                          - protein search, using sw model
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1 EEVVPXGXDYS 11
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Sequence 25088, A sequence 3, Applit Sequence 1, Applit Sequence 2, Applit Sequence 1, Applit Sequence 1, Applit Sequence 1, Applit Sequence 17, Applit Sequence 17, Applit Sequence 17, Applit Sequence 11, Applit Sequence 17, Applit Sequence 18, Applit Sequence 17, Applit Sequence 17, Applit Sequence 18, A	NCES RELATING TO STICS AND THERAPEUTICS	gth 181; Indels 0; Gaps 0;	
425 4 US-09-252-991A-25088 478 3 US-09-083-448-1 478 3 US-09-083-448-1 478 4 US-09-083-448-3 478 4 US-09-083-55-1 478 4 US-09-813-555-3 478 4 US-09-813-555-3 478 4 US-09-813-555-3 478 4 US-09-813-555-3 478 4 US-09-813-555-3 478 4 US-09-813-556-3 1049 4 US-09-813-2658-1 1049 4 US-09-814-268-3 1068 2 US-08-142-11 1068 2 US-08-142-77-7 1068 3 US-09-134-77-7 1068 3 US-09-314-272-8	SULT 1  -09-134-000C-4848 Sequence 4848, Application US/09134000C Sequence 4848, Application US/09134000C Sequence 4848, Application US/09134000C GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC AND AMINO ACID SEQUENCES TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTIC TITLE OF INVENTION: NUCLEIC 32796-032 CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT PILING DATE: 1998-08-13 SPROR APPLICATION NUMBER: US 60/055,778 FRICK APPLICATION NUMBER: US 60/055,778 NUMBER OF SEQ ID NOS: 6812 SOFTWARE: Patentin version 3.1 IENGTH: 181 TYPE: PRT ORGANISM: Enterococcus faecalis -09-134-000C-4848	74.0%; Score 37; DB 4; Len 70.0%; Pred. No. 5.1; vative 0; Mismatches 3; Y 10 Y 154	lication US/08569147 77 77 77 77 77 77 77 71 710N: NUTION: HUMANISED ANTIBODIES NOGCOCK Washburn Kurtz Mackiewicz & No. 6180377ris, LLP No. 6180377ris, LLP No. 6180377ris, LAP No. 6180377ris, LAP No. 6180377ris, LAP Nocceptable 1.S.A. ABLE FORM: 1.S.A. 118M PC compatible 118M PC compatible 118T PC compatible 118T PC DOS/MS-DOS
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272 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	RESULT 1  US-09-134-000C-4848  Sequence 4848  Patent No. 6617156  GENERAL INFORMATION: APPLICANT: LVAIN DOUGETE-Stamm TITLE OF INVENTION: FILE REFREENCE: 027956-032  CURRENT APPLICATION INVERS: US 67  FRIOR REFREENCE: 02796-03.  CURRENT PILING DATE: 1998-08-08-08-08-08-08-08-08-08-08-08-08-08	Query Match Best Local S Matches 7 Qy 1	RESULT 2 US-08-569-147-76 Sequence 76, Application 1 EDEACH NO. 6180377 GENERAL INFORMATION: APPLICANT: TITLE OF INVENTION: HITTLE OF INVENTION: HITTLE OF INVENTION: HITTLE OF SEQUENCES: ADDRESSEE: Woodcock ADDRESSEE: No. 6180: STREET: One Liberty CITY: Philadelphia STREET: One Liberty CITY: Philadelphia STREET: One Liberty CITY: Philadelphia STREET: ONE STREET: PROPERTIENT STREET: PROPE

RESULT 4

193-09-114-001C-5124

196-09-114-001C-5124

Requence 5124, Application US/09134001C

Requence 5124, Application US/09134001C

Requence 5124, Application US/09134001C

REACHT No. 6380370

GENERAL INFORMATION:

TILLS OF INVENTION:

TILLS OF INVENTION:

PRICE REPERENCE: GTC-07

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

RIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

LENGTH: 139

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Gaps

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64.0%; Score 32; DB 4; Length 139; 55.6%; Pred. No. 38; tive 2; Mismatches 2; Indels

Query Match Best Local Similarity 55.6 Matches 5, Conservative

3 VVPXGXDYS 11

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; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5124

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Gaps

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SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,147
FILING DATE: 25-March-1996
ATTORNEY/ABORT INFORMATION:
ATTORNEY/ABORT INFORMATION:
NAME: Trujill, Doren Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-310
TELEPAX: (215) 568-310
TELEPAX: (215) 568-310
TELEPAX: (215) 568-310
INFORMATION FOR SEQ ID NO: 76:
LENGTH: 140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 3; Length 140;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMANISED ANTIBODIES
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woo 6180377xis, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 82, Application US/08569147
Patent No. 6180377
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                      66.0%;
75.0%;
                                                                                                                                                                                                                                                                                                         ; LENGTH: 140 amino acids
; TYPE: amino acid
TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-76
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 WPTGFDY 129
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US-08-569-147-82
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## PRICANT Human Genome Sciences, Inc.
### APPLICANT Human Genome Sciences, Inc.
### TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
### TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
### FILE REFERENCE: Pab461PCT
### CURRENT APPLICATION NUMBER: 0010-04-24
### PRIOR APPLICATION NUMBER: PCT/US99/06199
### PRIOR APPLICATION NUMBER: 60/080,296
### PRIOR PILING DATE: 1999-03-18
### PRIOR PILING DATE: 1998-04-01
### PRIOR PILING DATE: 1998-05-07
### PRIOR PILING: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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Pred. No. 92;
2; Mismatches 2; Indels
                                                                                                   RESULT 5
US-09-8310-217-14
Sequence 14, Application US/09830217
; Partent No. 6521441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 4, Application US/09408020; Patent No. 6632937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-830-217-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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195 IVPFGRDYN 203
32 IVPEGHDYN 40
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US-09-408-020-4
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels
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MOLECULE TYPE: protein US-08-569-147-82

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340 Kingsland Street
                          Nutley
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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Sequence 4318 Application US/09134000C

Sequence 4318 Application US/09134000C

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: STATEMOCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: 1998-08-13

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT PILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

NUMBER OF SEQ ID NOS: 6812

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Parentin version 3.1

SEQ ID NO 4318

LENGTH: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                  APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Ronald V.
APPLICANT: Schlebar, Christa
APPLICANT: Schlebar, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REPERBNCE: DCORP, 002A
CURRENT APPLICATION NUMBER: US/09/408,020
CURRENT FILING DATE: 1999-09-29
PRIOR PELLING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC_FEATURE
1. LOCATION: (2)...(2)
2. CTHER INFORMATION: Amino acid 2 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-4318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08459146
Patent No. 586405
GENERAL INFORMATION:
APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION: Hypovirulence
NUMBER OF SEQUENCES:
ADDRESSE: George M. Gould, Esq., Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                        64.0%; Score 32; DB 4; Length 3472; 45.5%; Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.0%; Score 31; DB 4; Length 303; Best Local Similarity 40.0%; Pred. No. 1.5e+02; Matches 4; Conservative 3; Mismatches 3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-09-408-020-4
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 45.5-
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2294 EDVIPRGISFS 2304
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-134-000C-4318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-08-459-146-2
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Gaps
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J Gequence 2, Application US/08459065

J Sequence 2, Application US/08459065

J GENERAL INFORMATION:

J APPLICANT: Choi, Gil Ho

APPLICANT: Nuss, Donald Lee

J TITLE OF INVENTION: Genetically Engineered Transmissible

TITLE OF INVENTION US. 3

SCHARET: Alo Kingsland Street

COUNTRY: US.A.

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 02-04945,065

FILING DATE: 02-04943;

FRIOR APPLICATION: 435

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 622;
               COUNTY: U. S.A.

COUNTY: U. S.A.

COUNTY: U. S.A.

COMPUTER READBLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DATE RC-BOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION: 435

PRICA APPLICATION: 435

PRICA APPLICATION DATA:

APPLICATION NUMBER: US 07/832,117

FILING DATE: GG-FEB-1992

ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Endothia parasitica (Cryphonectria ) ORGANISM: parasitica) ; STRAIN: EP713 US-08-459-146-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.0%; Score 31; DB 2;
85.7%; Pred. No. 3.3e+02;
iive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: ROSEMEN, CALHETINE R
REGIGTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8589
TELECOMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 622 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
New Jersey
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 EEVVPAG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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Sequence 2, Application US/09617594A Patent No. 6541458 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecalis US-08-963-851-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Feline calicivirus US-09-617-594A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428 EELTPAG-DYS 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPXGXDYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-621-976-4604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
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US-99-413-814-86

US-99-413-814-86

Eatent No. 622504

GENERAL INPORMATION:

APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH

APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH

APPLICANT: Brandt, Petra

APPLICANT: Brandt, Petra

APPLICANT: Brandt, Petra

APPLICANT: Dougherty, Brian A

APPLICANT: Cino, Paul M

APPLICANT: Cino, Paul M

APPLICANT: Hofle, Gerhard

APPLICANT: Hofle, Gerhard

APPLICANT: Reichenbach, Hans

TITLE OF INVENTION: Dacchim

APPLICANT: Reichenbach, Hans

TITLE OF INVENTION: Dacthim

TITLE OF INVENTION: DAS sequences for enzymatic synthesis of polyketide compounds

TITLE OF INVENTION: 1992-10-07

CURRENT APPLICATION NUMBER: US/09/413,814

CURRENT APPLICATION NUMBER: DE 198 46 493.2

BARLIER FILING DATE: 1998-10-09

NUMBER OF SEQ ID NOS: 107

SERLIER APPLICATION VUMBER: 1988-10-09

NUMBER OF SEQ ID NOS: 107

SEQ ID NO 86

LENGTHARE: Patentin Ver. 2.1

SEQ ID NO 86

LENGTHARE: DE IND 805

LENGTHARE DE IND 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.0%; Score 31; DB 3; Length 739; Best Local Similarity 62.5%; Pred. No. 4e+02; Matches 5; Conservative 1; Mismatches 2; Indels
PILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, Catherine R
REGISTRATION NUMBER: 34,240
REPERENCE/DOCKET NUMBER: 34,240
REPERENCE/DOCKET NUMBER: 34,240
REPERENCE/DOCKET NUMBER: 35.20
TELEPHONE: (201) 235-6209
TELEPHONE: (201) 235-6209
TELEPHONE: (201) 235-6209
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Endothia parasitica (Cryphonectria ORGANISM: Endothia parasitica)
STRANISM: BP713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Sorangium cellulosum
US-09-413-814-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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RESULT 11 US-09-617-594A-2

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APPLICANT: Audonnet, et al.

TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT FILLE REFERENCE: 454313-3151.1

FILE REPRENCE: 454313-3151.1

CURRENT APPLICATION NUMBER: US/09/617,594A

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: France 00 01761

PRIOR PILING DATE: 2000-03-30

PRIOR FILING DATE: 2000-02-11

PRIOR PILING DATE: 2000-02-11

PRIOR PILING DATE: 1999-07-16

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 2

LENGTHALE: PATENTIN VERSION 3.0

SEQ ID NO 2

LENGTH: 669
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Pred. No. 4.5e+02;
1; Mismatches 2; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08963851
Facent No. 6300116
GENERAL INFORMATION:
APPLICANT: HALKIER, TORDEN
APPLICANT: HALKIER, TORDEN
APPLICANT: HALKIER, TORDEN
APPLICANT: HANDENSEN, PETER KAMP
TITLE OF INVENTION: PROTERS WAPP
TITLE OF INVENTION: PROTERS WAPP
TITLE OF INVENTION: PROTESS US/08/963,851
CURRENT FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 357-11-04
SOFTWARE: FASTERQ for Windows Version 3.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4604, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REPERROCE: GENSET. 054FR2
CURRENT APPLICATION NUMBER: US/09/621,976
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Pred. No. 83;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                        3; Indels
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Patent No. 6448230
FERREAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REPERBREE: PS00391.03
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
FERLIER FILING DATE: 1998-09-11
FERLIER PELLING DATE: 1998-03-12
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-03-04
EARLIER FILING DATE: 1997-03-05-05
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER PELLING DATE: 1997-05-30
EARLIER PELLING DATE: 1997-05-30
EARLIER PELLING DATE: 1997-05-30
EARLIER FILING DATE:
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Patent No. 6448230
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P1.US
                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                     50.08;
CURRENT FILING DATE: 2000-1
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4604
LENGTH: 120
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Best Local Similarity 85.7.
5. Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EVVPXGXDYS 11
                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-09-621-976-4604
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US-09-152-060-68
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US-09-152-060-85
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ORGANISM: Homo sapiens
PERATURE:
NAME/KEY: SITE
LOCATION: (67)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PERATURE:
NAME/KEY: SITE
LOCATION: (89)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-152-060-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%; Score 30; DB 4; Length 121; 85.7%; Pred. No. 83; 1; Indels :ive 0; Mismatches 1; Indels
S DATE: 1998-09-11
CATION NUMBER: PCT/US98/04858
                                  EARLIER FILING DATE: 1998-03-12
EARLIER PILING DATE: 1998-03-12
EARLIER PILING DATE: 1998-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER PILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER PILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER PILING DATE: 1997-06-05
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER PILING DATE: 1997-06-05
EARLIER APPLICATION NUMBER: 60/066,970
EARLIER PILING DATE: 1997-06-05
EARLIER APPLICATION NUMBER: 60/066,970
EARLIER PILING DATE: 1997-01-19
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: June 3, 2004, 12:03:09 Job time: 11.8 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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94.0%; Score 47;
JS-09-909-164-31
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Query Match
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June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 5
Sequence 6
Sequence 6
Sequence 6
Sequence 7
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-35
US-09-909-164-43
US-09-909-164-41
US-09-909-164-81
US-09-909-164-81
US-09-909-164-12
US-09-909-164-13
US-09-909-164-27
US-09-909-164-27
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                                                                                                  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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50
1 EEVVPXGXDYS 11
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Match Length
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Perfect score:
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Sequence 31, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

TITLE OP INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TITLE OP INVENTION: NOVEL PEPTIDES

CURRENT APPLICATION NUMBER: 60/220,101

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 3:

LENGTH: 11

LENGTH: 11

LENGTH: 11
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50,
51,
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US-09-909-164-28
US-09-909-164-39
US-09-909-164-39
US-09-909-164-39
US-09-909-164-36
US-09-909-164-5
US-09-909-164-19
US-09-909-164-19
US-09-909-164-19
US-09-909-164-19
US-09-909-164-19
US-09-909-164-38
US-09-909-164-38
US-09-909-164-39
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1) - (1)
OTHER INFORMATION: ACETYLATION
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: artificial sequence
     NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Length 11;

DB 12;

400

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RESULT 4

US-09-909-164-40

US-09-909-164-40

Sequence 40, Application US/09909164

Sequence 40, Application US/09909164

Publication No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Low, Odile E

APPLICANT: Brunck, Terence K

ITLE REFERENCE: 1001192-105

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT PILING DATE: 2003-03-25

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 40

LENGTH: 11

LENGTH: 11
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OTHER INFORMATION: 11-mer synthesized according to example 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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INFORMATION: norvaline-(CO)
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CTHER INFORMATION: D-amino acid

US-09-909-164-35
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LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
                                                                                                   TYPE: PRT
ORGANISM: artificial sequence
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NAME/KEY: MISC FEATURE
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NAME/KEY: MOD_RES
LOCATION: (11)..(1
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                                                                                                                                                                                     US-09-909-164-32
US-09-909-164-32
Squence 3.2, Application US/09909164
Spublication No. US2002068702A1
GENERAL INFORMATION:
APPLICANT: Lin-Wilby, Marguerita
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
SCOTTARRE: Patentin version 3.1
SCOTTARRE: Patentin version 3.1
SEQ ID NO 32
LENGTH: Lin-Wilby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-09-909-164-35
S-09-909-164-35
S-09-909-164-35
Sequence 35, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Lim-Wilby, Terence K
TILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERBNCE: IN01192-US
CURRENT PELLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
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GCANISM: artificial sequence
PEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
94.0%; Score 47; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 1; Indels
  Pred. No. 0.0049;
0; Mismatches 1; Indels
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NAME/KEY: MISC_FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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NAME/KEY: MISC FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
US-09-909-164-32
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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US-09-909-164-12
US-09-909-164-12

| Sequence 12, Application US/09909164
| Publication No. US20020068702A1
| GENERAL INFORMATION:
| APPLICANT: Lim-Wilby, Marguerita
| TILE OF INTENTION NUMBER: US/09/909,164
| CURRENT APPLICATION NUMBER: 60/220,101
| PRIOR FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 12
| LENGTH: 11
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ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
                                                                                                                                                                                                                                                                   FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
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Pred. No. 0.008;
0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIA VERSION 3.1
SEQ ID NO 8
LENGTH: 11
                                                                                                                                                                                                                                                                                                       PERTURE:
NAME/KEY: MOD_RES
LOCATION: (1). (1)
PERTURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
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LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 90.9%;
Matches 10; Conservative
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NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDATION
US-09-909-164-8
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Sequence 41. Application US/09909164

Sublication No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE REPERENCE: IN01122-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 11

LEVENTH: 11
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US-09-009-164-8
US-09-009-164-8
; Pagenance 8, Application US/09909164
; Publication No. US20020068702A1
; GENBERAL INFORMATION:
; GENBERAL INFORMATION:
; APPLICANT: Corvas International, Inc.
; APPLICANT: Lim.Wilby, Marguerita
; APPLICANT: Levy, Odile E
; APPLICANT: Brunck, Texence K
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; FILE REFERENCE: IN01192-US
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
CTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
                                                                                     Score 47; DB 12; Length 11; Pred. No. 0.0049; 0; Mismatches 1; Indels
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94.0%; Score 47; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 1; Indels
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OTHER INFORMATION: norvaline-(CO)
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; OTHER INFORMATION: D-amino acids
US-09-909-164-41
           ; OTHER INFORMATION: D-amino acid US-09-909-164-40
                                                                                     Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: artificial sequence
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Sequence 18, Application US/09909164

Publication No. USZ0020068702A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lim.Wilby, Marguerita

APPLICANT: Levy, Odile B

APPLICANT: Levy, Odile B

APPLICANT: Levy, Odile B

APPLICANT: Levy, Odile B

TILE REFERENCE: INO192-US

FILE REFERENCE: INO192-US

CURRENT APPLICATION NUMBER: 60/220,101

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR FILING DATE: 2000-07-21

NUMBER: OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

SEQ ID NO 18
APPLICANT: Levy, odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: INOL192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTION OF: 62
SOFTWARE: PATENTION OF: 52
SOFTWARE: PATENTION OF: 52
SOFTWARE: PATENTION OF: 52
SOFTWARE: PATENTION OF: 52
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SOFTWARE: PATENTION OF: 55
SOFTWARE: PATENTION OF:
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PREADANES:
PRATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 11;
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OTHER INFORMATION: D-amino acid
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 90.9
Matches 10, Conservative
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NAME/KEY: MOD_RES
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US-09-909-164-18
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; Sequence 13, Application US/09909164
; Publication No. US2020068702A1
; GENERAL INFORMATION:
    APPLICANT: Corvas International, Inc.
    APPLICANT: Lin-Wilby, Marguerita
    APPLICANT: Lin-Wilby, Marguerita
    APPLICANT: Brunck, Terence K
    TILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
    TILE PETERROCE: IN01192-US
    CURRENT APPLICATION NUMBER: US/09/909,164
    CURRENT FILING DATE: 2000-03-25
    PRIOR APPLICATION NUMBER: 60/220,101
    PRIOR PILING DATE: 2000-07-21
    NUMBER OF SEQ ID NOS: 62
    SOFTWARE: PatentIn version 3.1
    SEQ ID NO 13
    LENGTH: 11
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                                                                                                                                                                                                                                                             Score 46; DB 12; Length 11;
Pred. No. 0.008;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/09909164 Publication No. US20020068702A1 GENERAL INFORMATION:
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LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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                                         OTHER INFORMATION: norvaline-(CO)
                                                                                                 NAME/KEY: MISC_FEATURE

LOCATION: (8)..(8)

COTHER INFORMATION: D-amino acid
US-09-909-164-12
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NAME/KEX: MOD RES
LOCATION: (1): (1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 11
TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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NAME/KEY: MOD RES
LOCATION: (11). (11)
OTHER INFORMATION: AMIDATION
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EEVVPXGMDYS 11
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Best Local Similarity (
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APPLICANT: Levy, Odile B
APPLICANT: Brunck, Terence K
TITLE OF INVEXTION NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01122-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 26
LENGTH: 11
FIRE PRT
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APPLICANT: Lim-Wibby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICANTON NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 00/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTION NOS: 62
LENGTWARE: PATENTION NOS: 62
LENGTWARE: PATENTION NOS: 62
LENGTH: 11
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Pred, No. 0.008;
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OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: D-amino acid
US-09-909-164-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.9.
...hes 10; Conservative
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Squence 22, Application US/09909164

Squence 22, Application No. US20020068702A1

SENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Lim-Wilby, Marguerita

APPLICANT: Levy, Odile E

APPLICANT: Levy, Odile E

TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C

TITLE REPERENCE: INO192-US

TURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: 60/220,101

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1
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NAME/KEY: NOD_RES
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
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                                                                                                                                                                                                                                                                       Score 46; DB 12; Length 11;
Pred. No. 0.008;
0; Mismatches 1; Indels
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Sequence 26, Application US/09909164
Sequence 26, Application US/0909164
Publication No. US20020068702A1
GENERAL INPORMATION:
APPLICANT: Corras International, Inc.
APPLICANT: Lim-Wilby, Marguerita
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LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
FBAUTURE:
                                                                                                                                                           NAME/KEY: MISC_FEATURE
COCATION: (6)...(6)
CTHER INFORMATION: norvaline-(CO)
US-09-909-164-18
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OTHER INFORMATION: D-amino acid

US-09-909-164-22
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: MOD RES
LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
                                                                                                              OTHER INFORMATION: AMIDATION FEATURE:
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Best Local Similarity
Matches 10; Conserv
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LENGTH: 11
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APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPRESENCE: INOIL92-US
CURRENT PILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PARENTIN Version 3.1
SSQ ID NO 46
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1
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LOCATION: (11)...(11)
COTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: NOTVALINE-(CO)
                                                                 Sequence 46, Application US/09909164; Publication No. US20020068702A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE
LOCATION: (8)...(9)
OTHER INFORMATION: D-amino acids
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: artificial sequence
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LOCATION: (8)...(8)
COTHER INFORMATION: Met(0)
US-09-909-164-46
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APPLICANT: Corvas International, Inc.
APPLICANT: Lim.wilby, Marguerita
APPLICANT: Levy, Odile E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: INVINCE PATE: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 45
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Pred. No. 0.008;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION:
                    FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)._(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                   NAME/KEY: MISC_FEATURE
) LOCATION: (8)..(9)
) CTHER INFORMATION: D-amino acids
US-09-909-164-27
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NAME/KEY: MISC_FEATURE
LOCATION: (8)..(8)
OTHER INFORMATION: D-amino acid
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LOCATION: (1) (1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
FRATURE:
OTHER INFORMATION: AMIDATION
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Best Local Similarity 100.
Matches 11; Conservative
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NAME/KEY: MISC FEATURE
LOCATION: (8)...(8)
OTHER INFORMATION: Met (0)
US-09-909-164-45
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US-09-909-164-45
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Gaps ö

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

3, 2004, 11:35:47 ; Search time 9 Seconds June . 0

Run

(without alignments) 117.567 Million cell updates/sec

US-09-909-164-46 50 1 EEVVPXGXDYS 11 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sednence:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	conserved hypothet	6-0-methylguanine-	5	succinate dehydrog		disease resistance	Vl protein - tobac	hypothetical prote	pothe	unknown protein (i	ferrisiderophore r	peptidoglycan-bind	fat facets (faf) s	trans-regulatory s	thiol peroxidases	thiol peroxidases	conserved hypothet	hypothetical prote	hypothetical prote	acyl-CoA dehydroge	probable alkaline	ATP-dependent DNA	probable chitinase	prot	plastocyanin b - L		plastocyanin b pre	d hyp	hypothetical prote
SUMMARIES		D69551	AG3104	D98182	F81138	T48898	T48899	A42452	S54619	A96001	A96546	F82491	H87660	B49132	VKLJSI	AG1272	AH1635	AD0454	857810	\$40753	DERTCM	H72784	AF3286	D82246	T20173	0021	3825	5820		95
	DB	!																										~		
	Length	363	290	290	587	906	806	102	156	247	257	394	433	2747	124	165	165	196	225	327	421	440	1028	1088	1150	66	155	168	196	301
ok	Query Match	72.0	70.0	70.0		•	70.0	•	•			68.0	68.0			•	٠	٠	66.0	٠	٠	•	66.0	٠	66.0	•	•	64.0	•	64.0
	Score	36	35	35	35	35	35	34	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	33	32	32	32	32	32
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hypothetical prote hypothetical prote probable hexosyltr in-lactate dehydrog hypothetical prote toll protein - Hae ABC transporter AT oligopeptidase [improtein B012.3 [ipprobable membrane hypothetical 367K projectin - fruit	response regulator S-adenosylmethioni Conserved hypothet hypothetical prote
F84330 AH1912 G65250 G65250 T24111 F64064 E86665 H84350 G86551 F69009	
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AL IGNMENTS

Conserved hypothetical protein AF2411 - Archaeoglobus fulgidus
CiSpecies: Archaeoglobus fulgidus
CiAccession: D65521
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodso
CiAccession: D65521
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
Ashathors: Utterbrack, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeA;Accession: D65551
A;Accession: D65551
A;Accession: D65551
A;Relences: DNA
A;Residues: 1-363 https://doi.org/10.1097/ba.NID:g2689432; PIDN:AAB91255.1; PIDI:g26506]

Gaps ; Score 36; DB 2; Length 363; Pred. No. 9.1; 2; Mismatches 3; Indels 72.0%; 54.5%; Query Match
Best Local Similarity 54.5.
The Conservative

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1 EEVVPXGXDYS 11 ઠે 엄

120 ENIVPYGIDFS 130

AG3104 6-O-methylguanine-DNA methyltransferase [imported] - Agrobacterium tumefaciens (strain (C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

Claccession: AG3104
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel starp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2011
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, B.W. Ayılıtle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. AyReference number: AB2577; MUID:21608550; PMID:11743193 AyAccession: AG3104

A; Status: preliminary A; Molecule type: DNA

A;Gross-references: GB:AE008689; PIDN:AAL45253.1; PID:g17742937; GSPDB:GN00187 A;Experimental source: strain C58 (Dupont) A; Residues: 1-290 < KUR>

A; Map position: linear chromosome

Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative

1 EEVVPXGXDY 10 |:: | | || 9 EDITPIGSDY 18

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RESULT 7
42452
V1 protein - tobacco yellow dwarf virus (strain Australia)
V2 protein - tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A;Ticle: The mucleotide sequence of the infectious cloned DNA component of tobacco yell
A;Reference number: A42452; MUID:92188538; PMID:1546458
A;Accession: A42452
A;Molecule type: DNA
A;Residues: 1-102 <MOR>
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A;Title: Intragenic recombination and diversifying selection contribute to the evolutic A;Reference number: Z24999; MUID:99030193; PMID:9811794
A;Reference number: Z24999; MUID:99030193; PMID:9811794
A;Reteus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-908 cMCD>
disease resistance protein RPPB (validated) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Un-2000 #sequence_revision 02-Un-2000 #text_change 21-Uul-2000
C;Accession: T4889B
R;McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dang Plant Cell 10, 1861-1874, 1998
A;Title: Intragenic recombination and diversifying selection contribute to the evolutic A;Reference number: Z24999; MUID:99030193; PMID:9811794
A;Accession: T4889
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Mclecule type: DNA
A;Residues: 1-906 cMCD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AF089710; NID:g3928861; PIDN:AAC83165.1; PID:g3928862 A;Experimental source: Landsberg erecta C;Genetics: A;Gene: RPP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF089711; NID:g3901293; PIDN:AAC78631.1; PID:g3901294 A;Experimental source: Columbia C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease resistance protein rpp8 [similarity] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C;Accession: T48899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Description: promotes resistance to Peronospora parasitica
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Pred. No. 41;
2; Mismatches
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Local Similarity 60.0%;
les 6; Conservative 2
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Best Local Similarity 60.0
Matches 6; Conservative
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881 EKLVPGGEDY 890
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C;Function:
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C; Function:
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A; A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: A81000; MUID:2017575; PMID:10710307
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-587 < TET>
A; Cross-references: GB:AE002446; GB:AE002098; NID:g7226185; PIDN:AAF41356.1; PID:g722618
A; Experimental source: serogroup B, strain MC58
A; Experimental source: serogroup B, strain MC58
A; Mannocon
                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Agrobacterium tumefaciens
C;Apcession: Dogues: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: Dogues
C;Accession: Dogues
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2333-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Accession: D98182
                                                                                                                                                                                                                                                                                                                                                                                                           (Bt
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                                                                                                                                                                                                                                                                                                                                                                                                    O6-methylguanine-DNA methyltransferase PA2118 [imported] - Agrobacterium tumefaciens
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C;Genetics:
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Pred. No. 25;
0; Mismatches 3; Indels
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                                                   Length 290;
                                                                                                                 3; Indels
                                                   Score 35; DB 2;
Pred. No. 12;
2; Mismatches
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A;Gene: AGR L 818 A;Map position: linear chromosome

Query Match Best Loc Matches

A Status: preliminary A Molecule type: DNA A, Residues: 1-290 <KUR>

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Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative

Gene: NMB0950

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unknown protein [imported] - Arabidopsis thaliana
(Species Arabidopsis thaliana (mouse-ear cress)
(Species Arabidopsis thaliana (mouse-ear cress)
(Species Arabidopsis thaliana (mouse-ear cress)
(Species Arabidopsis thaliana)
(Species Arabidopsis Arabidopsis thaliana)
(Species Arabidopsis A.; Backer, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Huddes, B.; Huizar, L.; Conwar, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Aratheas B.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.S., Li, J.H.; Di, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Sinin, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Reference and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cispecies: Vibrio cholerae
Cispecies: Vibrio sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Cispacession: F82491
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
R;Heidelberg, J.F.; Eisen, J.A.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:AE004358; GB:AE003853; NID:g9657566; PIDN:AAF96096.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ferrisiderophore reductase VCA0183 [imported] - Vibrio cholerae (strain N16961 serogrouf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 2
C;Superfamily: flavohemoglobin; cytochrome-b5 reductase homology; globin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AE005173; NID: g11094688; PIDN: AAG29624.1; GSPDB: GN00141
                                                                                                                               Gaps
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                                                                               Length 247;
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Pred. No. 27;
0; Mismatches 3; Indels
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                                                                               5
                                                                         Score 34; DB 2
Pred. No. 16;
1; Mismatches
                                                                         68.0%;
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Best Local Similarity 66.7%;
Matches 6; Conservative (
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54.5%;
                                                                                                     Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                                                                                                                                    48 EDVEPRGADY
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A; Molecule type: DNA
A; Residues: 1-257 <STC
A;Gene: SMb21444
A;Genome: plasmid
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A, Map position: 1
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                                                                            Query Match
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K.Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A.Title: The complete sequence of the 1,683-kb psymB megaplasmid from the N2-fixing endc A; Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Residues: 1-156 <2EM
A,Crosa-references: EMBL:274920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR01
A,Experimental source: strain S288C
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C;Species: Sinorhizoblum meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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                                                                                                                                                                                                                                                                                                                                                nypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
N,Alternate names: hypothetical protein O2612; hypothetical protein YOL303.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4,Accession: S54619
4,Molecule type: DNA
4,Redidues: 1-156 CDEH
4,Redidues: 1-156 CDEH
7,Redidues: BMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
submitted to the Protein Sequence Database, July 1996
A;Reference number: $66877
                                                                                                                                                                                                                                                                                                                                                                                                      Species: Saccharomyces cerevisiae
:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
                                                                                                        Gaps
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  A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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                                                  Length 102;
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                                                  Score 34; DB 2;
Pred. No. 6.1;
2; Mismatches
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Pred. No. 9.6;
1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: hypothetical protein YOR013w
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66.7%;
                                                Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 60...
6; Conservative
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RESULT 12

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Cispedes: Listeria monocycogenes
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
Cipacession: AG1272
C
NiAlternate names: anti-repression trans-activator; art protein; trey protein; trey protein; Species: simian immunodeficiency virus SIVCp2
A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-62p-1991 #sequence_revision 30-5ep-1991 #text_change 16-Jul-1999
C;Accession: S09988
R;Must, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: S09983; MUID:90259077; PMID:2188136
A;Accession: S09983; MUID:90259077; PMID:2188136
A;Accession: S09989
A;Reference number: S09983; MUID:90259077; PMID:2188136
A;Accession: S09988
A;Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36405.1; PID:9763085
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thiol peroxidases homolog 1mo1583 [imported] - Listeria monocytogenes (strain EGD-e)
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A;Cross-references: GB:NC_003210; PIDN:CAC99661.1; PID:g16411012; GSPDB:GN00177
A;Experimental source: strain EGD-e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: AIDS trans-regulatory splicing protein C;Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.0%; Score 33; DB 1; Length 124; 60.0%; Pred. No. 12; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.0%; Score 33; DB 2; Length 165; 66.7%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETVPAGGNYS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EVVPXGXDYS 11
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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e: 9 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: rev; trs; art
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A; Gene: lmo1583
C; Superfact
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                                                                                                                                                                                                                                                                                                                                                                                        peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus
Cispecies: Caulobacter crescentus
Cispecies: Caulobacter crescentus
Cispecies: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
CiAccession: H8766
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
N, J.; Ermclaeva, M.; White, O.; Salzborg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CyAccession: B49132; A49132

RyFischer-Vize, J.A.; Rubin, G.M.; Lehmann, R.
Development 116, 985-1000, 1992
A;Title: The fat facets gene is required for Drosophila eye and embryo development.
A;Tottle: The fat facets gene is required for Drosophila eye and embryo development.
A;Contents: isogenic st
A;Accession: B49132
A;Actus: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-2747 effs.
A;Contents: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:127839)
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A;Molecule type: nucleic acid
A;Residues: 1-2704, 'Wr, 2707,'ANNV' <F12>
A;Cross-references: GB:L04958; NID:g157410; PIDN:AAF01346.1; PID:g6013475
A;Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:129029)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Moleoule type: DNA
A;Residues: 1-433 <STO>
A;Cross-references: GB:AE005673; NID:g13425020; PIDN:AAK25284.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fat facets (faf) splice form 1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Length 433; 3; Indels

7

Score 34; DB Pred. No. 30; 2; Mismatches

Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative

C;Genetics: A;Gene: CC3322

266 EVILPPGFDYS 276

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1 EEVVPXGXDYS 11

trans-regulatory splicing protein - simian immunodeficiency virus SIVcpz

RESULT 14 VKLJSI

| :|| | |:| EVIVPDGODFS 1404

1 EEVVPXGXDYS 11

68.0%; Score 34; DB 2; Length 2747; 54.5%; Pred. No. 2.2e+02; ive 2; Mismatches 3; Indels

C; Keywords: alternative splicing

Local Similarity 54.

Best Loca Matches

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June 3, 2004, 11:32:06; Search time 4.86667 Seconds (without alignments) 117.693 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                OM protein - protein search, using sw model
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BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-909-164-46 50 1 EEVVPXGXDYS 11 Title: Perfect score: Scoring table: Sequence:

141681 Total number of hits satisfying chosen parameters: 141681 seqs, 52070155 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	s arabidopsi	8w4j9	-	Q8rg86 fusobacteri				chimpanze			_				Q99x15 streptococc		hordeun	Pin auluqoq 070119	Q919i2 salmonella			haemo	pomod	рошоц	thern	cryp		Bu8	pantoea	P20422 daucus caro	p£0	3330 archaeo	Q04667 rattus norv
	ai.		RPP8_ARATH		CARB FUSIN	Y11K TYDVA	HMPA_VIBCH	FAF DROME	REV_SIVCZ	TPX_LISIN	TPX_LISMO	YK14 CAEEL	ACDM RAT	SYR STRP3	SYR_STRP8	SYR_STRPY	PLAS ORYSA	PLAS_HORVU	PLAT_POPNI	YJAG SALTY	DDL GLOVI	SUGT MOUSE		A10A_HUMAN	CHAC HUMAN		YHA1 CRYPA	ACDM_HUMAN	ACDM_PIG	TR2M_PANAY	PLAS DAUCA	TKNK HUMAN	Æ	HES3_RAT
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	Match																		64.0															
,	Score	35	35	35	35	34	34	34	33	33	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	31	31	31	31	31	30	30	30	30
Result	No.		73	3	4	ហ	9	7	00	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	26	27	28	29	30	31	32	33

P14194 bacillus su P08203 escherichia P06190 salmonella C921e3 helicobacte P5606 helicobacte P5606 helicobacte P56308 lymnaea sta P38174 saccharomyc O5250 halomonas e Q92eu7 halomonas e C95865 bacillus su O15231 homo sapien P53998 kluyveromyc
CTC_BACSU ARAD ECOLI ARAD ECOLI SCOA_HELPY SCOA_HELPY OVUH LYMST AMP2_YEAST ECB2_HALEL ECB1_HALEL FOLC_BACSU Z185_HUMAN
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ALIGNMENTS

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EMBL, AB015468, BAB10695.1; -.
EMBL, AK117163, BAC41841.1; -.
InterPro, IPR000767, Disease_resist.
InterPro, IPR01611, LRR. 8888888888

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EMBL; AF089710; AAC83165.1; -.
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STRAIN-CV. COlumbia. and cv. Landsberg erecta;

STRAIN-CV. Columbia. and cv. Landsberg erecta;

MCDOWELLINE=99030193; PubMed=9811794;

MCDOWell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,

Holub E.B., Dangl J.L.;

"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPPB locus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cooley M.B., Pathirans S., Wu H.-J., Kachroo P., Klessig D.F.; "Members of the Arabidopsis HRT/RPP8 family of resistance genes confer resistance to both viral and comycete pathogens."; Plant Cell 12:663-676(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSGW475; OSGW475; OSGSY3; OSGSY4; OSGSY4; OSGW475; OSGW476; OSGW47
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STRAIN=cv. Columbia;
MEDDINE=22954850; PubMed=14593172;
Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                      70.0%; Score 35; DB 1; Length 908; 60.0%; Pred. No. 18;
                           Pfam; PF00560; LRR; 2.
PRIMIS; PR00331; NB-ARC; 1.
PRINTS; PR00334; DERSASRSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
DOMAIN 10 45 LEUCINE-ZIPPER.
DOMAIN 175 599 LRR 1.
REPEAT 600 623 LRR 1.
REPEAT 842 867 LRR 3.
REPEAT 842 867 LRR 3.
NP BIND 192 199 ATP (POTENTIAL); SEQUENCE 908 AA; 104448 MW; 3111991B17239693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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MEDLINE=20271766; PubMed=10810142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis.";
Plant Cell 10:1861-1874(1998).
   InterPro; IPR002182; NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 60.0 es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 7:31-63(2000).
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Chan M. W., Quant H.L. Tripp W., Chang C.H., Lead J.M., Potismi M.J.,

A. Marwa T., Bank H.L. Tripp W., Chang J.M., Abtyma S., Ansari Y.,

A. Marwa T., Bank J., Banca C., Conders C.S., Deng J.M., Abtyma S.P., Carnica P.,

A. Mayahizaki Y., Johnson-1900an C., Hisaku W. W., Isla S. W., Karnes M.,

A. Marshizaki Y., Chomson-1900an C., Hisaku W. W., Isla S. W., Karnes M.,

A. Mann S., Koosema E., Islaida J., Jiang P.K., Jones T. San K., Sank J.,

Banch S. W., Chomson-1900an C., Hisaku W. W., Isla S. W., Karnes M.,

Mann S., Koosema E., Islaida J., Jiang P.K., Jones T., Karnes M.,

Mannes K., Wayabers B. W. Anabachogia A., Edec J., R. Manmara Y.,

Bacto W., Manne K., Yangers B. W. Anabachogia A., Edec J., R. Manmara Y.,

Bacto W., Manne K., Yangers B. W. Anabachogia A., Edec J., R. Manmara Y.,

Bacto W., Hida K., Katou W., Sakurai T., Akiyama K., Ishida J.,

B. SEQUENCE FROM N. A. (ISOPOW).

B. SEGURING FROM N. (ISO
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us-09-909-164-46.rsp

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                                                                                                                                                                           Dark -> KGE (in Cv. Di-1/) and Cv.

Landsberg erecta).

GKGV -> EKGI (in cv. Landsberg erecta).

C -> R (in cv. Landsberg erecta).

E -> D (in cv. Landsberg erecta).

R -> D (in cv. Di-17).

G -> Q (in cv. Di-17).

G -> V (in cv. Di-17).

R -> T (in cv. Di-17).

R -> F (in cv. Di-17).

R -> P (in cv. Di-17).

R -> P (in cv. Di-17).

R -> P (in cv. Di-17).

R -> F (in cv. Di-17).

R -> F (in cv. Di-17).

R -> K (in cv. Di-17).

R -> K (in cv. Di-17).

R -> V (in cv. Di-17).

R -> C (in cv. Di-17 and cv. Landsberg erecta).

R -> C (in cv. Di-17 and cv. Landsberg erecta).
                                                                                                                               isoform 2),
/Frid=VSP_001171.
Missing (in isoform 2),
/Frid=VSP_007172.
IDGQL -> VDEQI (in cv. Landsberg erecta).
G -> E (in cv. Di-17).
SGK -> RGE (in cv. Di-17)
                                                                                                                                                                                                                                                                                                                                                                                                                     erecta).

C -> S (in cv. Di-17 and cv. Landsberg erecta).

T -> I (in cv. Di-17).

S -> R (in cv. Di-17).

S -> R (in cv. Di-17).

H -> Q (in cv. Di-17).

I -> L (in cv. Landsberg erecta).

KNXT -> RNNA (in cv. Di-17).

K -> N (in cv. Landsberg erecta).

K -> N (in cv. Landsberg erecta).
                                                                                                                   ATP (POTENTIAL).
WKMLLTSRNEGVGIH -> ELLWYIHEALFLLNS (in
                                                                                                                                                                                                                                                                                                                                                                                                          -> N (in cv. Landsberg erecta).
                                                                                                                                                                                                                                                                                                                    erecta).
C -> R (in cv. Di-17 and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                         -> F (in cv. Di-17 and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                                           Landsberg erecta).

E.GYYS -> KITYQB (in cv. Di-17).

A -> V (in cv. Landsberg erecta).

E -> Q (in cv. Landsberg erecta).

DNYLSWQ -> NYKIRWH (in cv. Di-17).

MY -> SH (in cv. Landsberg erecta).
                                                                                                                                                                                                                                                                                                                                              erecta).
DSEISTYSLFY -> YSKISAYDLFN (in cv.
erecta).
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29
87
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85
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REPEAT
REPEAT
NP BIND
VARSPLIC
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatcphyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

Sucosids II; Brassicales; Brassicaceae; Arabidopsis.
PRF -> SRFK (in cv. Di-17).
Y -> F (in cv. Di-17).
S -> Y (in cv. landeberg erecta).
C -> S (in cv. Landeberg cv. Landeberg
                                                                                                                                                                                                      Score 35; DB 1; Length 908;
Pred. No. 18;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | homologs; | homologs; | homologs; | homologs; | homologs; | miterPro; | IRRO01611; | LRR. | litterPro; | LRR. | litterPro; | litte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.0%; Score 35; DB 1; Length 910; 60.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation update)
Disease resistance protein RPH8A (RPP8 homolog A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 910 AA.
                                                                                                                                              erecta).
                                                                                                                                                                                                              70.0%;
                                                                                                                                                                                                                                            Best Local Similarity 60.0
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                     883 EKLVPGGEDY 892
                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGXDY 10
   564
584
595
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Best Local Similarity
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P59584;
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VARIANT
VARIANT
VARIANT
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RP8H ARATH
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ALLOSTERIC DOMAIN.

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16-OCT-2001
16-OCT-2001
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Si
Matches 6
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SEQUENCE
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Q9KMY3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
Y11K TYDVA
ID Y11K TYD
AC P31619;
DOMAIN
REPEAT
REPEAT
NP BIND
NP BIND
NBTAL
METAL
METAL
METAL
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HMPA_VIBCH
   844444444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21866394; DubMed=11889109; MEDLINE-21866394; DubMed=11889109; MEDLINE-21866394; DubMed=11889109; MEDLINE-21866394; DubMed=11889109; MEDLINE-21866394; DubMed=11889109; MEDLINE-21866394; DubMed=11889109; Martanal V., Anderson A., Bartman A., Chagan Y., Chaga O., Goltsman B., Bernal A., Larsen N., Walumas T., Pusch G., Haselkorn R., Larsen M., Kypides N., Walumas T., Pusch G., Haselkorn R., Chonce sequence and analysis of the oral bacterium Fusobacterium Genome sequence and analysis of the oral bacterium Fusobacterium or nucleatum strain ATCZ 25586 [2]; J. Bacteriol. 184:2005-2018 [2002].

J. Bacteriol. 184:2005-2018 [2002].

J. Bacteriol. 184:2005-2018 [2002].

J. Bacteriol. 184:2005-2018 [2002].

J. CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + COPACTOR: Binds a manganese ions per subunit (By similarity).

J. PATHWAY: Arginine biosynthesis; first step.

J. SUBUNIT: Composed of two chains; the small (or glutamine) chain promptes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain contains the sarbamoyl phosphate (By similarity).
       ô
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PÉGMI, PFUZIT.

PÉGMI, PROJUGUS, CPSASE.

PRINTS, PRO0098; CPSASE.

TICRRAMS; TICRO1369; CPSASE.

TICRRAMS; TICRO1369; CPSASE.

PROSITE; PSO0086; CPSASE.1; 2.

PROSITE; PSO0086; CPSASE.2; 2.

PROSITE; PSO0086; PYLIMIDATE DIOSYNTHERIC DOMAIN.

ATD-binding; Manganese; Complete proteome.

CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

402 546 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (BC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                           PRT; 1058 AA.

    -i- SIMILARITY: Belongs to the carB family.

   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE010554; AAL94625.1; ALT_INIT.
HAMAP; MF_01210; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF 01210; -; 1.
InterPro; IPR006275; CarA L glu.
InterPro; IPR005481; CPase L
InterPro; IPR005481; CPase L D2.
InterPro; IPR005481; CPase L D3.
InterPro; IPR005481; MS II.
InterPro; IPR00481; MS II.
Pfam; PP00289; CPsase L Chain; 2.
Pfam; PP02784; CPsase L D3; 1.
Pfam; PP02784; CPsase L D3; 1.
   6; Conservative
                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                              ввѕ Екцурссвый в94
                                                               1 EEVVPXGXDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusobacterium.
NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                        CARB FUSNN
QBRGB6;
                                                                                                                                                                                                                         RESULT 4
CORR FUSNN
CORR FUSNN
CORR FUSNN
CORR FUSNN
CORR FUSND
CORR BACKED
CO
   Matches
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                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-92188538; PubMed-1546458; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonus plants."; virology 187:633-642(1992).
ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                            70.0%; Score 35; DB 1; Length 1058; 60.0%; Pred. No. 22; 2; Indels ive 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ll protein. 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses, ssDNA viruses, Geminiviridae, Mastrevirus.
NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Se or send an email to license@lsb-sib.ch).
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InterPro; IPR002621; Gemini mov.
Pfan; PF01708; Gemini mov; I.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Guery Local Similarity 60.00,
                                                                                                                                                                                                                                                                                                  Local Similarity 60.0
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                                                                                                           2 EVVPXGXDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EVVPXGXDYS 11
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                                                                                SEQUENCE FROM N.A.
STRAIRE 1 TOV NIL6661 / Serctype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                 cholerae.";
Nature 406:477-483(2000).
-!- DOMAIN: CONSISTS OF TWO DISTINCT DOMAINS; ONE IS A HEME-CONTAINING OXYGEN BINDING DOMAIN IN THE N-TERMINAL REGION AND THE OTHER IS AN FAD-CONTAINING REDUCTASE DOMAIN FOUND IN THE C-TERMINAL REGION.
-!- SMILARITY: BELONGS TO THE GLOBIN FAMILY. TWO-DOMAIN FLAVOHEMOPROTEINS SUBFAMILY.
-!- SIMILARITY: 10 A NUMBER OF FAD/NAD(P) FLAVOPROTEIN OXIDOREDUCTASES.
                                                                                                                                                                                                       'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
IRON (HEME PROXIMAL LIGAND)
(BY SIMILARITY).
NADP (RIBOSE PRAT) (BY SIMILARITY)
DDA3490PAE28823A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00311; FPNCR.
PRINTS; PR00410; PHEHYDRXLASE.
PR05ITE; PS01033; GLOBIN; 1.
Oxidoreductase; NADP; Heme; Flavoprotein; FAD; Iron transport;
Oxygen transport; Transport; Complete proteome.
DOMAIN
 Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin).
                                Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.0%; Score 34; DB 1; Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRON (HEME DISTAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR008333; FAD_binding_6.
InterPro; IPR001709; FPN cyt_redctse.
InterPro; IPR0010971; Globin.
InterPro; IPR001433; Oxxed FAD/NAD(P).
InterPro; IPR00121; Phe_hydroxylase.
Pfam; PF00970; FAD_binding_6; 1.
Pfam; PF00047; Globin; 1.
Pfam; PF000175; NAD_binding_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AE004358, AAF96096.1; -. PIR; F82491, F82491.
HSSP, P39662; ICQX.
TIGR, VCA0183; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44191 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
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394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
                       Vibrio cholerae.
            OR VCA0183.
                                                          NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
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STANDEMER FROM NA. S.

STANDEMER FROM NA. S.

STANDEMER STORE TO SE. LIP PW. Hoskins R.A., Galle R.F.,

Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celliker S.E., Holt R.A., Formy G. Chen L.X.

Adams M.D., Celliker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Abhurner M., Henderson S.N.,

Sutton G.G., Wortman J.E., Tandell M.D., Zhang Q., Chen L.X.

A Bandon R.C., Regers Y.-H.C., Bazel R.G., Chempe M., Petelfer B.D.,

Man K.H., Doyle C., Bazer E.G., Helt G., Walson C.R., Miklos G.L.G.,

Man K.H., Doyle C., Bazer E.G., Helt G., Walson C.R., Miklos G.L.G.,

Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Boctlain M.R., Boure J., Bayraktaroglu L., Bessley E.M.,

Ballew R.M., Cavley B., Buller H., Caddeu E., Center A., Chandra I.,

Buttis K.C., Busam D.A., Buller H., Caddeu E., Center A., Chandra I.,

Buttis K.C., Busam D.A., Buller H., Caddeu E., Dovttis P.,

Buttis K.C., Busam D.A., Buller H., Caddeu E., Dovttis P.,

Buttis K.C., Busam D.A., Hell M. J., Helman T.J., Hernandez J.R., Duck S.M.,

Cherry J.M., Cavley S., Dahlker C., Down P., Dew I., Dietz S.M.,

de Pablos B., Delcher A., Howland T.J., Hernandez J.R., Houck J.,

A Barris N.L., Harnan T.J., Hernandez J.R., Houck J.,

A Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,

A Harris N.L., Harvey D.A., Helman T.J., Marny D.J.A., Kennison J.A.,

A Harris N.L., Harvey D.A., Helman T.G., Warny E., Mornison D.A.,

A Harris N.L., Martel B.B., Molloch T.C., Moriel J., Mornison J.A., Mollon D.L.,

A Harris N. Moly M., Murphy B., Murphy L., Marny D.M., Nelson D.L.,

A Harris N. Molson K.A., Nixon K., Muskern D., Scheler F., Shen H.,

A Reiner K., Remington K.A., Nixon K., Warny D.W., Nelson D.K.,

Balazolo M., Pittman G.S., Pan S., Pollor, Scheler F., Shen H.,

Spier E., Spradling A.C., Stapleton M., Stupsk M., Stupsk M., Shen H.,

A Mang Z.-Y., Massarman D.A., Weinstock G.M., Walssenbach J.,

Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,

A Harris W. Walley B
P55824; Q9V9T6; Q9V0Z7;
01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3,1.2.15)
Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3,1.2.15)
(Ubiquitin thiolesterase FAF) (Ubiquitin-specific processing protease
FAF) (Bobiquitinating enzyme FAF) (Fat facets protein).
FAF OR BCDNA:LD2582 OR CG1945.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Weoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
PSPydroidea; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS, AND ALTERNATIVE SPLICING.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra C.D., Tupy Y., Kaninker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND TISSUE SPECIFICITY. TISSUE-Eye imaginal disk;
MEDLINE-93202020; Pubmed 195747;
Fischer-Vise J.A., Rubin G.M., Lehmann R.;
"The fat facets gene is required for Drosophila eye and embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development.";
Development 116:985-1000(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Gaps

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3; Indela

0; Mismatches Pred. No. 13;

6; Conservative

Matches

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2778 AA.

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RESULT 7

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TPX_LISIN
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DT 28-FB
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EMBL; L04959; AAF01345.1; -

EMBL; L04950; AAF01347.1; -

EMBL; L04950; AAF01347.1; -

EMBL; L04950; AAF01347.1; -

EMBL; L04950; AAF01348.1; -

EMBL; L04950; AAF01348.1; -

EMBL; AE003779; AAN14291.1; -

EMBL; AE003779; AAN14291.1; -

EMBL; AE0000532; faf,

EMBL; AE000533; CH4_2.1; 1.

EMBL; AE00033; CH4_2.1; 1.

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| SEQUENCE OF 1089-2778 FROM N.A. (ISOFORM 1).
| STRAIN=Berkeley; | Strain=2015(12); | PubMed=10731138; | STRAIN=Berkeley; | PubMed=10731138; | Strain=20156012; | PubMed=10731138; | Strain=20156012; | PubMed=10731138; | Strain=20156012; | PubMed=10731138; | Strain=20156012; | Strain=20156012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-mib.ch/announce/or send an email to license@isb-sib.ch).
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-i- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-i- SIMILARITY: Belongs to peptidase family C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing, Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                         Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P55824-2; Sequence=VSP_005270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sold=P55824-3; Sequence=VSP_005269;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ubiquitin + a thiol.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----
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                      IATAATLEPÄGNSELTTWVEKNLIISQENPQAKSSLQ -> SQRQQL (in isoform 2). /FTdd=vSP 005270.  
E > D (TR REF. I). 
T > S (IN REF. I) AAF01345). 
MW, FFB90438BA53A02B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 345:356-359(1990).

-I- FUNCTIONALLY TO RELIEVE
NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.

-I- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.

-I- PFM: Phosphoprotein whose state of phosphorylation is mediated by a specific serine kinase activity present in the nucleus.
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90259077; PubMed=2188136;
Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-359(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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PIR, S09988; VKLJSI.
HIV, X52154; REV$CET.
InterPro; IPR000625; REV_protein.
Pfam; PF00424; REV; 1.
Pramscription regulation; AIDS; Phosphorylation; Nuclear protein.
SEQUENCE 124 AA; 13701 MW; FS877DIBDF65A7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
REV protein (Anti-repression transactivator protein) (ART/TRS).
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                                                                                                                                                                                                           Score 34; DB 1; Length 2778; Pred. No. 97; 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.0%; Score 33; DB 1; Length 124; 60.0%; Pred. No. 6.2; arive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimpanzee immunodeficiency virus (SIV(cp2)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11723;
/FTId=VSP_005269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                   68.0%;
54.5%;
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2725 2725
2778 AA; 311139
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                                                                                                                                                                                                                                                                          Conservative
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ETVPAGGNYS 116
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                                                                                                                                                                                                              Query Match
Best Local Similarity
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P17280;
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                                                                                                            CONFLICT
CONFLICT
SEQUENCE
                               VARSPLIC
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Nature 368:32-38(1994)
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YK14_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BYBL outstated to the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                       Gaps
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MEDLINE=21537279; PubMed=11679669;
Glaeer P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Glaeer P., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antioxidant; Oxidoreductase; Peroxidase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.0%; Score 33; DB 1; Length 165; 66.7%; Pred. No. 8.4; 2; Indels cive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listeria monocytogenes.
Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
NCBL_TaxID=1639;
                                                                               Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77705B7CD8BC8F4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
TPX OR LMO1583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 AA
Probable thiol peroxidase (EC 1.11.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL596169; CAC96856.1; -.
PIR; AH1635; AH1635.
Listilist; LINO1625; -.
HAMAP; MF 00269; -; 1.
InterPro; IPR000866; AhpC-TSA.
Pfam; PF00578; AhpC-TSA.
PROSITE; PS00278; AhpC-TSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 AA; 18162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 EVVPEGSDH 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EVVPXGXDY 10
                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                         Listeria innocua.
                                                                                                     NCBI_TaxID=1642;
                           PX OR LIN1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPX LISMO
                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPX_LISMO
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Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Briian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Gobbel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Khinh M., Khust F., Kurapkat G., Andtournam A., Mata Vicente J., Ng E., Nedjari H., A Nordalak G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Remmel B., Rose M., Schlueter T., Simces N., Tierrez A., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P., Comparative genomics of Listeria species.";

G. Gomparative genomics of Listeria species.";

G. I- FUNCTION: Has antioxidant activity. Could remove peroxides or H(2)O(2) (By similarity).

C. I- SIMILARITY: Belongs to the ahpc/tsa family. Tpx subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=SHISTOL N2;
WHOLINE=SHISTOL N2;
Wilson R., Ainscough R., Canderson K., Baynes C., Berks M.,
Wilson R., Ainscough R., Candell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardher A., Green P., Hawkins T., Hillier L., Jier M.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer B., Staden R.,
Sulston J., Thierry Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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SEQUENCE 165 AA, 18133 MW, 77705B7CC46D424D CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.0%; Score 33; DB 1; Length 165; Best Local Similarity 66.7%; Pred. No. 8.4; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YXI4_CAREL STANDARD; PRT; 327 AA. 234338.
P34338.
P494384 (Rel. 28, Created)
O1-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C15H7.4 in chromosome III.
Caenorhabditis elegana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listilist; LM001583; -.
HAMAP; MF_00269; -; 1.
InterPro; IPR000866; AhpC-TSA.
InterPro; IPR002065; IPX.
Pfam; PF00578; AhpC-TSA; 1.
PROSITE; PS01265; TPX; 1.
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ACT SITE
SEQUENCE
                                                                                                                                                                                  ACT_SITE
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                           Matches
ઠે
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                              01-AUG-1988 (Rel. 08, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor (EC_1.3.99.3) (MCAD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Homotetramer.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
of different substrate specificities are present in mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liol. Chem. 262:10104-10108(1987). FUNCTION: This enzyme is specific for acyl chain lengths of 4 to
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver;
MEDLINE-67280028; PubMed=3611054;
Matsubara Y., Kraus J.P., Ozasa H., Glassberg R., Finocchiaro G.,
Ikeda Y., Mole J., Rosenberg L.E., Tanaka K.;
"Molecular cloning and nucleotide sequence of cDNA encoding the
entire precursor of rat liver medium chain acyl coenzyme A
                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
                                                                                                                                                                                             66.0%; Score 33; DB 1; Length 327; 63.6%; Pred. No. 17;
                                                                                                                                                                                                                           3; Indels
                                                                                                                                PIR; S40753; S40753.

Wormbep; 015H7.4; CB00082.

Hypothetical protein.

SEQUENCE 327 AA; 35566 MW; 716BC2BDD2E9607E CRC64;
                                                                                                                                                                                                                                                                                                                                                 421 AA
                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, J02791; AAA40670.1; -. PIR, A28436; DERTCM. HSSP; P11310; LEGD.
                                                                                                                    EMBL; Z22173; CAA80126.1; -.
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                KEVVPNGGDKS 185
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                      1 EEVVPXGXDYS 11
                                                                                                                                                                                                                Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - 1 - COFACTOR: FAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dehydrogenase.";
J. Biol. Chem. 20
                                                                                                                                                                                                                                                                                                                                               ACDM RAT
P08503;
                                                                                                                                                                                                                                                                                 175
                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                     ACDM_RAT
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CSTRAIN=SSI-1 / Secotype M3;

MEDLINE=22683278; PubMed=12799345;

MEDLINE=22683278; PubMed=12799345;

MEDLINE=22683278; PubMed=12799345;

MARAGAWA I., Kawabata K., Yamashita A., Nakata M., Tomiyasu Y.,

MARAGAWA II., Kattori M., Hamada S.;

Hayashi H., Hattori M., Hamada S.;

Machanen sequence of an M3 strain of Streptococcus pyogenes reveals at a neoperace of an M3 strain of Streptococcus pyogenes reveals at a neoperace grand of an M3 strain of Streptococcus pyogenes reveals at not phage evolution.";

Targe-scale genomic rearrangement in invasive strains and new insights into phage evolution.";

Genome Res 13:1042-1055(2003)

Genome Res 13:10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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28-FEB-2003 (Rel. 41, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
ARGS OR SPYM3_1809 OR SPS1807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 193 FORMS A HYDROCEN-BOND WITH THE FLAVIN N($) OF THE FAD COFACTOR (BY SIMILARITY) 401 BASE (BY SIMILARITY). 421 AA, 46555 MW; 2CF076F8C919BDE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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STRAIN=MGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
MEDLINE=22133808; PubMed=12122206;
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
Genome sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MITOCHONDRION.
ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN
SPECIFIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
R InterPro; IPR006099; Acyl-CoA_dh.
R InterPro; IPR006090; Acyl-CoA_dh.C.
R InterPro; IPR006091; Acyl-CoA_dh.M.
InterPro; IPR006091; Acyl-CoA_dh.M.
R Pfam; PF00441; Acyl-CoA_dh; 1.
R Pfam; PF00770; Acyl-CoA_dh; 1.
R PROSITE; PS00073; Acyl-CoA_Dh; 1.
R PROSITE; PS00073; Acyl-CoA_Dh; 1.
R PROSITE; PS00073; Acyl-CoA_Dh; 1.
R Mitcochondrion; Transit peptide.
TRANBIT
1 25 MITOCHOURION.
T CHAIN 26 421 Acyl-CoA_DEHYDROGENASE, MEDIUM-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.0%; Score 33; DB 1; Length 421; 50.0%; Pred. No. 22; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes (serotype M3).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 50.0 nes 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGXDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||::|
58 EEIIPVAPDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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NCBI_TaxID=198466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRP3
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
SYR_STRPY
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                      EMBL; AE014171; AAM80416.1; -.

R EMBL; AP005146; BACG4902.1; -.

R INTERPO: JEN001279; ANG LENNA-SYNL_1C.

R INTERPO: IPR005148; N. ANG LENNA-SYNL_1C.

R INTERPO: IPR005148; N. ANG LENNA-SYNL_1G.

R INTERPO: IPR005149; TRNA-SYNL_1G.

R INTERPO: IPR005199; TRNA-SYNL_1G.

R INTERPO: IPR00519; TRNA-SYNL_1G.

R PÉAM; PF00750; TRNA-SYNL_1G.

R PÉAM; PF00750; TRNA-SYNL_1G.

R PRINTS; PR01038; TRNA-SYNL_1G.

R RINTS; PR01038; TRNASYNTHARG.

R RINTS; PR01078; AA TRNA LIGASE I; FALSE NEG.

R PROSTIE; PS00178; AA TRNA LIGASE I; FALSE NEG.

W Aminoacyl-trNA synthétase; Proteīn biosynthesis; Ligase; AIP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seres 2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginyl--FRNA synthetase (EC 6.11.19) (Arginine--tRNA ligase) (ArgRS).
ARGS OR SPYMI8_2183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chaussee M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., "Kapur V., Daly J.A., Vary L.G., Museer J.M.; Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outbreaks.";

proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).

proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).

-!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP + diphosphate + L-arginyl-tRNA(Arg).

-!- SUBUNIT: Monomer (By aimlarity).

-!- SUBCELULIAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 66.0%; Score 33; DB 1; Length 563; 45.5%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                           121 131 "HIGH" REGION.
563 AA; 63134 MW; BOB7DEC31A9DCF63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 563 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Best Local Similarity
Matches 5; Conserv
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EMBL; AE010119; AAL98627.1; -. HAMAP; MF_00123; -; 1.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@l8b-sib.ch).
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Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(201).

-! CATALYNIC ACTIVITY: AIP + L-arginine + tRNA(Arg) = AMP + diphosphate + L-arginyl-tRNA(Arg).

-! SUBCELLULAR LOCATION: Cytoplasmic.
-! SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
ARGS OR SPY2151.
                                                                                                                                          Pfam; PF03485; N-Arg; 1.
Pfam; PF03485; N-Arg; 1.
Pfam; PF05746; tRNA-synt 1d; 1.
Prin; PF03746; tRNA-synt 1d; 2.
PRINTS; PR01038; TRNASYNTHARG:
TIGRAPMs; TIGR00456; args; 1.
PROSTIE; PS00178; AA TRNA LIGASE 1; PALSE NEG.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      563 AA; 63134 MW; FECAF176A68D8B5B CRC64;
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InterPro; IPR001278; Arg_trNA-synt_lc.
InterPro; IPR001278; N.
InterPro; IPR006348; N.
InterPro; IPR006909; tRNA-synt_ld_C.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR001278; Arg_tRNA-synt_lo.
InterPro; IPR005148; N.
InterPro; IPR001909; tRNA-synt_ld_C.
InterPro; IPR001412; tRNA-synt_l.
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MEDLINE=21192684; PubMed=11296296;
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Pfam; PF03485; N-AEG; 1.
Pfam; PF05750; tRNA-synt_1d; 1.
Pfam; PF05746; tRNA-synt_1d_C; 1.
PTGREPMS; PRO138; TRNASYNTHARG.
TIGREPMS; TIGRO0456; args; 1.
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HSSP; Q05506; 1BS2.
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Best Local Similarity 45.5
Matches 5; Conservative
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Q99XL5;
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DR PROSITE, PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.

KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.

KW Complete proteome.

121 131

SQ SEQUENCE 563 AA; 63120 MW; E0F2CAC28D03B613 CRC64;

Query Match

G6.0%; Score 33; DB 1; Length 563;

Best Local Similarity 45.5%; Pred. No. 30;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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Search completed: June 3, 2004, 11:49:56 Job time : 4.86667 secs

1 EEVVPXGXDYS 11 |:|: | ||: 94 EQVITAGSDYA 104

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                                                           June 3, 2004, 11:35:06; Search time 29.8667 Seconds (without alignments) 116.206 Million cell updates/sec
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                                                                                                                                                                                                       1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                  1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                      OM protein - protein search, using sw model
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O52367
Q8ESV7
O30260
Q946J7
Q8DIHO
Q9XST4
Q81033
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Gapop 10.0 , Gapext 0.5
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sp fungl: *
sp human: *
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sp organelle: *
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DB 16; Length 149;

74.0%; Score 37;

Query Match

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STRAIN-VC-16 / DSM 4304 / ATCC 49558; Milte O., Nelson K.E., Kleathway 13; PubMed=389475; White O., Nelson K.E., Kleachum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Kerlavage A.R., Graham D.E., Kyrpides N.C., Pleischmann R.D., Ouackenbuhb J., Lee N.H., Sutton G.G., 2111 S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Kirkness E.R., Gocayne J.D., Weidman J.F., Mobonald L., Utterback T., Overbeek R., Gocayne J.D., Weidman J.F., Mobonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
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Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q946J7;
01-DBC-2001 (TrEMBLrel. 19, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
31-Agaroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34).
HMGR1.
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                                                                                                                                                                                                        Score 36; DB 16; Length 319;
Pred. No. 20;
2; Mismatches 2; Indels
Nucleic Acids Res. 30:3927-3935(2002).
EMBL; AP004594; BAC12465.1; -.
InterPro; IPR001279; Blactmase-like.
Pfam; PF00753; lactmase-B; 1.
Hypothetical protein; Complete protecme.
SEQUENCE 319 AA; 35617 MW; 3BDAE4BF13E79B37 CRC64;
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PIR; D69551; D69551.
ITGR; AF2411; D69551.
InterPro; IPR002103; Bac_luciferase.
Pfam; PR00296; bac_luciferase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCbl_TaxID=2234;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;
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Best Local Similarity 60.v-
Local Similarity 60.v-
6; Conservative
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Q946J7
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GO, GO:0064621; C:extrachronosomal DNA; IEA.

GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.

GO; GO:0016491; F:oxidored dehydrogenase activity, zinc-dependent; IEA.

GO; GO:0016491; F:oxidored dehydrogenase activity; IEA.

InterPro: IPR002283; ADH zinc.

InterPro: IPR0022885; ADH zinc.

InterPro: IPR002085; ADH zinc.

PROSTIR: PG00059; ADH zinc.

Metal-binding; Oxidoreductase; Zinc; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CFN299;
Rosenblueth M., Hynes M.F., Martinez-Romero E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: ZINC (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY.
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STRAINSHIEBBAI / DSM 14371 / JCM 11309;
STRAINSHIEBBAI / DSM 14371 / JCM 11309;
MEDLINE-22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
                                                Gaps
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobium/Agrobacterium group; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 AA; 31092 MW; 49B2F8117C33AE87 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Hypothetical conserved protein.
                                                                                                                                                                                                                                                                                                                                                                      01-UTN-1998 (TrEMBLrel. 06, Created)
01-UTN-1998 (TrEMBLrel. 06, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
Aryl-alcohol dehydrogenase homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.0%; Score 36; DB 2; 50.0%; Pred. No. 19;
                Pred. No. 5.2;
); Mismatches
                                                                                                                                                                                                                                                                                                                      298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
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                70.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
                Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                 113 EEVVPTSEDY 122
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                                                                                                          1 EEVVPXGXDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pRtrCFN299a.
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SEQUENCE
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Q8ESV7

RESULT 3 Q8ESV7

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Complete proteome.
SEQUENCE 1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64;
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                                                      72.0%;
                                  Query Match
Best Local Similarity 63.00,
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Best Local Similarity 54.5
Best Local 6; Conservative
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16 EDYVPSGGEYS 26
                                                                                                                                           1 EEVVPXGXDYS 11
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SEQUENCE FROM N.A.
STRAIN=Jersey;
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                                                                                                                                                                                                    Andrographis paniculata.";

Andrographis paniculata.";

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF98919; AALISONS.2;

EMBL, AF98919; AALISONS.2;

CO; GO: 10016021; C:integral to membrane; IEA.

GO; GO: 10016021; C:integral to membrane; IEA.

GO; GO: 10016021; C:integral to membrane; IEA.

GO; GO: 10016021; C:integral to membrane; IEA.

R GO; GO: 10016021; F:hydroxymethylglutaryl-CoA reductase (NADPH). .; IEA.

R GO; GO: 10016020; F:hydroxymethylglutaryl-CoA reductase activity; IEA.

GO; GO: 10016020; F:hydroxymethylglutaryl-CoA red.

InterPro; IPR009021; HMG-CoA red.

InterPro; IPR009023; HMG-CoA Rob. Dind.

InterPro; IPR009023; HMG-CoA Rob. Dind.

InterPro; IPR009023; HMG-CoA Rob. Dind.

InterPro; IPR009023; HMG-CoA Rob. II.

R FR0311F; PS001318; HMG-COA REDUCTASE 1; 1.

BOR PR031TE; PS001318; HMG-COA REDUCTASE 2; 1.

R RNSITE; PS001318; HMG-COA REDUCTASE 2; 1.

R RNSITE; PS001318; HMG-COA REDUCTASE 2; 1.

R RNSITE; PS00151; HMG-COA REDUCTASE 2; 1.

R RNSITE; PS00151; HMG-COA REDUCTASE 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Makamura Y., Xaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Nakamura Y., Xaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Kawashima K., Kimura T., Kishida Y., Kiqokawa C., Kohara M., Matsumoto M., Matsumot A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Makamosynechococcus elongatus BP-1.";

DNA Res. 9:123-130(12002)

I. DNA Res. 9:123-130(12002)

I. DNA Res. 9:123-130(12001)

R. GO:0005215; F:transporter activity; IEA.

GO:0005215; F:transporter activity; IEA.

R. GO:0005216; R:transporter activity; IEA.

InterPro; IPRO01036; Acritinin res.

InterPro; IPRO01036; Acritinin res.

InterPro; IPRO01036; Acritinin res.

R. FIGNYS; PRO0702; ACRIFIANTRP.

R. TIGREPAMS; TIGRO0915; 2A0602; 1.
  Andrographis paniculata.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids;
Jamids; Lamiales; Acanthaceae; Acanthoideae; Ruellieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.0%; Score 36; DB 10; Length 595; 70.0%; Pred. No. 42; 3; Indels tive 0; Mismatches 3; Indels
                                                                                                                                                                    Krishnan S., Banerjee N.S.;
"3-hydroxy-3-methylglutaryl coenzyme A reductase gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                595 AA; 63268 MW; 19A3EA572F67AB2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBDIHO;
01-MAR-2003 (TYEMBLrel. 23, Created)
01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-UUN-2003 (TYEMBLrel. 24, Last annotation update)
Multidrug efflux transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1044 AA.
                                                                                Andrographinae, Andrographis
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Best Local Similarity
                                                                                                                                [1]
SEQUENCE FROM N.A.
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MEDLINE=20422104; PubMed=10964405;
Pichon B., Mercan D., Pouillon V., Christophe-Hobertus C.,
Christophe D.;
"A method for the large-scale cloning of nuclear proteins and nuclear targeting sequences on a functional basis.";
Anal Biochem. 284:231-23(2000).
EMBL; AJ388531; CAB46833.1;
NON_TER 78
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                                                        Gaps
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01-MAR. 2003 (TrEMBLrel. 23, Last sequence update)
01-MAR. 2003 (TrEMBLrel. 23, Last annotation update)
Human-type bont protein.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
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Score 36; DB 16; Length 1044; Pred. No. 79;
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70.0%; Score 35; DB 6; Length 175;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 6; Length 78;
Pred. No. 6.8;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iwashita S., Itoh T.;
"A LINE-mediated gene diversity.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB081003; BAC11552.1;
SEQUENCE 175 AA; 19529 MW; CE7283CB98393BE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 78 AA; 8895 MW; B62486313555FBA1 CRC64;
                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1997 homologous protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 AA.
                                                        1; Mismatches
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Q81031

RESULT 281031

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MEDLINE=21608551. PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Hinkle G., Gattung S., Miller N., Halling C.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
                                                                                                                                                                                                                                                                                                                                        Ueno S., Kimura J., Kurohmaru M., Fukuta K., Iwashita S.;
"Gene organization of the chevrotain bcnt whose paralogue in
ruminantia includes an endonuclease domain of RTE-1 in the protein.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

BENBL; AB103377; BAC57061.1; -.
NON TER
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The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE 21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L., Wood D.W., Zahou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chanman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Lim J.J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Trao Y., Eiddle P., Jung M., Krespan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Dolan M.V.,
Q867A5 PRELIMINARY; PRT; 281 AA.

AC Q867A5 TEMBLEL: 24, Created)
DT 01-JUN-2003 (TEMBLEL: 24, Last sequence update)
DT 01-JUN-2003 (TEMBLEL: 24, Last annotation update)
DT 01-JUN-2003 (TEMBLEL: 24, Last annotation update)
DT Human-type Bont (Fragment)
DS Tragilla javanicus (Lesser Malay chevrotain).
S Tragilla javanyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Bukaryota; Butheria; Cetartiodactyla; Ruminantia; Tragulina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.NCBI _TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.0%; Score 35; DB 6; Length 281; 54.5%; Pred. No. 29; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 AA; 31557 MW; 8133A9BAFF7509A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
6-O-methylguanine-DNA methyltransferase.
ADA OR ATUT459 OR AGR L 318.
Agrobacterium tumefaciens (strain C58 / ATCC 33970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 AA.
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                                                                                                                                                                                                                                Tragulidae, Tragulus.
NCBL TaxID=9849;
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Q8U7J0
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MEDLINE=97160586; PubMed=9006920;

NEDLINE=97160586; PubMed=9006920;

Nobukuni T., Kobayashi M., Oomori A., Ichinose S., Iwanaga T.,

Nobukuni T., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.;

Takahashi I., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.;

Takahashi I., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.;

"An Alu-linked repetitive sequence corresponding to 280 amino acids is expressed in a novel bovine protein, but not in its human homologue.";

J. Biol. Chem. 272.2801-2807(1997).

EMBL; D85939; BAA20069.1;

SEQUENCE 217 AA; 24061 MW; E404BA2E35497828 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JU., 1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
P97 homologous protein.
P97 homologous protein.
Enkaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 6; Length 215;
Pred. No. 22;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=RZPD #750;
Iwashita S., Itoh T., Sezaki M., Oshima K., Hashimoto E. Iwashita S., Itoh T., Rasul T., Hashimoto K.;
"A LINE-mediated gene diversity.";
"A LINE-mediated gene diversity.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB081095; BAC15593.1;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 AA; 23822 MW; 7287C8B98E9D05C8 CRC64;
                                                                                                                                                                                         QBI031;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
H-MAR-2003 (TrEMBLrel. 23, Last annotation update)
H-type bcnt protein (Fragment).
                                                                                                                                                                     215 AA
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.0%;
54.5%;
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16 EDYVPSGGEYS 26
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16 EDYVPSGGEYS 26
            1 EEVVPXGXDYS 11
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hes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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RESULT 10

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Best Loca Matches

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RESULT 11

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STRAIN=MCSB / Serogroup B;
STRAIN=MCSB / Serogroup B;
STRAIN=MCSB / Serogroup B;
MEDLINH=201755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gawinn M.L., DeBoy K., Peterson J.D., Hickey E.K., Nelson W.C., Gazberg S.L., White O., Pleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark B.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gotton M.D., Traser C.M., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;
Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                 SEQUENCE FROM N.A.
MEDLINE=98367221; PubMed=9602175;
Takahashi I., Nobukuni T., Ohmori H., Kobayashi M., Tanaka S.,
Ohshima K., Okada N., Masui T., Hashimoto K., Iwashita S.;
"Existence of a bovine LINE repetitive insert that appears in the cDNA of bovine protein BCNT in ruminant, but not in human, genomes.";
Gene 211:387-394(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Kalnine N., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
Phelan M., Farmer A.,
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB009285; BAA31867.1; ---
EMBL; BC000991; AAH00991.1; ---
EMBL; BT009819, AAB88821.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Neisseria.
NCBI_TaxID=491,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%; Score 35; DB 4; Length 299; 54.5%; Pred. No. 32; ive 2; Mismatches 3; Indels
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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GO; GO:0015036, F:disulfide oxidoreductase activity, IEA.
GO; GO:0006118, P:electron transport; IEA.
InterPro; IPR003953; FAD bind2.
InterPro; IPR001327; FAD_pyr_redox.
                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:1873; CFDP1.
SEQUENCE 299 AA; 33593 MW; F4A9E928B669451A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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EMBL, AE002446; AAF41356.1; -.
PIR; F81138; F81138.
HSSP; P00363; IKF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis (serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 287:1809-1815(2000)
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                         IISSUE-Placenta;
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                                                                             PIR; D98182; D98182.

PIR; D98182; D98182.

OG GO:0005622; C:intracellular; IEA.

GO; GO:0003908; F:methylated-DNA-[protein]-cysteine S-methylt. . .; IEA.

GO; GO:0003168; F:methyltransferase activity; IEA.

GO; GO:0005188; F:transferase activity; IEA.

GO; GO:0006281; F:transferase activity; IEA.

GO; GO:0006281; F:transferase activity; IEA.

GO; GO:0006281; F:DNA repair; IEA.

GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.

InterPro: IPR001005; HTHARAC.

InterPro: IPR001497; Methyltransf_1.

Pfam; PP00165; HTH AraC; 2.

Pfam; PP001055; Methyltransf_1: 1.
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Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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TIGREAMS; TIGR00589; ogt; 1.
PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
Methyltransferase; Transferase; Complete proteome.
SEQUENCE 290 Aa; 31587 MW; B626592EF519977F CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
BCNT protein (CRANIOFACIAL development protein 1).
BCNT.
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Last annotation update)
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                                   EMBL; AE009374; AAL45253.1; -. EMBL; AE008240; AAK88982.1; -.
        294:2323-2328(2001).
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 54.5
Matches 6; Conservative
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        Science
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29UEE9
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Gaps

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DR InterPro; IPR0019952; FRD/SDH_FAD_BS.

DR InterPro; IPR001100; Pyr_redox.

DR Fam; PF004901; Bucc_DH_flav_C.

DR Pfam; PF004910; Bucc_DH_flav_C.

DR PRINTS; PR004910; Bucc_DH_flav_C: 1.

DR PRINTS; PR00411; PNDRDTASE1.

DR PRSTTE; PS00504; FRD SDH FAD BINDING; 1.

ROSTTE; PS00504; FRD SDH FAD BINDING; 1.

RAD; Flavoprotein; OxidoreducTase; Complete proteome.

SQ SEQUENCE 587 AA; 64502 MW; 9581701B08069003 CRC64;
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 Query Match
 70.0%;
 Score 35;
 DB 16;
 Length 587;

 Best Local Similarity 70.0%;
 Pred. No. 68;
 Alsmatches 3;
 Indels

 Matches 7;
 Conservative 0;
 Mismatches 3;
 Indels

 Qy
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 Db
 366 EVVVPQGEDY 375
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0; Gaps

Search completed: June 3, 2004, 11:57:35 Job time : 30.8667 secs

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Abb80525 Hepatitis
Abb80562 Hepatitis
Abb80566 Hepatitis
Abb80566 Hepatitis
Abb80567 Hepatitis
Abb80567 Hepatitis
Abb80569 Hepatitis
Abb80569 Hepatitis
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Abb80567 Hepatitis
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                                                              June 3, 2004, 11:31:01; Search time 45.933 Seconds (without alignments) 67.664 Million cell updates/sec
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                                                                                                                                                                                                                   1586107
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                           1586107 seqs, 282547505 residues
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Maximum Match 100%
Listing first 45 summaries
                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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52
1 EEVVPXGMSYS 11
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Match Length
           Copyright
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44	23	52 Hepatit	45 Hepatit	30 Hepatit	42 Hepatit	43 Hepatit	38 Hepatit	48 Hepatit	47 Hepatit	56 Hepatiti	57 Hepatit	37 Hepatit	51 Hepatit	47	810 Hepatitis	621 Novel hum	73 K		546 Hepatitis	
Abb80544	Abb805	Abb805	Abb805	308ddA	4bb805	Abb805	Abb805:	Abb805		Abb805	Abb805			Abb805	Aau768	_	Abg081	Abg058	_	
ABB80544	ABB80553	ABB80552	ABB80545	ABB80530	ABB80542	ABB80543	ABB80538	ABB80548	ABB80547	ABB80556	ABB80557	ABB80537	ABB80551	ABB80541	AAU76810	ABG03621	ABG08173	ABG05826	ABB80546	
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84.6	84.6						78.8							•		o,	9	. 6.94		
44	44	44	44	42	41	41	41	40	40	40	40	40	40	40	40	40	40	40	39	
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                           Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5
                                                                                                                                                                          note= "N-terminal acetyl"
                                                                                                                                                                                                                                                          /note= "C-terminal amide"
                                                                                                                                                                                                                                   'note= "D-form residue"
                                                                                                                                                     Location/Qualifiers
ABB80525 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                19-JUL-2001; 2001WO-US023169.
                                                                                                                                                                                                                                                                                                                                                        21-JUL-2000; 2000US-0220101P.
                                            08-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Lim-Wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                              (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-361643/39.
                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                Modified-site
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                                                                                                                               Synthetic.
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                        ABB80525;
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Indels

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Mismatches

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have viruide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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Best Local Similarity
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Pred. No. 0.002;
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96.2%; Score 50; DB 5; 100.0%; Pred. No. 0.002;

Query Match Best Local Similarity

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            ABB80566 standard; peptide; 11 AA.
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                             /note= "Valyl carbonyl forming keto-amide linkage with residue 7"
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'note= "N-terminal acetyl"
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                     ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C ^{\circ}
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n. 0.002;
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             (CORV-) CORVAS INT INC.
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                                                                                                                                                                                                                                                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
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               "C-terminal amide"
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                                                                                                                                                                                                        Brunck TK;
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                                                                                                                                                                         (CORV-) CORVAS INT INC
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Query Match

Best Loc Matches

protease

ABB80567;

RESULT 7

virucide.

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Gaps

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ABB80526 standard; peptide; 11 AA
                                                                                                          21-JUL-2000; 2000US-0220101P.
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                                                                                                                            protease
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ABB80526
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virus
ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
  Novel peptide
                                                  protease
                         activity
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Claim 17; Page 65; 69pp; English

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha **Etoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

Sequence 11 AA;

ö Gape ö DB 5; Length 11; 0.002; hes 0; Indels Query Match 96.2%; Score 50; DB Best Local Similarity 100.0%; Pred. No. 0.(Matches 11; Conservative 0; Mismatches

1 EEVVPXGMSYS

1 EEVVPXGMSYS 11

(first entry) ABB80526

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide. Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6

Synthetic

note= "N-terminal acetyl" Location/Qualifiers Key Modified-site Modified-site

note= "Norvalyl carbonyl forming keto-amide linkage with residue 7" note= "D-form residue" note= "D-form residue" residue Misc-difference 9 Misc-difference

WO200208251-A2

/note= "C-terminal amide"

31-JAN-2002

19-JUL-2001; 2001WO-US023169

CORV-) CORVAS INT INC

Brunck Levy OE, Lim-Wilby M,

Ĭ,

ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C virus WPI; 2002-361643/39. Novel peptide activity usefu

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus

Sequence 11 AA;

Claim 17; Page 65; 69pp; English.

protease

Claim 17; Page 64; 69pp; English

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      The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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virucide.
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                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44
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                                                                                                                               96.2%; Score 50; DB 5; Length 11; 100.0%; Pred. No. 0.002; ive 0; Mismatches 0; Indels
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residue 7"
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Best Local Similarity
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Best Loc Matches

RESULT

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                                                                                   Hepatitis C virus, HCV, serine protease, inhibitor; alpha-ketoamide, virucide.
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                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
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Pred. No. 0.013;
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                             standard; peptide; 11 AA.
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90.9%;
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Best Local Similarity
Matches 10: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Alpha-propynyl-glycinyl-carbonyl residue forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48.
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
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                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
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Brunck TK,

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                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ingredient
                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have viruside activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.5%; Score 46; DB 5; Length 11; 90.9%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-terminal acetyl"
                                 'note= "N-terminal acetyl"
                                                                                                                                            /note= "C-terminal amide"
                                                                                             'note= "D-form residue"
                                                                                                                        /note= "D-form residue"
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          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB80528 standard; peptide; 11
                                                                                                                                                                                                                                                21-JUL-2000; 2000US-0220101P.
                                                                                                                                                                                                                        19-JUL-2001; 2001WO-US023169.
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                                                                                                                                                                                                                                                                                                  Lim-Wilby M, Levy OE,
                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEVVPXGMDYS
                                                                                                                                                                                                                                                                                                                         WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                            Misc-difference
                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11 AA;
                                                                                                                                                                        WO200208251-A2
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Modified-site
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Modified-site
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Gaps

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Score 46; DB 5; Length 11; Pred. No. 0.013; 0; Mismatches 1; Indels

88.5%; 90.9%;

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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus
                          /note= "C-terminal amide"
       /note= "D-form residue"
11
                                                                                                                                                                                     Claim 17; Page 64; 69pp; English.
                                                                                         21-JUL-2000, 2000US-0220101P.
                                                                          19-JUL-2001, 2001WO-US023169
residue 7"
                                                                                                                        Lim-Wilby M, Levy OE,
                                                                                                        (CORV-) CORVAS INT INC.
                                                                                                                                        WPI; 2002-361643/39.
       Misc-difference
                                            WO200208251-A2
                      Modified-site
                                                            31-JAN-2002.
                                                                                                                                                                      protease.
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Brunck TK;

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus Gaps ; 0 88.5%; Score 46; DB 5; Length 11; 90.9%; Pred. No. 0.013; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.9
Matches 10; Conservative Sequence 11 AA;

1 EEVVPXGMSYS 11

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1 EEVVPXGMDYS 11

Search completed: June 3, 2004, 11:48:25 Job time: 45.9333 secs

us-09-909-164-47.rai

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ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Enterococcus faecalis
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54.5%;
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2294 EDVIPRGISFS 2304
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Best Local Similarity
Matches 6; Conserv
RESULT 2
US-09-134-000C-3738
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US-09-408-020-4
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Sequence 3738, Ap
Sequence 2902, Ap
Sequence 2902, Ap
Sequence 7885, Ap
Sequence 3, Appli
Sequence 236, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66, Appl
66, Appl
23, Appl
4, Appli
4, Appli
7, Appli
21, Appli
21, Appli
                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                       (without alignments)
48.399 Million cell updates/sec
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Sequence 4, R
Sequence 4, R
Sequence 7, Sequence 21,
Sequence 21,
Sequence 21,
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Sequence 2
Sequence 2
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                                                              June 3, 2004, 11:36:47; Search time 11.7333 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                       /cgm2 6/ptodata/2/iaa/5A COMB.pep:*
/cgm2 6/ptodata/2/iaa/5B COMB.pep:*
/cgm2 6/ptodata/2/iaa/6A COMB.pep:*
/cgm2 6/ptodata/2/iaa/6A COMB.pep:*
/cgm2 6/ptodata/2/iaa/PcTUS COMB.pep:*
/cgm2 6/ptodata/2/iaa/PcTUS COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-134-000C-3738
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US-08-637-759B-236
US-08-871-355A-236
US-09-201-945-236
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US-09-521-650-66
US-09-18-888-66
US-08-98-84-4
US-08-460-694-4
US-08-460-744-4
US-08-133-977-7
US-08-133-977-7
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US-08-463-772-21
PCT-US93-05000-21
US-08-464-517-22
US-08-246-361A-22
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US-09-328-352-7885
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                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-228-986-73
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Maximum Match 100%
Listing first 45 summaries
                                              - protein search, using sw model
                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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52
1 EEVVPXGMSYS 11
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Match Length DB
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Perfect score:
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No.
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) ORGANISM: Acinetobacter baumannii
US-09-328-352-7885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 5; Conserv
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US-09-760-946-2
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| Patent No. 6673910
| GENERAL INFORMATION:
| APPLICANT: Gary L. Breton et al. |
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR |
| TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS |
| CURRENT APPLICATION NUMBER: US/09/540,236 |
| CURRENT FILING DATE: 2000-04-04 |
| SEQ ID NOS: 3840 |
| SEQ ID NO 2902 |
| LENGTH: 1191
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 73, Application US/09228986

Parent NO. 6159198

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: US 1000/1020
TITLE OF INVENTION: UNDER: US/09/228,986
CURRENT APPLICATION UNDER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 73
LENGTH: 947
                             ) LUCATION: (327)..(328)
) OTHER INFORMATION: Amino acids 327 & 328 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-3738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                               Query Match 69.2%; Score 36; DB 4; Length 382; Best Local Similarity 66.7%; Pred. No. 22; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.4%; Score 34; DB 4; Length 947; Best Local Similarity. 66.7%; Pred. No. 1.6e+02; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                               332 LIPEGMSYS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pinus radiata
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US-09-540-236-2902
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                                                                                                                                                                                                                                                 3 VVPXGMSYS 11
                        NAME/KEY: MISC FEATURE LOCATION: (327)..(328)
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US-09-540-236-2902
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US-09-228-986-73
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FEATURE:
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RESULT 5 US-09-328-352-7885

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Sequence 7885, Application US/09328352
Fatent No. 6562958
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7885
LENGTH: 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Transtriator, Youla S.

APPLICANT: Transtriator, Youla S.

APPLICANT: Generon, Dale R.

APPLICANT: Generon, Dale R.

APPLICANT: Glico, Elies

APPLICANT: Glico, Elies

APPLICANT: Himme, Teddy

APPLICANT: Himme Peddy

FILE REFERENCE: 13/076-1-C1

CURRENT FILING NUMBER: US 09/542,675

PRIOR FILING DATE: 2000-04-03

PRIOR FILING DATE: 1999-04-06

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.1

SEQ ID NO 2:

LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.4%; Score 34; DB 4; Length 140
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels
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APPLICANT: Teantrizos, Youla S.
APPLICANT: Cameron, Dale R.
APPLICANT: Faucher, Anne-Marie
APPLICANT: Ghiro, Elise
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63.5%;
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Best Local Similarity 60.07
                    45 amino acids
                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
SEQUENCE CHARACTERISTICS:
                                                       STRANDEDRESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-637-759B-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                              1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                       1 EEISPLGWSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEISPLGWSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                       amino acid
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                       LENGTH:
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                APPLICANT: Halmos, Teddy
APPLICANT: Halmos, Teddy
APPLICANT: Linas-Brunet, Montse
TITLE OF INVENTION: Macrocyclic Peptides Active Against the Hepatitis C Virus
FILE REFERENCE: 13/076-1-C1
CURRENT APPLICATION NUMBER: US/09/760,946
CURRENT FILING DATE: 2001-08-23
PRIOR PILING DATE: 2000-04-03
PRIOR PILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) LOCATION: (10)
; OTHER INFORMATION: Tyr at position 10 is iodinated with I-125
US-09-760-946-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.5%; Score 33; DB 4; Length 12; Best Local Similarity 45.5%; Pred. No. 1.7; Matches 5; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 236, Application US/08637759B
Sequence 236, Application US/08637759B
Sequence 236, Application US/08637759B
Setent No. 5876331
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE PADRESS: 51
CORRESPONDENCE PATERAL PADRESS: 51
COUNTRY: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STREET: 1201 West Peachtree Street
CITY: Atlanta
STREET: 1201 West Peachtree Street
COUNTRY: USA
ZIP: 30309-3450
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EADABLE FORM:
MEDIUM TYPE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION NUMBER: DEC-1995
FILING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: BPMS 101
FELECAMUNICATION INFORMATION:
TELECHMICATION NUMBER: BPMS 101
TELECHMICATION NUMBER: BPMS 101
TELECHMICATION NUMBER: RPMS 101
TELECHMICATION NUMBER: BPMS 101
TELECHMICATION NUMBER: A35
INFORMATION FOR SEQ ID NO: 236:
                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1) CTHER INFORMATION: Asp at position 1 is biotinylated NAME/KEY: MOD RES LOCATION: (10)
                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Tracer for NS3 protease assay
NAME/KEY: MOD_RES
Goudreau, Nathalie
                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                SEQ ID NO 3
LENGTH: 12
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Pred. No. 7.8;
1; Mismatches 3; Indels
Score 33; DB 2; Length 45;
Pred. No. 7.8;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                       Sequence 236, Application US/08871355A

Sequence 236, Application US/08871355A

Patent No. 6015669

GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: 2200 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STRATE: Georgia
COUNTRY: USA

COUNTER: Georgia
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: 09-UN-1997
FILING DATE: 09-UN-1997
CLASSIFICATION DATE: 09-UN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 4.5.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERNICE/DOCKET NUMBER: RPMS 101 CO
TELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8795
; INPORVATION POR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
TENETHON FOR SEQ ID NO: 236:
TENETHON FOR SEQ ID NO: 236:
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3; Mismatches

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52 KEICPGGMGYT 62
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                                                                      1 EEVVPXGMSYS 11
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5177197-30
;Patent No. !
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   Matches
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PAPILICANT: KANZAKI, TETSUTO; CLOFSSON, ANDERS; MOREN, ANITA;
PREMSTEDT, CHRISTER: HELLMAN, ULF; MIXAZONO, KOHEI; CLAESSON-WELSH,
PREMSTEDT, CARL-HERNERK

HUMAN; HELDIN, CARL-HERNERK

HUMAN; TREADER OF SEQUENCES: 153

CURRENT ARGOWITH FACTOR-BETA1-BINDING PROTEIN
NUMBER OF SEQUENCES: 53

CURRENT APPLICATION NOTAS: 18/07/487,343

FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 4; Length 45; Pred. No. 7.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945 FILING DATE: CLASSIPICATION:
                                                              Sequence 236, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Atlanta
STATE: Georgia
CCUVIRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISCRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: REPMS 101
TELECOMMUNICATION INFORMATION:
TELEFHONE: (404) 873-8794
TELEFHORE: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 AND AND ADDRESSIVED TO ADDRESSIVE
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TYPE: amino acid
STRANDEDNESS: single
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Matches 6; Conservative
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HYPOTHETICAL: NO
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Score 33; DB 6; Length 65; Pred. No. 12;

63.5%;

Query Match Best Local Similarity

5177197-51

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or Fluorescent Reporter Molecules and
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Patent No. 6335429

GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Weber, Cai, Xiong
APPLICANT: Weber, Colm F.W.
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Caing, Han-Zhong
TITLE OF INVENTION: Or File Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
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                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
1S-09-357-952-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Description of Artificial Sequence:Synthetic , OTHER INFORMATION: Peptide US-09-521-650-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%; Score 32; DB 4; Length 10; 50.0%; Pred. No. 2.3; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                        Score 32, DB 3; Length 10;
Pred. No. 2.3;
3; Mismatches 2; Indels
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative
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ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 5, Conservative
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Search completed: June 3, 2004, 12:03:09 Job time: 11.8 secs

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Query Match
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                                                                                                          June 3, 2004, 11:57:42; Search time 33.7333 Seconds (without alignments) 91.741 Million cell updates/sec
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Sequence 6, 8
Sequence 10, 8
Sequence 47, 8
Sequence 49, 8
Sequence 50, 8
Sequence 51, 8
Sequence 51, 8
Sequence 11, 8
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-164-6
US-09-909-164-10
US-09-909-164-40
US-09-909-164-40
US-09-909-164-49
US-09-909-164-49
US-09-909-164-52
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                                                                                                                                                                                                                                                                                                                                                                 otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      1155919 seqs, 281338677 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                    finimum DB seq length: 0 taximum DB seq length: 2000000000
                                                                                                                                                                                       US-09-909-164-47
52
1 EEVVPXGMSYS 11
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Match Length DB
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Verfect score:
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No.
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Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl
19,	20,	23,	24,	28,	29,	33,	36,	37,	43,	14,	22,	26,	27,	61,	62,	21,	25,	31,	32,	32,	4,	4	d,	4	30,	34,	38,	39,	42,
Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence		Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence						
-09-909-164-1	-09-909-164-2	-09-909-164-2	-09-909-164-2	-09-909-164-2	-09-909-164-2	-09-909-164-3	-909-164-3	-09-909-164-3	-09-909-164-4	-09-909-164-1	-09-909-164-2	-09-909-164-2	-09-909-164-2	-09-909-164-6	-09-909-164-6	-09-909-164-2	-09-909-164-2	-09-909-164-3	-09-909-164-3	-09-909-164-3	-09-909-164-4	-09-909-164-4	-09-909-164-4	-09-909-164-4	-909-164-3	-09-909-164-	-09-909-164-3	-09-909-164-3	-09-909-164-4
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ALIGNMENTS

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Sequence 5, Application US/09909164
; Sequence 5, Application US/09909164
; Publication No. US20020068702A1
; Publication No. US20020068702A1
; GENERAL INFORMATION:
    APPLICANT: Lim-Wilby, Marguerita
    CURRENT APPLICANTON NUMBER: 60/220,101
    PRIOR PILING DATE: 2000-07-21
    NUMBER OF SEQ ID NOS: 62
    SEQ ID NOS: 62
    SEQ ID NO 5
    ARGUERITAL NUMBER: Marguerita
    ARGUERITAL NUMBER: Marguerital Number: Margueri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: 11-mer synthesized according to example 1 FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE
LOCATION: (6)._(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MOD_RES
LOCATION: (1)_.(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: artificial sequence
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OCHER INFORMATION: AMIDATION US-09-909-164-5
US-09-909-164-5
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Length 11;

DB 12;

Score 50;

96.2%;

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Nacoust 30-164-10

US-09-909-164-10

US-09-909-164-10

US-09-909-164-10

US-09-909-164-10

US-09-909-164-10

US-09-909-164-10

US-09-909-164-10

US-09-104-10

US-09-104-10

APPLICANT: Corvas International, Inc.

APPLICANT: Lin-Wilby, Marguerita

APPLICANT: Lin-Wilby, Marguerita

APPLICANT: Lin-Wilby, Marguerita

APPLICANT: Levy, Odile E

ITLE REFERENCE: INO1192-US

FILE REFERENCE: INO1192-US

CURRENT PELIAG DATE: 2003-03-25

PRIOR PPLICATION NUMBER: 60/220,101

PRIOR PLILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

LENGTH: 11

LENGTH: 11
                                                                                                                                            FEATURE:
OFFIER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11) ... (11)
OTHER INFORMATION: AMIDATION
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96.2%; Score 50; DB 12; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0014;

Matches 11; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: D-amino acid
US-09-909-164-9
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NAMES/KEY: MOD RES
LOCATION: (1) .. (1)
OCHER INFORMATION: ACETYLATION
FRATURE:
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
                                                                                                 TYPE: PRT ORGANISM: artificial sequence
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LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
FRATURE:
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                                                                                                                                                                                                                                        Sequence 6, Application US/0990164
Publication No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corves International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/090,164
CURRENT FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATEURIN Version 3.1
SEQ ID NO 64
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Publication No. US20020068702A1

Publication No. US20020068702A1

Publication No. US20020068702A1

Publication No. US20020068702A1

APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT APPLICATION NUMBER: US/09/909,164
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OTHER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
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  Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2000-07-21
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NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE LOCATION: (9). . . (9) OTHER INFORMATION: D-amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD RES
LOCATION: (1) (1)
THER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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LOCATION: (11). (11)
CTHER INFORMATION: AMIDATION
US-09-909-16-6
                                                                           1 EEVVPXGMSYS 11
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Sequence 49, Application US/09909164
Sequence 49, Application US/09909164
Publication No. US200200668702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REPERENCE: IN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3:1
SEQ ID NO 49
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                                                                                                                                                     TYPE: PRT
ORGANIEM: artificial sequence
ERATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 96.2%; Score 50; DB 12; Length 11; 1 Similarity 100.0%; Pred. No. 0.0014; 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , CURTION: (6) ...(5) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) ...(6) .
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NAME/KEY: MOD RES
LOCATION: (1) OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (11) (11)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAMEKEY: MISC FEATURE
LOCATION: (6)...(6)
CTER INFORMATION: leucine-(CO)
US-09-909-164-48
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NAME/KEY: MOD RES
LOCATION: (1) .. (1)
OTHER INFORMATION: ACETYLATION
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME CITY. MOD RES LOCATION: (11). (11) OTHER INFORMATION: AMIDATION FEATURE:
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Best Local Similarity
Matches 11; Conserva
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Sequence 200 of Application US/09909164

Sequence 300 of Application No. US20020068702A1

GENERAL INFORMATION:
APPLICANT: Corvas international, Inc.
APPLICANT: Levy, Odile E
APPLICANT: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ. ID NOS: 66-2
SOFTWARE: Patentin version 3.1
SEQ ID NO 47
LENGTH: 11
TYPE: PRT
CONTANT SET ENT
CONTANTS ATTIFICIAL SEQUENCE
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S-09-909-164-48
Sequence 48, Application US/09909164
Dublication No. US20020068702A1
GENERAL INFORMATION:
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile E
APPLICANT: Levy, Odile E
APPLICANT: Lim-Wilby, NoveL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01192-US
CURRENT PELLING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: 60/220,101
PRIOR PILING DATE: 2000-07-21
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                                                                                                                         Length 11;
                                                                                                                                                                                              0; Indels
                                                                                                                     Query Match 96.2%; Score 50; DB 12; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0
        OTHER INFORMATION: D-amino acids IS-09-909-164-10
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (6).7(6)
OTHER INFORMATION: valine-(CO)
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IS-09-909-164-47
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Sequence 52, Application US/0990164

Publication No. US20020068702A1

Generation No. US20020068702A1

GENERAL INFORMATION:

APPLICANT: Corvas International, Inc.

APPLICANT: Lim-Wilby, Marguerita

CURRENT APPLICATION NUMBER: 105/09/20,101

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PatentIn version 3.1

SEQ ID NO 52

LENGTH: Lim-Wilby, Marguerita

Marguerita

Marguerita

Seq ID NO 52
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96.2%; Score 50; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0014;
tive 0; Mismatches 0
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i OTHER INFORMATION: propynyl glycine-(CO)
US-09-909-164-52
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Publication No. US20020068702A1
                                                                                         LOCATION: (1) ... (1)
COTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: NOD RES
COCATION: (11). (11)
OTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: AND RES
COCATION: (11). (11)
COTHER INFORMATION: AMIDATION
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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NAME/KRY: MOD RES
NACATION: (11).
OTHER INFORMATION: AMIDATION
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Best Local Similarity 100.
Matches 11; Conservative
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                                               NAME/KEY: MOD_RES
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US-09-909-164-8
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FRICK PRILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SEQ ID NO 50

LENGTH: 11

LENGTH: 11
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Sequence 51, Application US/0999164
Sequence 51, Application US/0999164
Sequence 51, Application US/0999164
Sequence 51, Application US/0909164
Sequence 51, Application US/0900168702A1
SET INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: L
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NAME/STREE:
NAME/STRE
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96.2%; Score 50; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 51
LENGTH: 11
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ORGANISM: artificial sequence
FEATURE:
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EEVVPXGMSYS 11
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NAME/KEY: MISC_FEATURE
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RESULT 13
US-09-164-13
US-09-909-164-13
isquence 13, Application US/09909164
isquence 13, Application US/09909164
isquence 13, Application No. US20020068702A1
isquence 13, Application
isquence 13, Application
isquence 13, Application
isquence 12, Application NUMBER: US/09/909,164
isquence 12, Application NUMBER: 00/220,101
isquence 12, Application NUMBER: 00/220,101
isquence 13, Application NUMBER: 00/220,101
isquence 14, Application NUMBER: 00/220,101

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NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
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Pred. No. 0.0091;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 12; Length 11; Pred. No. 0.0091; 0; Mismatches 1; Indels
                                                                                                              FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
CTHER INFORMATION: norvaline-(CO)
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)...(8)
COCATION: (8)...(8)
COTHER INFORMATION: D-amino acid
US-09-909-164-12
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OTHER INFORMATION: norvaline-(CO)
FEATURE:
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Best Local Similarity 90.9%;
Matches 10; Conservative
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LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
NAME/KEY: MOD RES
LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
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    APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Lim-wilby, Marguerita
APPLICANT: Levo, Oddile R
APPLICANT: Levo, Oddile R
APPLICANT: Brunck, Terence K
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROFEASE INHIBITORS OF HEPATITIS C
GURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 00/20,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
LENGTH: 11
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NAME/KRY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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88.5%; Score 46; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 1; Indels
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LICCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
FEATURE:
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LOCATION: (9). (9)
OTHER INFORMATION: D-amino acid
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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JS-09-909-164-8
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LOCATION: (11)..(:
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Gaps
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Pred. No. 0.015;
0; Mismatches 1; Indels
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COTHER INFORMATION: ACETYLATION FRATURE: NAME/KEY: MOD RES INCATION: (11). (11) OTHER INFORMATION: AMIDATION FRATURE:
                                                                                                                                                 LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
                                                                                                                                                                                                            FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (8)..(8)
OTHER INFORMATION: D-amino acid
US-09-909-164-11
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Sequence 7, Application US/09909164
Sequence 7, Application No. US20020068702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: NOUVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: L05/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 7
ILENGTH: 11
ILENGTH: 11
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TOGRANSM: artificial sequence
PEATURE:
OTHER INFORMATION: 11-mer synthesized according to example 1
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86.5%; Score 45; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels
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LOCATION: (1) ...(1)

OTHER INFORMATION: ACETYLATION

FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (6) ...(6)

OTHER INFORMATION: norvaline-(CO)

FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (9) ...(9)

OTHER INFORMATION: D-amino acid

FEATURE:

NAME/KEY: MOD RES

NAME/KEY: MOD RES
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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 protein search, using sw model OM protein Run on:

June 3, 2004, 11:35:47 ; Search time 9 Seconds
(without alignments)
117.567 Million cell updates/sec

US-09-909-164-47 52 1 REVVPXGMSYS 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

hypothetical prote masking protein pr hypothetical prote	transport protein rho protein GDF-di hypothetical prote cyclin D2 ; rat	cyclin D2 - rat cyclin D2 - mouse cyclin D2 - human cyclin D1 - Affica	Cyclin D2 - chicke Cyclin D2 - chicke Cyclin D1 - zebra Cyclin D3 - human Cyclin D1 - human
2 T04456 2 A38261 2 E97333	2 PQ0616 2 T01457 2 B72481	2 IS8372 2 A41984 2 A42822 2 S57922	2 S57925 2 JC4579 2 S62730 2 B42822 2 A38977
1548 1712 84	175 223 279 288	289 289 299	2002 2002 2002 2002 2002
63.5 63.5 53.5	100 100 100 100 100 100 100 100 100 100	611.5 611.5 611.5 611.5 611.5	61.5 61.5 61.5 61.5 61.5 61.5
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ALIGNMENTS

hypothetical 367K protein - Cenarchaeum symbiosum C;Species: Cenarchaeum symbiosum C;Species: Cenarchaeum symbiosum C;Species: Cenarchaeum symbiosum C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000 C;Date: 11-Jan-2000 C;Peston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V. J. Bacteriol. 180, 5003-5009, 1998 C;Peston C;

ö Gaps ö Score 38; DB 2; Length 3472; Pred. No. 60; 4; Mismatches 1; Indels Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative

1 EEVVPXGMSYS 11 ઠે

2294 EDVIPRGISFS 2304 g

T39116
probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
probable sulfate permease - fission yeast (Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T39116
K;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, November 1999
A;Reference number: Z21829
A;Accession: T39116

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mostatues: 1-840 c.MBL.
A;Rostiques: 1-840 c.MBL.AL122779; PIDN:CAB60015.1; GSPDB:GN00066; SPDB:SPAC869.05c
A;Experimental source: strain 972h-; cosmid c869

C,Genetics: A,Gene: SPDB:SPAC869.05c

A; Map position: 1

Gaps ; 0 Query Match 71.2%; Score 37; DB 2; Length 840; Best Local Similarity 77.8%; Pred. No. 21; Matches 7; Conservative 1; Mismatches 1; Indels

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||| ||||: 135 VVPQGMSYA 143 3 VVPXGMSYS 11 ઠે g ó

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A, Map position: 5
A, Introns: 23/3; 56/3; 113/3; 257/2
Query Match
Best Local Similarity 60.0°
Matches 6; Conservative
                                                                                                                                                                        1276 EQKIPMGMSY 1285
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C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Date: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A;Teile: The nucleotide sequence of the infectious cloned DNA component of tobacco yelld
A;Reference number: A42452; MUID:92188538; PMID:1546458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cispecies: Clostridium acetobutylicum
Cibate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
Cibate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
Cibate: B97355
Rivoling, J.; Brecon, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
Jaly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA segregation ATPase, FtsK/SpoilIE family, YUKA B. subtilis ortholog [imported] - Clos
                                                                                                                                                                                                                                                                                                                                                                                                                              "Cross-references: EMBL:AL031261; PIDN:CAA20298.1; GSPDB:GN00067; SPDB:SPBC3H7.02. Experimental source: strain 972h-; cosmid c3H7
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A;Molecule type: DNA
A;Residues: 1-1498 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAKB1629.1; PID:g15026814; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC624
                                                                                     ulfate permease - fission yeast (Schizosaccharomyces pombe)
; Species: Schizosaccharomyces pombe
; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
; Accession: T40413
; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
ubmitted to the EMBL Data Library, August 1998
; Reference number: Z21926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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A,Molecule Vype: DDA
A,Residues: 1-102 <MOR>
A,Cross-references: GB:M81103; NID:g335283; PIDN;AAA47947.1; PID:g335284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cuery Match 71.2%; Score 37; DB 2; Length 877; Best Local Similarity 77.8%; Pred No. 22; Matches 7; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                     Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: SPDB:SPBC3H7.02
                                                                                                                                                                                                                                                                                                             Accession: T40413
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                              ESULT 3
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A;Cross-references: EMBL: Z81109; PIDN: CAB03241.1; GSPDB:GN00023; CESP:R10D12.10 A;Experimental source: clone R10D12
                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein precursor (clone TPP11) - tomato
C.Speciese Lycopersicon esculentum (tomato)
C.Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C.Accession: S57810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein R10D12.10 - Caenorhabditis elegans
C,Spacies Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24111
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: 322293; I78656
R;Mitchimore, C:; Traboni, C:; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1.225 «MIL»
A;Residues: 1.225 «MIL»
A;Cross-references: EMBL:U20592; NID:g924625; PIDN:AAA80497.1; PID:g924626
C;Superfamily: plant Kunitz-type proteinase inhibitor
                                                                                    0; Gaps
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Plant Mol. Biol. 28, 691-711, 1995
A;Title: Nature and regulation of pistil-expressed genes in tomato.
A;Reference number: S57808; WUID:95375233; PMID:7647301
69.2%; Score 36; DB 2; Length 1498; 60.0%; Pred. No. 63; 2; Indels tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.3%; Score 35; DB 2; Length 225; Best Local Similarity 54.5%; Pred. No. 13; Matches 6; Conservative 3; Mismatches 2; Indels
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A;Molecule type: DNA
A;Residues: 1-425 <WIL>
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A;Reference number: 219842
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ESULT 15
1S-09-164-11
Sequence 11, Application US/09909164
Sequence 11, Application US/09909164
Sequence 11, Application No. USZ0020068702A1
GENERAL INFORMATION:
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, NowHER: US/09/909,164
TITLE OF INVENTION: NOWHER: US/09/909,164
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 11
LENGTH: 11
LENGTH: 11
                                                                                                                       APPLICANT: Corvas International, Inc.
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lew, Odile E
APPLICANT: Lew, Odile E
APPLICANT: Lew, Odile E
APPLICANT: Lew, Odile E
APPLICANT: New, Develope E
APPLICANT: NOWEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT APPLICATION NUMBER: 60/220,101
PRIOR APPLICATION NUMBER: 60/220,101
NUMBER OF SEQ ID NOS: 62
SEQ ID NOS: 62
SEQ ID NO 7
LENGTH: 11
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SSULT 14
3.09-164-7
Sequence 7, Application US/09909164
Enblication No. US20020068702A1
GENERAL INFORMATION:
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LOCATION: (6). (6)
OTHER INFORMATION: norvaline-(CO)
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NAME/FRY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: D-amino acid
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OTHER INFORMATION: ACETYLATION
FRATURE:
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LOCATION: (11)...(11)
OTHER INFORMATION: AMIDATION
IS-09-909-164-7
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Best Local Similarity 90.9'
Matches 10; Conservative
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NAME/KEY: MOD_RES
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Query Match 86.5%; Score 45; DB 12; Length 11; Best Local Similarity 90.9%; Pred. No. 0.015; Matches 10; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                    ; NAME/KEY: MISC_FEATURE
; LOCATION: (6)...(6)
; OTHER INFORMATION: norvaline-(CO)
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (8)...(8)
; OTHER INFORMATION: D-amino acid
US-09-909-164-11
LOCATION: (1) ... (1)
COTHER INFORMATION: ACETYLATION
PEATURE:
NAME/KEY: MOD RES
LOCATION: (11)... (11)
OTHER INFORMATION: AMIDATION
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Sequence 13, Application US/09909164

Sequence 13, Application Work 052020068702A1

GENERAL INFORMATION

APPLICANT: Corvas International, Inc.

APPLICANT: Lewy, Odile B.

APPLICANT: Lewy, Odile B.

APPLICANT: Brunck, Terence K.

ITILE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C.

FILE REFERENCE: IN 1001192-US

CURRENT APPLICATION NUMBER: US/09/909,164

CURRENT FILING DATE: 2003-03-25

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin version 3.1

LENGTH: 11

LENGTH: 11
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Pred. No. 0.0091;
0; Mismatches 1; Indels
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                                                                                                                                                    LOCATION: (11)..(11)
OTHER INFORMATION: AMIDATION
FRATURE:
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-(CO)
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COTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)
COTHER INFORMATION: AMIDATION
FEATURE:
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NAME/KEY: NISC FEATURE
LOCATION: (8)..(8)
. CTHER INFORMATION: D-amino acid
US-09-909-164-12
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Best Local Similarity 90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Levy, Odile B
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
TITLE REPERENCE: IUN01192-US
CURRENT APPLICATION NUMBER: US/09/909,164
CURRENT FILING DATE: 2003-03-25
PRIOR PLLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 11
TYPF: LENGTH: 11
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US-09-164-12
Sequence 12, Application US/09909164
Sequence 12, Application US/09909164
Publication No. US20020068702A1
GENERAL INFORMATION
APPLICANT: Corvas International, Inc.
APPLICANT: Lim-Wilby, Marguerita
APPLICANT: Low, Odile E
TITLE OF INVENTION: NOVEL PEPTIDES AS NS-3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
GURRENT APPLICATION NUMBER: US/09/909,164
CURRENT PILING DATE: 2003-03-25
FRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 11
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FIFTER INFORMATION: 11-mer synthesized according to example 1
FEATURE:
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88.5%; Score 46; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 1; Indels
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE: NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: norvaline-(CO)
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LOCATION: (9). 7(9)
OTHER INFORMATION: D-amino acid
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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LOCATION: (11)...(11)
CTHER INFORMATION: AMIDATION
US-09-909-164-8
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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M protein - protein search, using sw model

June 3, 2004, 11:35:47 ; Search time 9 Seconds no una

(without alignments) 117.567 Million cell updates/sec

US-09-909-164-47 52 1 BEVVPXGMSYS 11 Mitle: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 scoring table: sequence:

283366 seqs, 96191526 residues 3earched:

283366 fotal number of hits satisfying chosen parameters:

dinimum DB seq length: 0
Aaximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Jatabase :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	1	probable sulfate p	sulfate permease -	V1 protein - tobac	DNA segregation AT	hypothetical prote	hypothetical prote	Q,	topoisomerase IV s	DNA-binding protei	14	cell division inhi	probable ABC subst	hypothetical prote	_	_	щ.	_	hypothetical prote	_	hypothetical prote	imat	cdc37 protein - fi	iron(III) ABC tran	bacteriocin BCN5 -	ATP-dependent DNA	conserved hypothet		DNA-directed RNA p
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ALIGNMENTS

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Cincession: T31308
Rischieper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
J. Bacteriol. 180, 5003-5009, 1998
Arithe: Genomic analysis reveals chromosomal variation in natural populations of the uralyscence number: 220994; MUID: 94422450; PMID: 9748430
A; Reference number: Z20994; MUID: 98422450; PMID: 9748430
A; Accession: T31308
A; Residual type: DNA
A; Residual type: DNA
A; Residual type: DNA
A; Residual type: Carachaeum symbiosum hypothetical 367K protein
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Cibbecies: Schizosaccharomyces pombe
Cibbecies: Schizosaccharomyces pombe
Cibbecies: O3-bec-1999 #sequence_revision O3-bec-1999 #text_change O3-bec-1999
CiAccession: T39116
Riburt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, November 1999
A; Reference number: Z21829
A; Accession: T39116
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; McGenile type: DNA
A; Residues: 1-840 <-HUN>
A; Cross-references: EMBL:AL132779; PIDN:CAB60015.1; GSPDB:GN00066; SPDB:SPAC869.05c
Cigenetics: A; Accession A; Accessio
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hypothetical 367K protein - Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       739116
probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 73.1%; Score 38; DB 2; Length 3472; Local Similarity 54.5%; Pred. No. 60; les 6; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
71.2%; Score 37; DB 2; Length 840;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: SPDB:SPAC869.05c
A,Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Si
Matches 6;
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-877 <LYN>

A; Accession: T40413

7; Conservative

Best Local Similarity Matches 7; Conserv

Query Match

C;Genetics: A;Gene: SPDB:SPBC3H7.02 A;Map position: 2

148 VVPQGMSYA 156

3 VVPXGMSYS 11

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A;Accession: T24111
A;Status: preliminary; translated from GB/BMBL/DDBJ
A;Status: preliminary; translated from GB/BMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 < WIL>
A;Cross-references: ZMB1:281109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
A;Experimental source: clone R10D12
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                                                                                                                                                                                                                                                                                          hypothetical protein precursor (clone TPP11) - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Accession: S57810
R;Milligan, S.B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
A;Title: Nature and regulation of pistil-expressed genes in tomato.
A;Reference number: S57809; MUID:95375233; PMID:7647301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               zinc finger protein AT-BP2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: S22293; 1786066
R;Mitchelmore, C; Trabon1, C; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: EMEL:U20592, NID:g924625, PIDN:AAA80497.1, PID:g924626
C,Superfamily: plant Kunitz-type proteinase inhibitor
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Score 36; DB 2; Length 1498;
Pred. No. 63;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 67.3%; Score 35; DB 2; Length 425; Best Local Similarity 50.0%; Pred. No. 26; Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.3%; Score 35; DB 2; Length 225; 54.5%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 5
A;Introns: 23/3; 56/3; 113/3; 257/2
     Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                           1276 EQKIPMGMSY 1285
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                                                                                                         1 EEVVPXGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: Z19842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-225 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP:R10D12.10
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C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yelld
A;Reference number: A42452; MUID:92188538; PMID:1546458
                                                                                                                                                                                                                                                                                                                                                                          COSS-references: EMBL:AL031261; PIDN:CAA20298.1; GSPDB:GN00067; SPDB:SPBC3H7.02; Experimental source: strain 972h-; cosmid c3H7
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A;Molecule type: DNA
A;Residues: 1-1498 <KUR>
A;Residues: 1-1498 <KUR>
A;Cross-references: GB;AE001437; PIDN;AAK81629.1; PID:g15026814; GSPDB;GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                            C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40413
S*Lyne, M:; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
submitted to the EMBL Data Library, August 1998
A;Reference number: 221926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-102 <MOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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Pred, No. 3.5;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.2%; Score 37; DB 2; Length 877; 77.8%; Pred. No. 22; tive 1; Mismatches 1; Indels
                                                                                     - fission yeast (Schizosaccharomyces pombe)
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69.2**%**; 60.0**%**;

Query Match Best Local Similarity 60.0 Matches 6; Conservative

OVVPSGINYS 16

A; Gene: CAC3709

2 EVVPXGMSYS 11

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Map position: 15R Superfamily: hypothetical protein YOR013w
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Beet Local Similarity 66.79,
Beet Local Similarity 65.79,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [|| |::||
2405 VVPAGLTYS 2413
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**Cross-references: GB:AE003967; GB:AE003849; NID:g9106347; PIDN:AAF84162.1; GSPDB:GN001

**Stresidues: 1-749 «SIM»

**Cross-references: GB:AE003967; GB:AE003849; NID:g9106347; PIDN:AAF84162.1; GSPDB:GN001

**Stresidues: R.J. G. Reliach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Ariones, M.S.; Bueno, M.R.F.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H. S. Gensank, June 2000

**Authors: Ferreira, W.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.B.; Laigradthors: Martins, E.M.F.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Palmieri, D.A. odrigues, W.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Oliveira, R.G.; Santelli, R.V.; Sawasak, Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; Constitution M.A.; de Rosa Jr., V.E.; de Silva, M.A.; da Silva, M.A.; da Silva, M.A.; verjovski-Almeida, S.; Vettore, A.L.; Z.; Reference number: AS328
Fitle: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-;Reference number: 158280; MUID:91187610; PMID:1901405
;Accession: 822293
;Accession: 822293
;Molecule trype: mRNA
;Residues: 1-670 cMTI>
;Cross-references: PMBL:X54250; NID:957519; PIDN:CAA38151.1; PID:957520
;Note: the authors did not translate the codon for residue 1
;Superfamily: HIV-EP2 enhancer-binding protein
;Keywords: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: H82691

Janonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent anonymous, The Xylella fastidiosa.

Jitle: 406, 151-157, 2000

Title: The genome sequence of the plant pathogen Xylella fastidiosa.

Reference number: A82515; MUID:20365717; PMID:10910347

Note: for a complete list of authors see reference number A59328 below

Accession: H82691

Status: preliminary

Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194203
INA-binding protein PRDII-BF1 - human
INA-binding protein PRDII-BF1 - human
INA-binding protein and protein is the compatibility complex enhancer-binding protein 1
Indicate: 22-dun-1990 #sequence_revision 22-dun-1990 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    opoisomerase IV subunit XF1353 [imported] - Xylella fastidiosa (strain 9a5c) ;Species: Xylella fastidiosa ;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 43;
2, Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative 2
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 VVPAGLTYS 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EVVPXGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESULT 10
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A; Reference number: A34203; MUID:90169514; PMID:2106471
A; Reference number: A34203; MUID:90169514; PMID:2106471
A; Accession: A34203
A; Status: preliminary
A; Molecule type: mRNA
A; Readdues: 1-2717 < PMID:38017; PIDN:CAA35798.1; PID:g38018
A; Realdues: 1-2717 < PMID:A; Reference: EMBL.X51435; NID:g38017; PIDN:CAA35798.1; PID:g38018
A; Realdwin Jr., A.S.; LeClair, K.P.; Singh, H.; Sharp, P.A.
Mol. Cell. Biol. 10, 1406-1414, 1990
A; Title: A large protein containing zinc finger domains binds to related sequence elemen A; Reference number: A34779; MUID:90205817; PMID:2108316
A; Accession: A34779
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 801-1072, NV. 1074-1168, VK., 1170-1225, VV., 1227-1434, VN., 1436-1607, I', 1609-16
A; Cross-references: GB:M32019
C; Superfamily: HIV-EP2 enhancer-binding protein
C; Keywords: DNA binding; transcription regulation; zinc finger
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#169491
cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus
cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
C;Dates: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
B;Richark, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
B;Richmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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A;Molecule type: DNA
A;Residues: 1-156 cDEM>
A;Cross-references: EmBL;Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR01
A;Experimental source: strain S288C
C;Genetics:
A;Cross-references: SGD:S0005539
A;Map position: 15R
C;Superfamily: hypothetical protein YOR013w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bypotherical protein YOR013w - yeast (Gaccharomyces cerevisiae)
NyAlternate names: hypothetical protein O2612; hypothetical protein YOL303.3
C;Species: Saccharomyces cerevisiae
C;Date: 08-Unl-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S54619; 566879
R;de Haan, M.; Maarse, A.C.; Grivell, L.A.
Submitted to the EMBL Data Library, May 1995
A;Reference number: S54617
A;Accession: S54619
A;Medcule type: DNA
A;Residues: 1-156 cDEH>
A;Cross-references EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
Submitted to the Protein Sequence Database, July 1996
A;Reference number: S66877
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C;Accession: E90544
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pult A; Peference number: A99512; MUID:21267165; PMID:11353084
A;Accession: E90544
                                                                                                                              ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
                                                                                                                                                                         C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: June 3, 2004, 12:00:03
Job time: 9 secs
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Nature 390, 364-370, 1997

A,Authors: Utcerback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Wosse, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: H69491
                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Wolecule type: DNA
A;Residues: 1-252 «KLB
A;Cross-references: GB:AE000970; GB:AE000782; NID:g2689293; PIDN:AAB89318.1; PID:g264860
C;Superfamily: cell division inhibitor minD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ispecies: Ureaplasma urealyticum; in constant change 02-Sep-2000 #sequence_revision 20-Aug-2000 #sequence_revision 20-Aug-2000 #sequence_revision 20-Aug-2000 #sequence_revision 20-Aug-2000 #sequence_revision 20-Aug-2000 #sequence 01.5.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. inhitted to GenBank, February 2000 #sequence of Ureaplasma urealyticum: Alternate views of a min; Reference number: A82870
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,Species: Campylobacter jejuni
,Species: Campylobacter jejuni
,Date: 16-Aug-1996 #text_change 08-Oct-1999
,Accession: 140758; S47317
,Hani, E.K.; Chan, V.L.
. Bacteriol: 177, 2396-2402, 1995
. Title: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd; Reference number: 140758; MUID:95247673; PMID:7730270
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A;Molecule type: DNA
A;Residues: 1-544 <GLAS
A;Residues: 1-544 <GLASD02133; GB:AF222884; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
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Pred. No. 14;
2; Mismatches 2; Indels
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A;Molecule type: DNA
A;Residues: 1-94 <RES>
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55.6%;
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 55.0
Local 5; Conservative
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81 EVIPAGMS 88
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A;Genetic code: SGC3
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26 DIFPSGMSY 34

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A;Status: preliminary
A;Molecule type: DNA
A;Realdues: 1-16 <br/>Afresidues: 1-116 <br/>A;Cross-references: GB:AL445566; PID:g14089674; PIDN:CAC13434.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
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                                                                                                                                                                                                                           Score 33; DB 2; Length 116;
Pred. No. 17;
0; Mismatches 2; Indels
                                                                                                                                               A,Gene: MYPU 2610
A,Genetic code: SGC3
C,Superfamily: Bscherichia coli ribosomal protein L20
                                                                                                                                                                                                                                  Query Match 63.5%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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           075355 homo sapien
099616 homo sapien
p90818 crithidia f
P52384 human herpe
P52384 human herpe
P52544 human herpe
P52671 rattus norv
P28931 tomato aspe
P16916 escherichia
P16918 escherichia
                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (BC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
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TOLB HABIN
BENP3 HUMAN
S216 HUMAN
GSP CRIFA
PRTP HSV6U
PRTP HSV6Z
SCTI YEAST
EDD KAT
V1A TAV
RHSA ECOLI
RHSC ECOLI
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HAMAP, MP. 01210; ...
INTERPRO: IPR006275; Cara L glu.
INTERPRO: IPR005483; CPase L D2.
INTERPRO: IPR005480; CPase L D2.
INTERPRO: IPR005481; CPase L D2.
INTERPRO: IPR005481; CPase L D3.
INTERPRO: IPR005481; CPase L N.
INTERPRO: IPR005481; CASE L N.
INTERPRO: IPR005481; CASE L N.
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CPSase_L_D3; 1.
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PF02787; CPSase L
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Y11K_TYDYA
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Y11K_TYDYA
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ZEPI_HUMAN
A10A_HUMAN
RLZ0 WYCPU
YJ49G_ARCPU
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genome sequence of Schizosaccharomyces pombe.";
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FRANSMEM
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ID Y11K_TYDVA
AC P31619;
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SEQUENCE FROM N.A.

STRAIN=972;

MEDLINE=1848401; PubMed=11859360;

MODLINE=1848401; PubMed=11859360;

MOOG V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Bouros J., Peat N., Hayles J., Basham D., Bowman S., Bouros J., Peat N., Hayles J., Basham D., Bowman S., Collins M., Comnor R., Cronin A., Davis P., Felewell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Honloryd S., Honnes M., McDonald S., McLean J., Andlovd S., Mones M., Jones L., Jones M., Lather S., McDonald S., McLean J., Money P., Moule S., Mungall K., Murphy L., Niblet D., Odell C., Andlore M., Squares R., Seeger K., Sharp S., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor K., Taylor K., Malsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Wolckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mallbert H., Abelloffer J., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Berry M., Cadleu B., Dreanc S., Gloux S., Lelaure V., Mortier S., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Porsburg S.L., Cerrutti L., Lowe T., Moreno S., Armstrong J., Porsburg S.L., Shakovski G.V., Ussery D., Barrell B.G., Nurse P.; Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;
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DR PEAM; PF02142; MGS; 1.

DR PRINTS; PR00098; CPSASE.

DR PROSTE; PS00866; CPSASE.1.

DR PROSITE; PS00866; CPSASE.1; 2.

DR PROSITE; PS00867; CPSASE.2; 2.

KM Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KM Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KM Arginine biosynthesis; Complete protecome.

AP-binding; Manganese; Complete protecome.

AND ARBOXYPHOSPHATE SYNTHETIC DOMAIN.

CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

***CARFERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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ATP (POTENTIAL).
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MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
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MANGANESE 3 (BY SIMILARITY).
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Pred. No. 7;
3; Mismatches 1; Indels
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Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable sulfate permease C3H7.02.
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60.0%;
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Best Local Similarity
Matches 6; Conserv
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074377;
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MEDIINE-2188538; PubMed=1546458;

Morris B-2188538; PubMed=1546458;

Morris B-2.188538; Fichardson K.A., Haley A., Zhan X., Thomas J.E.;

"The nucleotide sequence of the infectious cloned DNA component of
"The nucleotide sequence of the infectious cloned DNA component of
infecting monococytedonus plants.";

Virology 187:633-642(1992).
                                                                                       -!- SUBCELLULAR LOCATION; Integral membrane protein (Potential). -!- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
Nature 415:871-880(2002)
-i- FUNCTION, HIGH APPINITY UPTAKE OF SULFATE INTO THE CELL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
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01-011.
01-011.1993 (Rel. 26, Last sequence update)
01-0CT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
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                                                                                                                                                                               -!- SIMILARITY: Contains 1 STAS domain.
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GeneDB SPombe; SPBC3H7, 02; -.
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulph_transpt.
Pfam; PF001140; STAS; 1.
Pfam; PF00116; Stlfate transp; 1.
TIGRFAMS; TIGR00815; SulP; 1.
PROSITE; PS01130; SLC36A; 1.
PROSITE; PS010130; STAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL031261; CAA20298.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sauer U., Duerre P.;
"Sequence and molecular characterization of a DNA region encoding a
"Sequence and molecular characterization acetobutylicum.";
small heat shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
-!- SIMILARITY: Contains 2 FtsK domains.
-!- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATC. 824 / DSM 792 / VKM B-1787;
MEDLINE=2135925; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennet G.N., Xoonin B.V., Sahth D.R.;
Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Pred. No. 1.6;
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16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical protein CAC3709.
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                                                                                                                                                                                                                                                                                                                                              3; Mismatches
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; PubMed=8501044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 183:4823-4838(2001)
                                                                                                                                                                                        PIR; A42452; A42452.
InterPro; IPR002621; Gemini mov.
Edm., PF01708; Gemini mov. I.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A4
                                                                                                                                                                                                                                                                                                       69.2%;
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Best Local Similarity 60.v.
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7 QVVPSGINYS 16
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EMBL; AE007866; AAK81629.1; -. EMBL; X65276; CAA46379.1; ALT_FRAME. PIR; B97355; B97355. InterPro; IPR002543; FteK_SpoIIIE.

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                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-077-2003 (Rel. 42, Last annotation update)
2inc finger protein 40 (Human immunodeficiency virus type I enhancer-
binding protein 1) (HIV-EPI) (Major histocompatibility complex binding
protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Biochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN T-CELL ACTIVATION.
--- SUBCELLULAR LOCATION: Nuclear.
--- INDUCTION: By mitogens and phorbol ester.
--- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH ZINC-FINGER IN-BETWEEN.
--- SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=90169514; PubMed=2106471;
ABD C.M., Maniatis T.;
"A DNA-binding protein containing two widely separated zinc finger
motifs that recognize the same DNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-52222684, PubMed-1567844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
Gronenborn A.M.;
                                                                                                                                                 ö
                               Complete proteome; Repeat.
                                                                                                                Score 36; DB 1; Length 1498;
Pred. No. 27;
2; Mismatches 2; Indels
                                                                        675 682 ATP (POTENTIAL).
1498 AA; 168968 MW; FF42037A335A9649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NNR OF 2113-2142.
MEDLINE=91064333, PubMed=2248949;
MEDLINEsti J.G., Clore G.M., Appella E., Sakaguchi K.,
Gronemborn A.M.;
                                                                                                                                                                                                                                                                                     2717 AA.
Pfam; PF01580; FtsK_SpoiliE; 2.
PROSITE; PS50901; FTSK; 2.
Hypothetical protein; ATP-binding; Cc
DOMAIN 655 857
FTSK 1.
DOMAIN 1001 1189
                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR OF 2087-2142
                                                                                                                     69.2%;
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                          1276 EQKIPMGMSY 1285
                                                                                                                                                                              1 EEVVPXGMSY 10
                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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9
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                                                            DOMAIN
NP BIND
SEQUENCE
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ZEP1_HUMAN
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Homo sapiens (Human)
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Best Local Similarity
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SEQUENCE FROM N.A.
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CARBOHYD
SEQUENCE
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   RE REPARENCE OF THE REP
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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# Min; 194440; -.

# GO; GO:0005634; C:nucleus; TAS.

# GO; GO:0005634; C:nucleus; TAS.

# GO; GO:0005634; C:nucleus; TAS.

# R GO; GO:000567; F:DRA binding; TAS.

# R GO; GO:00056; Zf-C2H2; Zf-C2H2;

# R PROSITE; PS00026; ZINC FINGER C2H2 1; 4.

# PROSITE; PS00026; ZINC FINGER C2H2 2; 4.

# Transcription regulation; ZinC-finger; Metal-binding; DNA-binding;

# Transcription regulation; ZinC-finger; Metal-binding; DNA-binding;

# Transcription regulation; ZinC-finger; Metal-binding; DNA-binding;

# TAN FING 434 456 C2H2-TYPE.

# ZN FING 2087 2109 C2H2-TYPE.

# ZN FING 2087 2109 C2H2-TYPE.

# ZN FING 2087 2109 C2H2-TYPE.

# DOMAIN 803 806 POLY-SER.
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MEDLINE=91129256; PubMed=1825178;
Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recognition elements of cys-14, the structural gene for sulfate permease II in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROBABLE REVISIONS.
MEDUINE-9418925.f. Pubmed-8140616;
Sandal N.N., Marcker K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 1; Length 2717;
Pred. No. 80;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297217 MW; D45D3CA951FEA561 CRC64;
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                                                                                                                                                                              EMBL; X51435; CAA35798.1; -
                                                                                                                                                                                                                                          PDB; 3ZNF; 15-JAN-92.
PDB; 4ZNF; 15-JAN-92.
PDB; 1BBO; 31-OCT-93.
TRANSPAC; 700497; --
Genew; HGNC:4920; HIVEPI.
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2405 WPAGLTYS 2413
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2115 2110
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2123 2121
2127 2131
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                                                                                                                                                                                                                   PIR; A34203; A34203
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Matches 6; Conserv
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HELIX
SEQUENCE
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permease II and a putative human tumour suppressor.";

Trends Biochem. Sci. 19:19-19(1994).

-!- PUNCTION: UPTAKE OF SULFATE INTO THE CELL.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- INDUCTION: Highly expressed, but only in cells subject to sulfur limitation, and it is turned on by the positive-acting Cys-3 sulfur regulatory protein.

-!- MISCELLANEOUS: SULPATE PERMEASE II IS MAINLY FOUND IN MYCELIA.

-!- SIMILARITY: Belongs to the SLC26A/SulP transporter (TC 2.A.53)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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O60312; Q96914;
O60312; Cooo (Rel. 39, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-Octential phospholipid-transporting ATPase VA (EC 3.6.3.1) (ATPVA)
ATP10A OR ATP1C OR ATPVC OR KIAA0566.
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POTENTIAL.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4FC604B60798CE77 CRC64;
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POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001902; Sulph_transpt.
PERM, PR00916; Sulfate_transp; 1.
TICRFAMB; TICR00815; SulP; 1.
PROSITE; PS01130; SLC26A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M59167; AAA33615.1; ALT_SEQ.
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SEQUENCE FROM N.A.
                      EMBL;
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R Genew, HGNC:13542; ATP10A.

R MIM; 605855; -

R MIM; 105830; -

R GO; GO:00004012; F:phospholipid-translocating ATPase activity; NAS.

R GO; GO:000830; F:phospholipid-translocating ATPase activity; NAS.

R InterPro; IPR00157; ATPase E1-E2.

R InterPro; IPR005839; F:phospholipid; 1.

RR INTS; PR00119; CATATPASE.

R TIGRPAMS; TIGR01652; ATPase P-type; 6.

R TIGRPAMS; TIGR0149; ATPASE E1-E2; 1.

R Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding; MILIGENE FAMILY.

TRANSMEM 87 106 CYTOPLASMIC (POTENTIAL).

T RRANSMEM 87 106 POTENTIAL).

T TRANSMEM 87 106 POTENTIAL).
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PHOSPHORYLATION (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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Pred. No. 70;
0; Mismatches 3; Indels
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18 Q -> R (IN REF. 4).
167687 MW; D4996A4D0635A68D CRC64;
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POTENTIAL.
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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                                                  AAK33100.1; JOINED.
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                      EMBL; AY029494 AAK33100.1;
EMBL; AY029495, AAK33100.1;
EMBL; AY029495, AAK33100.1;
EMBL; AY029496, AAK33100.1;
EMBL; AY029498, AAK33100.1;
EMBL; AY029498, AAK33100.1;
EMBL; AY029500, AAK33100.1;
EMBL; AY029501, AAK33100.1;
EMBL; AY029501, AAK33100.1;
EMBL; AY029503; AAK33100.1;
EMBL; AY029503; AAK33100.1;
EMBL; AY029503; AAK33100.1;
EMBL; AN0139503; AAK33100.1;
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Best Local Similarity 72....
Best & Conservative
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267
292
499
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RL20 MYCPU
ID RL20 MYCPU
AC Q98QV0;
DT 28-FEB-2003 (C)
DT 28-FEB-2003 (C)
DT 28-FEB-2003 (C)
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CONFLICT
SEQUENCE
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TRANSMEM
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TRANSMEM
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RT The complete sequences of 100 new cDNA clones from brain which can recomine to sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

LONA Res. 5:31-39(1998)

C. -- CATALIVITY ATP + H(2)0 = ADP + phosphate.

--- CATALIVITY ATP + H(2)0 = ADP + phosphate.

--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

C. -- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

C. -- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

C. -- SUBSTASE: Defects in ATP10A are a cause of Angelman syndrome (AS)

(MIN:105830]; also known as 'happy puppet syndrome'. AS is characterized by features of severe motor and intellectual retardation, microcephaly, frequent jerky limb movements and flapping of the arms and hands, hypotomia, hyperactivity, characterized by macrostomia, a large mandible and open-mouthed characterized by macrostomia, propensity for protruding the tongue ('tongue thrusting'), and an occipial groove.

-- SIMILARITY: Belongs to the cation transport ATPases family (P-type Contaction and pages and a propensity for protruction transport ATPases family (P-type Contaction and pages and a protein and a p
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                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

Attauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Attauener R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Attauener R.D., Caeberg B., Battow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Zeeberg B., Battow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

A Diatchenok L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Scares M.B., Tocanido M.F., Caeavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

Brownstein M.J., McEwan P.J., McEwnan K.J., Malek J.A., Glubaraene P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Rale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

Human and mouse cDNA sequences",

"The Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.; "The human aminophospholipid-transporting ATPase gene ATP10C maps adjacent to UBB3A and exhibits similar imprinted expression."; Am. J. Hum. Genet. 68:1501-1505(2001).
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AY029488, PAK33100.1; JOINED.
AY029491, PAK33100.1; JOINED.
AY029491, PAK33100.1; JOINED.
AY029491, PAK33100.1; JOINED.
AY029491, PAK33100.1; JOINED.
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MEDLINE=98290545; PubMed=9628581;
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EMBL; AY029504; AAX33100.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 337-1499 FROM N.A.
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AY029492; AAK33100.1;
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Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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MEDILNE=2012012: PubMed=10688204;
MEDILNE=2015012: PubMed=10688204;
MEDILNE=2015012: PubMed=10688204;
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campylobacter jejuni.
Badteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 160-253 FROM N.A.
STRAIN=ATCC 43431 / TGH 9011;
MEDLINE=95247673; PubMed=7730270;
MEDLINE=95247673; PubMed=7730270;
MEDLINE=95247673; PubMed=7730270;
MEDLINE=95247673; PubMed=9730270;
MEDLINE=9524761970; PubMed=9730270;
MEDLINE=9730270;
MEDLINE=9730270270;
MEDLINE=9730270;
MEDLINE=9730270270;
MEDLINE=9730270270;
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MEDLINE=973027027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TICR; AF1949; -.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 7 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 AA; 17588 MW; BBC17054810ADBF8 CRC64;
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11-OCT-2001 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CJ0990C.
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Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 177:2396-2402(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000968; AAB89307.1; -.
PIR; D69493; D69493.
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EESIPDGASY 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIR-C1-6 / DSM 4304 / ATCC 49558;
STRAIR-C1-6 / DSM 4304 / ATCC 49558;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Klenk H.-P., Clayton R.A., Tomb J.-F., White So., Nelson K.E.,
Kterchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                         Mycoplasna pulmonis.
Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
                                                                                                                                                                                                                                                                                                                           STRAIN-UAB CTIP;
MEDLING=21267165; PubMed=11353084;
MEDLING=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Gal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mypulat; MYPO 2610; -.
HAMAP; MF 00382; -; 1.
HINEFPLO; IPR005812; Ribosomal L20.
Fram; PF00453; Ribosomal L20; T.
PRINTS; PR00062; RIBOSOMELL20.
FRINTS; PR00062; RIBOSOMELL20.
TIGREAMS; TIGR01032; rplT_bact; 1.
FRICKPAMS; TIGR01032; rplT_bact; 1.
FRIBOSOME, PS00937; RIBOSOME, L20; 1.
FRIBOSOME, RS00937; RIBOSOME, L20; 1.
FRIBOSOME L20; I.
FRIBOSOME L20; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 116;
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Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           028330;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
AF1949.
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Pred. No. 8.1;
0; Mismatches
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PIR; E90544; E90544.
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77.8%;
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Best Local Similarity 77.00,
                                  50S ribosomal protein L20 RPLT OR MYPU 2610.
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                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                          NCBI_TaxID=2107;
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SEQUENCE FROM N.A. (ISOFORNS 1 AND 2).

STRAIN-CS7BL/6J; TISSUR=Embryonic head;

MEDIINE-21085660; PubMed=11217851.

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Raxawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Raxawa T., Rara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Psole G., Quackenbush J.,

Schriml D., Staubi F., Sizuki R., Tomita M., Wagner L., Washio T.,

Schriml D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni I., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodřiguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaii H., Kohtsuki S.,

Hayashizaki Y., Leelen M. M., Handel M., Hayashizaki Y., Kawaii Y., Kanii Y., Kawaii Y., Kawaii Y., Kawaii Y., Kawaii Y., Kawaii Y., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
the Buropean Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TISSUB-Ammanary fibroblast;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L. L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernen K.J., Malek J.J., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                     h similarity 55.6%; Pred. No. 18; 5, Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                 EMBL; AL139076; CAB73246.1; -.
EMBL; Z3640; CAA85392.1; -.
PIR; C81374; C81374.
HJV; 1,40758; 140758.
HYPOChetical proteome.
SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTX3_MOUSE STANDARD; PRT; 280 AA. Q9D387; Q9CXQ4; CPEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 110-OCT-2003 (Rel. 42, Last annotation update) Protein C20orf103 homolog precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 DIFPSGMSY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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Best Local Similarity
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOId=09D387-2; Sequence=VSP 003820; CAUTION: Ref.1 sequence differs from that shown due to frameshifts in positions 174 and 239.
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnits Butterfield Y.S.N., Krzywinski M.I., Skalska U., Snailus D.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-! SUBCELLULAR LOCATION: Type I membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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AROA VIBCH
AROA VIBCH
AROA VIBCH
AROA VIBCH
ACCA VIBCH
ACCA CONTROL
ACCA 
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E -> V (IN REF. 1; BAB31124)
Q -> P (IN REF. 1; BAB31124)
P -> A (IN REF. 1; BAB31124)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
PROTEIN C20ORF103 HOMOLOG.
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bvent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FA11D7BF9FD5CCEF
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SIGNAL 1 29 POTENTIAL.
CHAIN 30 280 PROTEIN C20ORF1
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Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9D387-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AKO14127; BAB29169.1; -.
EMBL; AKO16222; BAB31124.1; ALT_FRAME.
EMBL; BC004791; AAH04791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1920368; 3110035N03Rik.
MGD; MGI:1923411; 6330527006Rik.
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Best Local Similarity 75.v.
6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMSY 10
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280 AA;
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CONFLICT
CONFLICT
SEQUENCE
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DOMAIN
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                        SOLUTION SELECTION SELECTI
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98 DSAIPGGMSY 107
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                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNEL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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         SEQUENCE FROM N.A.
STRAINEET TOR NIGHT SEROTUPPE 01;
STRAINEET TOR NIGHG-10552301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Doddon R.D., Haft D.H., Hickey B.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
MCDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
                                                                                                                                                               Nature 406:477-483 (2000).
-!- CATALYTIC ATTUITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyviny1)-3-phosphoshikimate.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF_0210; -; 1.

INTER-PRO; IPRO006264; ArcA.

INTER-PRO; IPRO01986; EPSP synth.

Promon; PP001867; EPSP synthase; 1.

PROSTITE; PS00104; EPSP SYNTHASE 1; 1.

PROSTITE; PS00885; EPSP SYNTHASE 1; 1.

Archica mino acid biosynthasis; 7: arnsferase; Complete proteome. SEQUENCE 426 AA; 46101 MW; 38852D6483BFEIC3 CRC64;
                                                                                                                                       "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.5%; Score 33; DB 1; Length 426; 60.0%; Pred. No. 31; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Westwood P.K., Preston N.C., Fantes P.A.;
"Schizosaccharomyces pombe cdc37 gene.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                    sixth step.
--- SUBUNIT: Monomer (By similarity).
--- SUBUNIT: Monomer (CATION: Cytoplasmic (Probable).
--- SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE004251; AAF94882.1; -. PIR; D82163; D82163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 EFVIPAGOSY 232
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094740;
                                                                                                                                                       cholerae."
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CC37_SCHPO
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239 EVAPAGASYN 248
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417
477
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BCN5_CLOPE
ID _BCN5_C
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                                                                                                                                                                                                                                                                                                                                  MEDLINE=2298825; PubMed=12477932;
A Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
A Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
B Diatchencho L., Marusila K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchencho L., Marusila K., Farmer A.A., Rubin G.M., Hong L.,
B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernen K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=92214318; PubMed=10196275;
BLUMI R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regular
                                                                                                                                                                                 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Schatthauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            GSR2_HUMAN STANDARD; PRT; 478 AA.
C9NZM5; Q9BTC6; Q9HAX6; Q9NPP1; Q9NPR4; Q9UF12;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID=9606;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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(FTIG=VAR. 011486.

GGS -> HEĞ (IN REF. 2; AAH04229).

G -> R (IN REF. 3).

RRKEQLWEKLAKQGELPREYRRAQARLLANESATRAKPGPQD

RYERP -> SGRSSYGRSWPERASSPGGAQGPSPVAQPFCN
KGPNTAPGHRIAA (IN REF. 3).

SDNPLDRPLVGQDEFFLE -> LNNPDKPVVWPGCLFPG
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REIQ -> VLTVSCRGAPCPVMTPSLLPVPPRGYGRHHGCP
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EGNILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFR
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MEDLINE=88336297; PubMed=2901768;
MEDLINE=88336297; PubMed=2901768;
MEDRILET T., Cole S.T.;
"Complete nucleotide sequence and genetic organization of the bacteriocinogenic plasmid, plP404, from Clostridium perfringens."; Plasmid 19:134-150(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDI.INE-8705/020; PubMed=2877971;
Garnier T., Cole S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pIP404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IN REF. 3).
A -> S (IN REF. 2, AAHO4229)
D -> H (IN REF. 3).
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01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Bacteriocin BCN5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM, 605691, -.
GO, 60016622; C:intracellular; NAS.
Nuclear protein; Polymorphism.
VARLANT 389 389 R -> Q.
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EMBL, BC064229; AAH04229.1; --
EMBL, BC010095; AAH10095.1; --
EMBL, BC296124; AAG31413.1; --
EMBL, AL359335; CAB94786.1; --
EMBL, AL359336; CAB94787.1; --
EMBL, AL122063; CAB94787.1; --
SWISS-ZDPAGE; QBNZMS; HUMAN.
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                                                                          SEQUENCE OF 1-14 FROM N.A.
STRAIN=CRN50;
MEDLINE=S8039249; PubMed=2460717;
Garnier T., Cole S.T.;
"Studies of UV-inducible promoters from Clostridium perfringens in vivo and in vitro.";
wincrobiol. 2:607-614(1988).
-1- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
-1- INDUCTION: By UV irradiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%; Score 33; DB 1; Length 890; 66.7%; Pred. No. 67; tive 1; Mismatches 2; Indels
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SEQUENCE 890 AA; 96699 MW; P4E5E8971C31C6C6 CRC64;
perfringens and molecular genetic analysis of the bacteriocin-encoding gene. ", J. Bacteriol. 168:1189-1196 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M14481; AAA982481;
EMBL; M32882; AAA982491;
PIR; A30481; A30481;
InterPro; IPR000834; Peptidase_M14.
InterPro; IPR00084; Peptidase_M14.
InterPro; IPR002646; SH3 bac.
Pfam; PF00246; Zn_carbOpept; 1.
SNART; SM00287; SH3b; 3.
Antibiotic; Bacteriocin; Plasmid.
BOWAIN
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Best Local Similarity 66.77
Matches 6; Conservative
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Gaps

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Search completed: June 3, 2004, 11:49:56 Job time: 4.86667 Becs

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Q8dihO synechococc Q8dis7 bacillus ce Q9153 bacillus ce Q9154 trizobium 1 07405 cenarchaeum Q9ury8 schizosacch Q8ew4 mycoplasma Q8116 mus musculu Q8h24 mus musculu Q8bx35 mus musculu Q8bx7 pseudomona Q8957 pseudomona Q80547 qaenorlabdi Q8cud7 mus musculu Q89547 mus musculu Q80547 musculu Q80547 mus musculu Q80547 
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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2: Sp_bacteria:*
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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RESULT 1

Q726r0 homo sapien Q9bha3 plasmodium Q9bha5 plasmodium Q81587 plasmodium Q01487 rattus ratt Q8mi6 xanthomonas Q8mi2 xanthomonas Q8mi2 xanthomonas Q9dm6 xy1ella fas Q12479 saccharomyc Q97182 sulfolobus Q96mi1 homo sapien Q92md6 rhizobium m Q92md6 rhizobium m	Q98bp5 rhizobium 1 Q9pd2 ureaplasma Q7uwu7 rhodopirell Q9ur47 penicillium Q8q415 bifidobacte Q8xt05 ralstonia s Q8xt67 methanopyru Q8ppp5 xanthomonas Q8vua8 lactococous Q8ktq4 candidatus Q8re56 fusobacteri Q7sy67 xenopus lae Q7us52 synechococc
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## ALIGNMENTS

ORDINO	H0 H						
£	QBDIHO	PRELIMINARY;	::	PRT; 104	1044 AA.		
AC AC	QBDIHO;			;			
占	01-MAR-2003	(TrEMBLrel.	23,				
H	01-MAR-2003	_		Last sequenc	sequence update)		
Ιď	01-JUN-2003	(TrEMBLrel.	24,	ast	annotation update)	٠	
E E	Multidrug efflux transporter.	flux transp	ortei				
Z	TLL1618.	1	į	•			
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58	NOBI TexTD-32046.	anobacteria 2046.	5	oococcares;	Bacreria; Cyanobacreria; Unrocccares; Symeomococcas;		
Z.							
R.	SEQUENCE FROM N.A.	M N.A.					
RC	STRAIN=BP-1;						
ΣX	MEDLINE=22225144; PubMed=12240834;	5144; PubMe	d=122	40834;			
RA	Nakamura Y.,	Kaneko T.,	Sate	S., Ikeuch:	Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sas	W.	ر. د.
RA	Watanabe A.,	Iriguchi N	ζ. Σ	Iriguchi M., Kawashima K., Kimura T.,	Kimura T., Kie		
RA	Kiyokawa C.,	Kohara M.,	Mate	umoto M., Ma		zaki N.,	
R.	Shimpo S., Sugimoto M., Takeuchi C., Yamada M.,	ugimoto M.,	Take	uchi C., Yar	nada M., Tabata S.;		
RT	"Complete ge	nome struct	ure	f the therm	"Complete genome structure of the thermophilic cyanobacterium	cterium	
E.	Thermosynechococcus elongatus BP-1.";	ococcus elc	ongati	S BP-1.";			
RL	DNA Res. 9:123-130(2002).	23-130 (2002					
DR	EMBL; AP005374; BAC09170.1;	74; BAC0917	70.1;	·			
띪	GO; GO:0016021;	21; C:integ	yral t	C:integral to membrane;	IEA.		
DR	GO; GO:0005215;	15; F:trans	sporte	r activity;	IEA.		
DR.	GO; GO:0006810;	10; Pitrans	sport	IEA.			
Д Н	InterPro, IPR001036; Acrflvin_res.	R001036; Ac	rflvi	n_res.			
DR	InterPro; IPR004764; HAE1.	R004764; H	E1.				
DR.	Pfam; PF00873; ACR	3; ACR_trar	tran; 1.				
DR.	PRINTS; PR00702; ACRIFLAVINRP.	702; ACRIFI	AVIN	μ.			
DR	TIGRFAMS; TIGR00915; 2A0602; 1	GR00915; 27	10602				
3	Complete proteome.	teome.					
SQ	SEQUENCE 1	.,	113205 MW;		00E9C13F0F636D2F CRC64;	4;	
g,	Query Match		75.0%;	Score 39;	16;	Length 1044;	
M B	Best Local Similarity Matches 7; Conser	vat	53.55; ive	Fred. NO. 20; 2; Mismatches	ches 2; Indels	ls 0;	Gaps

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1 EEVVPXGMSY 10
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NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                  074056
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                                                                                                                                                                                                                                                                                                                                   RESULT 4
074056
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Q9URY8
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X MEDLINE=21082930; PubMed=11214968;
A REDLINE=21082930; PubMed=11214968;
A Ratanabe A., Idesawa Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
A Watanabe A., Idesawa Y., Isbikawa A., Kawashima K., Kimura T.,
A Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
A Kishida Y., Kiyokawa S., Nakazaki N., Shimpo S., Sugimoto M.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabara S.,
Tomplete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.",
DNA Res. 7:331-338(2000).
R EMBL; APRO3002: BABS0445.1; -.
R GO, GO:0006508; F:hydrolase activity; IEA.
R GO, GO:0006508; F:metallopeptidase activity; IEA.
R GO, GO:0006508; P:proteclysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=22608415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Ivanova N., Sorokin A., Anderson I.,
Kapatral V., Battacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Xyrpides N.;
Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriacae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 16; Length 344;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                               Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 AA; 38539 MW; C55268ACB7225995 CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                             01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence v
01-0CT-2003 (TrEMBLrel. 25, Last annotation
ABC transporter substrate-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AE017015; AAP12123.1; -.
INTERFO, IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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GO; GO:0006508; P:proteolysis and
InterPro; IPR002933; Peptidase_M20
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01-0CT-2001 (TrEMBLrel. 18,
01-0CT-2001 (TrEMBLrel. 18,
01-JUN-2003 (TrEMBLrel. 24,
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843 EEVLPNGIGYS 853
                                                                                                                                                                                PRELIMINARY;
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1 EEVVPXGMSYS 11
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Best Local Similarity
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MLR3583.
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                                                                                                                                                                                Q815A7
Q815A7;
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The modern of analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";

If J. Bacteriol. 180:5003-5009(1998).

B. D. Bacteriol. 200:5003-5009(1998).

B. D. Bacteriol. 200:5003-5009(1998).

B. PIR; T31308; T31308.

C. G. GO:0016009; C. Temebrane; IEA.

B. GO; GO:0005315; F. transporter activity; IEA.

B. GO; GO:0005315; F. transporter activity; IEA.

B. Rockery: JRR0013015; B.D. transporter activity; IEA.

B. Rockery: JRR001680; WD40.

S. MART; SM00320; WD40; 2.

B. ROGATE; PS00402; B.D. TRANSP_INN_MEMBR; 1.

R. WHypothetical protein.

S. SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
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                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conarchaeum symbiosum.
Archaea; Crenarchaeota; Thermoprotei; Cenarchaea; Cenarchaeaceae; Cenarchaeota; Normarchaeota; Normarchaeum.
NCBI_TaxID=46770;
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Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3472;
                                                                                               73.1%; Score 38; DB 16; Length 387; 60.0%; Pred. No. 15; tive 2; Mismatches 2; Indels
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Pfam; PF01546; Peptidase_M20; 1.
Hydrolase; Complete protecme.
SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
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Bukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Probable sulfate permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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Pred. No. 1.7e+02;
4; Mismatches 1;
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Best Local Similarity 54.5
Local Similarity 6.5
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Best Local Similarity 60.v
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484 AA
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Best Local Similarity 60...
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TISSUE=Salivary gland;
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                                                             SEQUENCE FROM N.A
   NCBI_TaxID=10090;
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Q8VD18
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Saaaki Y., Ishikawa J., Xamashita A., Oshima K., Kenri T., Furuya K., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
EMBL; AP004411; BAC44662.1;
InterPro; IPR008985; ConA like lec gl.
InterPro; IPR007326; Lipoprotein.17.
FO4200; Lipoprotein.17; 3.
Complete proteome.
SEQUENCE 1123 AA; 123636 MW; A4D707330E3DB4AC CRC64:
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
71.2%; Score 37; DB 3; Length 840;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 1; Indels
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132779; CAB60015.1; -.
PIR; T39116; T39116.
                                                                                                                                                                                                                                                                                                                                                                                                  840 AA; 93517 MW; ED4833E162B69077 CRC64;
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Last annotation update)
                                                                          Geneb Spendbe, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416, 193416,
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
MYPE 2560 paralog, 57%.
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Best Local Similarity 70...
Try Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Q8EWD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
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Q8R126
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STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                 Query Match

69.2%; Score 36; DB 11; Length 471;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to glioma tumor suppressor candidate region gene
GLTSCR2 OR AW536411.
TISSUB-Liver.
Strausberg R.;
Stubmitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
MGD; MGI:2154441; Gltscr2.
MGD; MGI:2154441; Gltscr2.
MGD; MGI:2154441; Gltscr2.
MON TER
1 BRQUENCE 471 AA; 54506 MW; E0DA685C374A9760 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC01-637; ARH17637.1; -. MDD; MGI:2154441; Gltscr2.
GROTTRICE 484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
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mobile DNA in the evolution of vancomycin-resistant
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           Role of
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0889X7
AC 0889X AC 0889X AC 0889X AC 0889X AC 0889X AC 01-UC DT 0
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STRAIN=VSB3 / ARCC 700802;
MEDLINE=22550837; PubMed=12663927;
MEDLINE=22550837; PubMed=12663927;
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolomay J., Madupu R.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus
NCBL_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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QBBK35;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
$\frac{1}{2}\text{Tull 1} \text{Tull 1} \text{Tull 24} \text{Last annotation update} \text{Similar to glioma tumor suppressor CANDIDATE region gene 2}
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL, AKO89461. BAC40367.1; -.
MGD, MGI:215441. G1tscr2.
SEQUENCE 484 AA; 55806 MW; B3056425B5EECAD8 CRC64;
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01-JUN-2003 (TYEMBLrel. 24, Created)
01-JUN-2003 (TYEMBLrel. 24, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Pheromone binding protein, putative.
EF0063.
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239 EVIPAGASYN 248
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Q8BK35
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           SOOCOS SELECTION OF SELECTION O
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STRAIM-DC30000;

Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,

Buell R., Uterback T., Van Aken S., Feldblyum T., Gwinn M.,

Berry K., Uterback T., Van Aken S., Feldblyum T., Gwinn M.,

Berry K., Deboy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,

Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,

Mite O., Fraser C., Collner A.,

Ricmplete sequence of Pseudomonas syringae.";

Lubmitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AE016858; AA054162.1; -..

BREI, AE016858; AA054162.1; -..

BRICH, AE016858; AA054162.1; -..

BRICH, PSPTO0620, -..

BRICH, AE016858; AA054162.1; -..

BRICH, AE016858; AA05418.1; -..

BRICH, AE016858; AE016858; AE016858; AE016888; AE0168888; AE016888; AE016888; AE016888; AE016888; AE016
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DNA-directed RNA polymerase, beta subunit.
RPOC OR PSPTO0620.
Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.2%; Score 36; DB 16; Length 559; 66.7%; Pred. No. 62; ive 2; Mismatches 1; Indels
Enteroccus faecalis.";
Science 299.2071-2074(2003).
EMBL; ABC016947; AAO79943.1; -.
TIGR; EPRO653 -.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPRO00914; SPP bac.5.
InterPro; IPRO00914; SPP bac.5.
Fram; PF04465; SPP bac.5.
PFam; PF004065; SPP bac.5.
PROSITE; PS00013; PROKĀR_LIPOPROTEIN; 1.
Complete proteome.
SEQUENCE 559 AA; 61476 MW; CC15418D33D53DE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1399 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 LIPEGMSYS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||| |:||
581 QVVPAGLSY 589
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Indels

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Pred. No. 41; 2; Mismatches

60.08;

Best Local Similarity 60.0 Matches 6; Conservative

:||| |: || 179 QVVPVGLGYS 188

2 EVVPXGMSYS 11

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                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypochetical protein precursor.
Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
Iamiids; Solanales; Solanaceae; Solanum.
11 TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

C STAILN-1976; ITSSUE=Pistil;

MEDLINE=95375233; PubMed=7647301;

Milligan S.B., Gasser C.S.;

Milligan S.B., Gasser C.S.;

T "Nature and requiation of pistil-expressed genes in tomato.";

Plant Mol. Biol. 28:691-711(1995).

R EMBL; U20592; AAA80497.1; ---

R PIR; S57810; S57810.

R Of GO:0004866; F:endopptidase inhibitor activity; IEA.

R InterPro; IPR002160; Kunitz_legume.

R PRINTS; PR00291; Kunitz_legume; 1.

R PRINTS; PR00291; Kunitz_legume; 1.

R PRINTS; SM00482; SII; 1.

SMART; SM00452; SII; 1.
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Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Hess W.R., Lindell D. Post A.F., Regala W., Shah M.
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipid and glycerol acyltransferase (From 'motifs_6.msf').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria, Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.3%; Score 35; DB 10; Length 225; 54.5%; Pred. No. 37; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Score 35; DB 16; Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 474:1042-1047(2003).
EMBL, BX572098; CAE21267.1; -.
Acyltransferase, Transferase, Complete proteome.
SEQUENCE 245 AA; 26907 MW; 106F7C4CBE2C6427 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25188 MW; 1074C261D20CFDAD CRC64;
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UNKNOWN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMSYS 11
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32 DEVVPNGKTYA 42
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225 AA;
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Best Local Similarity
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77V6Q4
ESULT 13
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Query Match

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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998). BMEL; 281109; CAB03241.1; -. BMEL; ZA111, TA4111. WormPep; R10D12.10; CE12699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Score 35; DB 5; Length 425; 50.0%; Pred. No. 75; 2; Indels sive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005524; F.ATP binding; IEA.
GO; GO:0004672; F:protein Kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                    Percy C.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Transferase. SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
                                                                                                                  Last sequence update)
Last annotation update)
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Prodom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
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Job time: 29.8667 secs
                                                                                             Created)
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MEDLINE=99069613; PubMed=9851916;
                                                                                           01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                              PRELIMINARY;
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                                                                                                                                                                                             R10D12.10.
Caenorhabditis elegans
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                                                                                                                                                                   R10D12.10 protein.
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                                                 Q9XVK4
RESULT 15
Q9XVK4
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